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OM nucleic - nucleic search, using sw model

Run on: November 8, 2002, 08:53:09 : Search time 71.703 Seconds
(without alignments) 8725.170 Million cell updates/sec

Title: US-09-924-400-303

Perfect score: 2040

Sequence: 1 atgtgtgtgtgtgtgtgtgtc.....aaaaaaaaaaaaaaaaaaaaa 2040

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 15

Total number of hits satisfying chosen parameters: 11554

Minimum DB seq length: 0

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Database : Issued_Patents.NA.*

1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/6C.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/6D.COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2040	100.0	2040	US-09-605-785-375	Sequence 375, App
2	2040	100.0	2040	US-09-439-313-375	Sequence 375, App
3	2040	100.0	2040	US-09-352-616A-375	Sequence 375, App
4	1551	76.0	2000	US-09-605-785-374	Sequence 374, App
5	1551	76.0	2000	US-09-439-313-374	Sequence 374, App
6	1551	76.0	2000	US-09-352-616A-374	Sequence 374, App
7	1128	55.3	1155	US-09-605-785-373	Sequence 373, App
8	1128	55.3	1155	US-09-439-313-373	Sequence 373, App
9	1128	55.3	1155	US-09-352-616A-373	Sequence 373, App
10	491	24.1	1512	US-09-605-785-368	Sequence 368, App
11	491	24.1	1512	US-09-439-313-368	Sequence 368, App
12	491	24.1	1512	US-09-352-616A-368	Sequence 368, App
13	491	24.1	1512	US-09-605-785-367	Sequence 367, App
14	252	12.4	1853	US-09-605-785-366	Sequence 366, App
15	252	12.4	1853	US-09-439-313-366	Sequence 366, App
16	252	12.4	1853	US-09-352-616A-366	Sequence 366, App
17	252	12.4	1853	US-09-605-785-365	Sequence 365, App
18	120	5.9	879	US-09-605-785-364	Sequence 364, App
19	120	5.9	879	US-09-439-313-364	Sequence 364, App
20	120	5.9	879	US-09-352-616A-364	Sequence 364, App
21	120	5.9	1059	US-09-605-785-372	Sequence 372, App
22	120	5.9	1059	US-09-439-313-372	Sequence 372, App
23	120	5.9	1851	US-08-991-789A-291	Sequence 291, App
24	120	5.9	1851	US-09-605-785-366	Sequence 366, App
25	120	5.9	1851	US-09-439-313-366	Sequence 366, App
26	120	5.9	1851	US-09-605-785-366	Sequence 366, App
27	120	5.9	1851	US-09-062-451-291	Sequence 291, App

c	28	120	5.9	1851	4	US-09-352-616A-366	Sequence 366, App
	29	120	5.9	1852	4	US-09-605-785-530	Sequence 530, App
	30	120	5.9	1852	4	US-09-439-313-530	Sequence 530, App
	31	120	5.9	1853	4	US-09-605-785-371	Sequence 371, App
	32	120	5.9	1853	4	US-09-439-313-371	Sequence 371, App
	33	120	5.9	1855	4	US-09-062-451-297	Sequence 297, App
	34	120	5.9	1855	4	US-09-352-616A-371	Sequence 371, App
	35	120	5.9	2184	4	US-09-605-785-370	Sequence 370, App
	36	120	5.9	2184	4	US-09-439-313-370	Sequence 370, App
	37	120	5.9	2184	4	US-09-062-451-296	Sequence 296, App
	38	120	5.9	2184	4	US-09-352-616A-370	Sequence 370, App
c	39	118	5.8	668	4	US-09-605-785-367	Sequence 367, App
c	40	118	5.8	668	4	US-09-439-313-367	Sequence 367, App
c	41	118	5.8	668	4	US-09-062-451-293	Sequence 293, App
c	42	118	5.8	668	4	US-09-352-616A-367	Sequence 367, App
c	43	109	5.3	454	4	US-08-991-789A-211	Sequence 211, App
c	44	109	5.3	454	4	US-09-062-451-211	Sequence 211, App
c	45	109	5.3	454	4	US-09-598-326-211	Sequence 211, App

ALIGNMENTS

RESULT 1
US-09-605-785-375
Sequence 375, Application US/09605785
Patent No. 6321716
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuguang
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darriick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-605-785-375
Query Match 100.0%; Score 2040; DB 4; Length 2040;
Best local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

121 AGCAAGTGGGACCTTCTGTGAGACGACGACGACTGTGTAAGACACTACGAGCAAG 180
121 AGCAAGTGGGACCTTCTGTGAGACGACGACGACTGTGTAAGACACTACGAGCAAG 180

; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-375

Query Match 100.0%; Score 2040; DB 4; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGGGGTTGAGTGGATTCATGCCGGCTGCTTCTGTGAAGAGCATTTGGTCTC 60
OY 61 AGGAGCAAGATGGGCAAGTGTGTGCGGTTGCTTCCCTGCTGAGAGGACGGCAAG 120
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DB 1441 AAACAGATGCCAAATATCTCTGAAAAACAGCAACCCAGAAACAGACTTAAAGCTG 1500
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DB 1501 TCAGAGAGAGTACCAAAAGGCTTGAAGGCACTGAAATGCGCAGCAAGAAAGATCT 1560
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Db 1981 GAGCTAGACAAATGAAACATCAGAGCCAGCTAAAAA 2040
RESULT 3
US-09-352-616A-375
Sequence 375, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yugu
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352, 616A
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-352-616A-375
Query Match 100.0%; Score 2040; DB 4; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 301 TGTGCTGCGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGTGGGCGCTTG 360
Db 301 TGTGCTGCGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGTGGGCGCTTG 360
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Db 361 GGAAGCTACAGATGAGTGCCTTCATGAGCCAGGTAACAGTCCCTGAGAGAGATCTG 420
QY 421 GAGAAGCTCCACAGAGTGTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATGCTATG 480
Db 421 GAGAAGCTCCACAGAGTGTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATGCTATG 480
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Db 1021 GCCAGAGATATGCTGTTCTAGTCATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
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QY 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAGGCGCTGAATAATGCGCCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAGGCGCTGAATAATGCGCCAGAGAAA 1200
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Db 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
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Db 1261 AAGCATGAAGATTAATTAATGTTGAGATTAATTAAGAAACCTGACTAATGCTGCTG 1320
QY 1321 AATGTGATTAATGATTAATTCCTCAAGAGAGAGCAAGCACTGGAATTCAGCAATTT 1380
Db 1321 AATGTGATTAATGATTAATTCCTCAAGAGAGAGCAAGCACTGGAATTCAGCAATTT 1380
QY 1381 CTTGACAAAGAAAGTGAAGATATCACAGAAATTTGCAATTAATTTCTGACTCAAGAA 1440
Db 1381 CTTGACAAAGAAAGTGAAGATATCACAGAAATTTGCAATTAATTTCTGACTCAAGAA 1440
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QY 1501 TCAGAGGAAGATGACAAAGGCTTGAGGCGAGTGAATAATGGCCAGCAGAGAAAGATCT 1560
Db 1501 TCAGAGGAAGATGACAAAGGCTTGAGGCGAGTGAATAATGGCCAGCAGAGAAAGATCT 1560
QY 1561 CAAGAACAGAAATTAATTAAGATGATGATGAGAGAGCTAAGAAATTTATGCGTATCGAA 1620
Db 1561 CAAGAACAGAAATTAATTAAGATGATGATGAGAGAGCTAAGAAATTTATGCGTATCGAA 1620
QY 1621 GAATGAAGAGAGAGAGAGTACTCATGTCGATTCCTCAAGAAACCTGACTAATGTCG 1680
Db 1621 GAATGAAGAGAGAGAGAGTACTCATGTCGATTCCTCAAGAAACCTGACTAATGTCG 1680
QY 1681 ACTGCTGCAATGATGATGATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAG 1740
Db 1681 ACTGCTGCAATGATGATGATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAG 1740

QY 1741 CAGCAATTTCTGACACTGAGATGAGATATCAGAGTACAGCAAAATGATCTCG 1800
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DB 1801 AAGCAATTTTGTGAAGAACAGAACTGGATATTTACAGATGAGATTTCTGATTCAGAA 1860
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QY 1981 GAGCTAGACACAAATGAAATCATCAGAGCCAGCTAAAAA 2040
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DB 1981 GAGCTAGACACAAATGAAATCATCAGAGCCAGCTAAAAA 2040

RESULT 4

US-09-605-785-374
Sequence 374, Application US/09605785
Patent No. 6321716

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Reiter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C16
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-605-785-374

Query Match 76.0%; Score 1551; DB 4; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTTGAGTGGATTCATGCGGCTGCTTCTGTAAGCAAGCATTTGCTTC 60
|||
DB 1 ATGTGTTGAGTGGATTCATGCGGCTGCTTCTTGTGAAGCAAGCATTTGCTTC 60
QY 61 AGGACCAAGATGGGCAAGTGTGTGCGTTGCTTCCCTGCTGAGGAGCGGCAAG 120
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DB 61 AGGACCAAGATGGGCAAGTGTGTGCGTTGCTTCCCTGCTGAGGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGACACAGCACTGCTATGAAGACTCAGAGCAAG 180
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QY 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAACGTG 240
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QY 361 GGAGACTACAGATGACAGTCTTCAATGAGCCAGGATCCAGTCCGTGAGAAATCTG 420
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DB 361 GGAGACTACAGATGACAGTCTTCAATGAGCCAGGATCCAGTCCGTGAGAAATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGTTGGGGTAAAGTCCCAAGAAAGATCTCATG 480
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DB 421 GACAAGCTCCACAGAGCTGCTGTTGGGGTAAAGTCCCAAGAAAGATCTCATG 480
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DB 541 TCTGCCAATGGGAATTCAGAAATGATGAAACTCTGCTGGAGAGAGATGCACTTAAT 600
QY 601 GTCTTGGACAAACAAAAGAGAGAGAGCTGATAAAGCCGTCAATGCCAGAAATGAA 660
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DB 601 GTCTTGGACAAACAAAAGAGAGAGAGCTGATAAAGCCGTCAATGCCAGAAATGAA 660
QY 661 TGTGCTTATGTTGTGCGAACAATGCGACTGATCCAAATTTCCAGATAGTGAAT 720
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DB 661 TGTGCTTATGTTGTGCGAACAATGCGACTGATCCAAATTTCCAGATAGTGAAT 720
QY 721 ACCACTGCTACAGCTATCTATGTAAGAAATTAATGAGCCAAAGCACTGCTTA 780
|||
DB 721 ACCACTGCTACAGCTATCTATGTAAGAAATTAATGAGCCAAAGCACTGCTTA 780
QY 781 TATGTTGCTGATATGAAATCAAAAAAACAAGATGGCTCACACACTGTTACTGGTGA 840
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DB 781 TATGTTGCTGATATGAAATCAAAAAAACAAGATGGCTCACACACTGTTACTGGTGA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAATCAAGAAAAAAGCAATTTAAATGA 900
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DB 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAATCAAGAAAAAAGCAATTTAAATGA 900
QY 901 CTGATATGATGAGAGAGCTGCTCATACTGCTGATGTTGATGATCAGCAAGTATA 960
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DB 901 CTGATATGATGAGAGAGCTGCTCATACTGCTGATGTTGATGATCAGCAAGTATA 960
QY 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAGAG 1020
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DB 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTATCATCTATGATTTGGCAGTTACTTTCTGACTAC 1080
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DB 1021 GCCAGAGATATGCTGTTTCTAGTATCATCTATGATTTGGCAGTTACTTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAAAATCTTCTGAAAACAGCAATCCAGAACAGCTTAAG 1140
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QY 1141 CTGACATCAGAGAGAGTACAAAAGTTCAAAAGCGTGAATAATGCCAGCAGAGAAA 1200
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DB 1141 CTGACATCAGAGAGAGTACAAAAGTTCAAAAGCGTGAATAATGCCAGCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACCAAAATTAATGAAGTGTGATAGAGAGTGAAGAAATGAAG 1260
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DB 1201 ATGTCTCAAGAACCAAAATTAATGAAGTGTGATAGAGAGTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTAATATGTGGATTTACTAAGAAACCTCAATATGTCTCACTGCTGC 1320

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Db 1261 AAGCATGAAGTAATATGATGGGATTACTAGAAACCTGACTAATGGTCACTGGCGC 1320
QY 1321 AATGATGATTAAGTAAATTCCTCAAGAGAGAGAGACACCTGAAATTCAGCAATTT 1380
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QY 1381 CCTGACAGCAAGAGAGAGATATCACAGAAATTTGGCAATTTCTGACTACAAAGAA 1440
Db 1381 CCTGACAGCAAGAGAGATATCACAGAAATTTGGCAATTTCTGACTACAAAGAA 1440
QY 1441 AAGCAATGCGCAAAATACTCTTGTGAAAACAGCAACCCAGACAGACTTAAAGCTGACA 1500
Db 1441 AAGCAATGCGCAAAATACTCTTGTGAAAACAGCAACCCAGACAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGGAAGATCACAAAGGCTTGAAGGCGATGAAATGGCCAGCCAGAG 1551
Db 1501 TCAGAGGAAGATCACAAAGGCTTGAAGGCGATGAAATGGCCAGCCAGAG 1551

RESULT 5
US-09-439-313-374
; Sequence 374 Application US/09439313
; Patent No. 6329305
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-374

Query Match 76.0%; Score 1551; DB 4; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTGGAGGTGATTCATGCGGGCTGCTCTTGTGTAAGAAGCCATTTGGTCTC 60
Db 1 ATGGTGGTGGAGGTGATTCATGCGGGCTGCTCTTGTGTAAGAAGCCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCCCTTCCCTGGCTGCGAGGGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGTGCTGCCCTTCCCTGGCTGCGAGGGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACACAGAGACTTGTCTGAAGACACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACACAGAGACTTGTCTGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
QY 241 GGGGCTTCTGGAGACGACGACTCTGCTATGAAGACACTCAGGAACAAGATGGGCAAG 300
Db 241 GGGGCTTCTGGAGACGACGACTCTGCTATGAAGACACTCAGGAACAAGATGGGCAAG 300

QY 301 TGGTGTCCACACTGCTTCCCTGCTGAGGGGAGGCGGCAAGAGCAAGGTGGCGCTTGG 360
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Db 661 TGTGCGTTAATGTTGCTGGAACATGGCAGTATCAATATTCAGATGATGAAAT 720
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Db 721 ACCACTGTGCACTACGTTATCTATTAAGAGATTAATTAATGGCCAAAGACAGCTCTTA 780
QY 781 TATGTCCTGATATGCAATCAAAAAACAAAGCATGCGCTCACACACTGTACTTGGTGA 840
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Db 1201 ATGCTTCAGAACACAGAAATTAATTAAGAGTGTGATGAGAGGTTGAAGAAATGAAG 1260
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Db 1261 AAGCATGAAAGTAAATATGTTGGATTAATCTGAAGAAACCTGACTATGTGTGCTGGC 1320
QY 1321 AATGATGATTAAGTAAATTTCTCAAGAGAGAGAGACACCTGAAATTCAGCAATTT 1380
Db 1321 AATGATGATTAAGTAAATTTCTCAAGAGAGAGAGACACCTGAAATTCAGCAATTT 1380
QY 1381 CCTGACAAAGAGAGATATCAAGAAATTTGGCAATTTCTGACTACAAAGAA 1440

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Db 1381 CCTGACAAGAAAGTGAAGATATCAGCAATTTGGGAATTTAGTTCTGACATCAAGAA 1440
Oy 1441 AAGAGATGCCAAATACCTCTCTGAAACAGACACCCGAAACAGACTTTAAAGCTGACA 1500
Db 1441 AAGAGATGCCAAATACCTCTCTGAAACAGACACCCGAAACAGACTTTAAAGCTGACA 1500
Oy 1501 TCAGAGGAAGAGTCAACAAGGCTTGAGGGCAGTGAATAATGGCAGCCAGAG 1551
Db 1501 TCAGAGGAAGAGTCAACAAGGCTTGAGGGCAGTGAATAATGGCAGCCAGAG 1551

RESULT 6
US-09-352-616A-374
; Sequence 374, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jlang, Yuguil
; APPLICANT: Xu, Jlangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352, 616A
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-374

Query Match 76.0%; Score 1551; DB 4; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAGGTGTTGAGGTGATTCATGCCGGCTGCTCTTCTGTGAAGAACCATTTGGTCTC 60
Db 1 AAGGTGTTGAGGTGATTCATGCCGGCTGCTCTTCTGTGAAGAACCATTTGGTCTC 60
Oy 61 AAGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGGAGCGGCAAG 120
Db 61 AAGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGGAGCGGCAAG 120
Oy 121 ACGAAGTGGGCACTTCTGAGACCAAGACGACTCTGTATGAAGCACTCAGAGCAAG 180
Db 121 ACGAAGTGGGCACTTCTGAGACCAAGACGACTCTGTATGAAGCACTCAGAGCAAG 180
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Db 601 GTCCCTTGACAAACAAAAGAGAGACAGCTGTATGAAGGCGGTACAAATGCCAGAAATGAA 660
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Db 661 TGTGCGTTAATGTTGCTGGAACATGGCAGCTGATCAAAATATTCAGATGATGGAAT 720
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Oy 781 TATGCTGTGATATCAATCAAAAAACAAGCATGGCTCACACACTGTTACTTGGTGA 840
Db 781 TATGCTGTGATATCAATCAAAAAACAAGCATGGCTCACACACTGTTACTTGGTGA 840
Oy 841 CATGACCAAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGACCAAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Oy 901 CTGGATAGATATGGAAGAGCTGCTCATATCTGCTGATGTTGTGATCAGCAATTA 960
Db 901 CTGGATAGATATGGAAGAGCTGCTCATATCTGCTGATGTTGTGATCAGCAATTA 960
Oy 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATGATATCTGAGACAG 1020
Db 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATGATATCTGAGACAG 1020
Oy 1021 GCCAGAGATATGCTGTTCTAGTCATCATATGATTAATTTCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTCTAGTCATCATATGATTAATTTCCAGTTACTTCTGACTAC 1080
Oy 1081 AAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATTCACAAACAGCTTAAAG 1140
Db 1081 AAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATTCACAAACAGCTTAAAG 1140
Oy 1141 CTGACATCAGAGGAAGTACCAAAAGTTCAAAAGCAGTGAATAATGCCAGCAGAGAAA 1200
Db 1141 CTGACATCAGAGGAAGTACCAAAAGTTCAAAAGCAGTGAATAATGCCAGCAGAGAAA 1200
Oy 1201 ATGTCTCAAGAACCAAGAAATTAATGAAGTGTGATGAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAGAAATTAATGAAGTGTGATGAGAGGTTGAAGAAATGAAG 1260
Oy 1261 AAGCATGAAAGTAATTAATGGGATTAATGAAGAAACCTGATGATGATGATGATGATG 1320
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Oy 1321 AATGTGATTAATGATTAATCTCAAAAGGAAGAGCAAGCAACCTGAAATTCAGCAATTT 1380
Db 1321 AATGTGATTAATGATTAATCTCAAAAGGAAGAGCAAGCAACCTGAAATTCAGCAATTT 1380
Oy 1381 CTTGACAAAGAAAGTAAAGATATCAAGAAATTTGGAATTAATTTCTGACTCAAAAGAA 1440
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Oy 1441 AAGCAATGCAAAATATCTTCTGAAAAACAGCAACCCAGAAACCACTTAAAGCTGACA 1500
Db 1441 AAGCAATGCAAAATATCTTCTGAAAAACAGCAACCCAGAAACCACTTAAAGCTGACA 1500
Oy 1501 TCAGAGGAAGAGTCAACAAGGCTTGAGGGCAGTGAATAATGGCAGCCAGAG 1551
Db 1501 TCAGAGGAAGAGTCAACAAGGCTTGAGGGCAGTGAATAATGGCAGCCAGAG 1551

RESULT 7
US-09-605-785-373


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; Sequence 373, Application US/09605785
; Patent No. 632176
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jlang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedavick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-605-785-373
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Query Match          55.3%; Score 1128; DB 4; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ATGGTGGTTGAGTTGATTCATCCGCGCTGCTCTTCTGTGAAGAGCCATTGGTCTC 60
DB 1 ATGGTGGTTGAGTTGATTCATCCGCGCTGCTCTTCTGTGAAGAGCCATTGGTCTC 60
QY 61 AGAGCAAGATGGGCAAGTGTGCTGCTCCCTGCTGCTGAGGAGCGGCAAG 120
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QY 361 GGAGACTACGATGACAGTGGCTTTCATGAGGCCAGGTACACGTCGCTGAGAGATCTG 420
DB 361 GGAGACTACGATGACAGTGGCTTTCATGAGGCCAGGTACACGTCGCTGAGAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGCTGGGAGTAAAGTCCCAAGAAAGATTCATGTCATG 480
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QY 481 CTCAGGGACACTGACGTGAACAAAGAGCAAGCAAGAAAGAGATGCTCTACATCTGGCC 540
DB 481 CTCAGGGACACTGACGTGAACAAAGAGCAAGCAAGAAAGAGATGCTCTACATCTGGCC 540
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QY 541 TCTGCCAATGGGAATTCAGAAGTAGTAATACTCTGCTGAGACAGATGTCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAGTAGTAATACTCTGCTGAGACAGATGTCAACTTAAT 600
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DB 661 TGTGCGTTAATGTTGCTGGAACATGGCAGCTGATCCAAATATATCCAGATGATGAAAT 720
QY 721 ACCACTGTGACACTACGCTATCTATATGAAGATAAATTAATGACCAAGCACTGCTTA 780
DB 721 ACCACTGTGACACTACGCTATCTATATGAAGATAAATTAATGACCAAGCACTGCTTA 780
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DB 901 CTGATAGATATGGAAGCACTGCTCATACCTGCTGATGTTGATGCAAGATATA 960
QY 961 GTGAGCTTCTACTTGAAGCAAAATATGATATCTTCTCAAGATCTATCTGAGACAG 1020
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QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAAATTTCCAGTTACTTTCGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAAATTTCCAGTTACTTTCGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAA 1128
DB 1081 AAAGAAAAACAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCAGAA 1128
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RESULT 8
US-09-439-313-373
; Sequence 373, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jlang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Stolk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-439-313-373
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Query Match          55.3%; Score 1128; DB 4; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 ATGTGTGATGATGATTCATGCCGGCTGCTTCTGTGAAGAAGCCATTTGGTTC 60
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OY 61 AGGACCAAGATGGGCAAGTGTGTCCGCTTCCCTGCTGCAGGAGAGCGGCAAG 120
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Db 841 CATGAGCAAAAACAGCAATGCTGAATTTTATCAAAAAAGCGAATTTAAATGCA 900
OY 901 CTGAGATAGATGAAGAGCTGCTCATACTGTGTATGTTGTTGAGATCAGCAATTA 960
    |||||||
Db 901 CTGAGATAGATGAAGAGCTGCTCATACTGTGTATGTTGTTGAGATCAGCAATTA 960
OY 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAG 1020
    |||||||
Db 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAG 1020
OY 1021 GCGAGAGATATGCTGTTCTAGTCAATCATGTAATTTGCCAGTTACTTTGACTAC 1080
    |||||||
Db 1021 GCGAGAGATATGCTGTTCTAGTCAATCATGTAATTTGCCAGTTACTTTGACTAC 1080
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OY 1081 AAAGAAAAACAGATGCTAAATAATCTCTGAAACAGCAATCCAGAA 1128
    |||||||
Db 1081 AAAGAAAAACAGATGCTAAATAATCTCTGAAACAGCAATCCAGAA 1128

RESULT 9
US-09-352-616A-373
; Sequence 373, Application US/09352616A
; Patent No. 6195278
; GENERAL INFORMATION:
; APPLICANT: Dillon, David C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuxi
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352, 616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-373
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Query Match 55.3%; Score 1128; DB 4; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1 ATGTGTGATGATGATTCATGCCGGCTGCTTCTGTGAAGAAGCCATTTGGTTC 60
    |||||||
Db 1 ATGTGTGATGATGATTCATGCCGGCTGCTTCTGTGAAGAAGCCATTTGGTTC 60
OY 61 AGGACCAAGATGGGCAAGTGTGTCCGCTTCCCTGCTGCAGGAGAGCGGCAAG 120
    |||||||
Db 61 AGGACCAAGATGGGCAAGTGTGTCCGCTTCCCTGCTGCAGGAGAGCGGCAAG 120
OY 121 AGCAACGTGGGCACTTCTGGAGACCAAGCACTGCTGTATGAAGACACTCAGAGCAAG 180
    |||||||
Db 121 AGCAACGTGGGCACTTCTGGAGACCAAGCACTGCTGTATGAAGACACTCAGAGCAAG 180
OY 181 ATGGCAAGTGTGGCGCCACTGCTTCCCTGCTGCAGGAGGAGTGGCAAGCAAGT 240
    |||||||
Db 181 ATGGCAAGTGTGGCGCCACTGCTTCCCTGCTGCAGGAGGAGTGGCAAGCAAGT 240
OY 241 GCGGCTTCTGAGACCAAGCACTGCTGTATGAAGTAAATTAATGAGCCAAAGCACTGCTTA 780
    |||||||
Db 241 GCGGCTTCTGAGACCAAGCACTGCTGTATGAAGTAAATTAATGAGCCAAAGCACTGCTTA 780
OY 301 TGTGCTGCTGCTGCTTCCCTGCTGCAGGAGGAGCGGCAAGCAAGTGGGCTTGG 360
    |||||||
Db 301 TGTGCTGCTGCTGCTTCCCTGCTGCAGGAGGAGCGGCAAGCAAGTGGGCTTGG 360
OY 361 GGAGACTAGATGACAGTGTCTTCAATGAGCCAGGTACAGTCCGTGGAGAGATCTG 420
    |||||||
Db 361 GGAGACTAGATGACAGTGTCTTCAATGAGCCAGGTACAGTCCGTGGAGAGATCTG 420
OY 421 GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAGATCTCATGCTATG 480
    |||||||
Db 421 GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAGATCTCATGCTATG 480
OY 481 CTCAGGAGACACTGAGCTGAACAAGAGCAAAAGAGACTGCTTACATCTGGCC 540
    |||||||
Db 481 CTCAGGAGACACTGAGCTGAACAAGAGCAAAAGAGACTGCTTACATCTGGCC 540
OY 541 TGTGCCAATGGGAATTCAGAAATGTAATTAATCTGCTGAGACAGATGTCACTTAAT 600
    |||||||
Db 541 TGTGCCAATGGGAATTCAGAAATGTAATTAATCTGCTGAGACAGATGTCACTTAAT 600
OY 601 GTCTTTGACAAACAAAAGAGACAGCTGTATAAAGCCGTACAAATGCCAGAAATGAA 660
    |||||||
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|||||
Db 601 GTCTTACAAACAAAAGAGACAGCTCTGTAAAGCCCGTACATGCCAGAGATGAA 660
Qy 661 TGTGCGTAAATGTGCGAAGACGACGATGCCAAATATCCAGATGATGAAAT 720
Db 661 TGTGCGTAAATGTGCGAAGACGACGATGCCAAATATCCAGATGATGAAAT 720
Qy 721 ACCACTGTGACACTACGCTATCTATATGAATGAATTAATGAGCAAGCACTGCTTA 780
Db 721 ACCACTGTGACACTACGCTATCTATATGAATGAATTAATGAGCAAGCACTGCTTA 780
Qy 781 TATGTCCTGATATGATCAATCAAAAACAGAGAGCCCTCACACACGTTACTTGCTTA 840
Db 781 TATGTCCTGATATGATCAATCAAAAACAGAGAGCCCTCACACACGTTACTTGCTTA 840
Qy 841 CATGAGCAAAAACAGAGAGCGTGAATTTTATCAAGAAAAAGGAATTTAAATGCA 900
Db 841 CATGAGCAAAAACAGAGAGCGTGAATTTTATCAAGAAAAAGGAATTTAAATGCA 900
Qy 901 CTGATGATATGAGAGAGCTGCTCTCATCTTCTGATGTTGATGATCAGCAAGTATA 960
Db 901 CTGATGATATGAGAGAGCTGCTCTCATCTTCTGATGTTGATGATCAGCAAGTATA 960
Qy 961 GTGAGCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
Db 961 GTGAGCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
Qy 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATCATGTAATTTCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATCATGTAATTTCCAGTTACTTCTGACTAC 1080
Qy 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGAAAAACAGCAATCCAGAA 1128
Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGAAAAACAGCAATCCAGAA 1128

```

RESULT 10

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; Sequence 368, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqul
; APPLICANT: Henderson, Robert A.
; APPLICANT: Katos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 368
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-605-785-368

```

Query Match 24.1%; Score 491; DB 4; Length 1512;
Best Local Similarity 99.4%; Pred. No. 8.9e-198;

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Matches 691: Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 34 TCTTCTGTAAGAACCATTTGTCTCAGAGCAAGATGGCAAGTGTGCTGCCGTTGC 93
Db 256 TCTTCTGTAAGAACCATTTGTCTCAGAGCAAGATGGCAAGTGTGCTGCCGTTGC 315
Qy 94 TTCCCTGCTCTCAGAGAGAGCGGCAAGACAGCAAGCTGGGCACTTCTGAGACCAAGCAGAC 153
Db 316 TTCCCTGCTCTCAGAGAGAGCGGCAAGACAGCAAGCTGGGCACTTCTGAGACCAAGCAGAC 375
Qy 154 TCTGCTATGAAGACACTCAGAGAGCAAGATGGGCAAGTGTGCTGCCGTTGCCGTTGC 213
Db 376 TCTGCTATGAAGACACTCAGAGAGCAAGATGGGCAAGTGTGCTGCCGTTGCCGTTGC 435
Qy 214 TGCAGGGGAGATGGCAAGAGCAAGCTGGGCAAGTGTGCTGAGACCAAGCAAGCTGCTATG 273
Db 436 TGCAGGGGAGATGGCAAGAGCAAGCTGGGCAAGTGTGCTGAGACCAAGCAAGCTGCTATG 495
Qy 274 AAGACACTCAGAGAACAGATGGGCAAGTGTGCTGAGACCAAGCTGCTGCTGAGAGGGG 333
Db 496 AAGACACTCAGAGAACAGATGGGCAAGTGTGCTGAGACCAAGCTGCTGCTGAGAGGGG 555
Qy 334 AGCGCAAGACAGAGTGGGGGCTTGGGAGACATACATGACATGACATGCTTATGAGAGCC 393
Db 556 AGCGCAAGACAGAGTGGGGGCTTGGGAGACATACATGACATGACATGCTTATGAGAGCC 615
Qy 394 AGGTACACAGCTGCTGAGAGATCTGGACAACTCCACAGAGCTGCTGAGAGGGTAA 453
Db 616 AGGTACACAGCTGCTGAGAGATCTGGACAACTCCACAGAGCTGCTGAGAGGGTAA 675
Qy 454 GTCCCCAGAAAGATCTCATCTGTCATGCTCAGGACACTGACGTAACAGAGAGCAAG 513
Db 676 GTCCCCAGAAAGATCTCATCTGTCATGCTCAGGACACTGACGTAACAGAGAGCAAG 735
Qy 514 CAAAAGAGATGCTCATCATCTGCGCTGCGCAATGGGAATTCAGAAATGTAATAACTC 573
Db 736 CAAAAGAGATGCTCATCATCTGCGCTGCGCAATGGGAATTCAGAAATGTAATAACTC 795
Qy 574 CTGCTGACAGACAGATGTCATTAATGCTCTTGACAAACAAAAGAGACAGCTGTGATA 633
Db 796 STGCTGACAGACAGATGTCATTAATGCTCTTGACAAACAAAAGAGACAGCTGTGATA 855
Qy 634 AAGCCCTGACAAATGCCAGAGAGATGTCGTTAATGTTGCTGGAACATGCACTGAT 693
Db 856 AAGCCCTGACAAATGCCAGAGAGATGTCGTTAATGTTGCTGGAACATGCACTGAT 915
Qy 694 CCAATATTCAGATGATGATGAATATACACTCT 728
Db 916 CCAATATTCAGATGATGATGAATATACACTCT 950

```

RESULT 11

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; Sequence 368, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqul
; APPLICANT: Reed, Steven G.
; APPLICANT: Katos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solik, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575

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SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 368
LENGTH: 1512
TYPE: DNA
ORGANISM: Homo sapien
US-09-439-313-368

Query Match 24.1%; Score 491; DB 4; Length 1512;
Best Local Similarity 99.4%; Pred. No. 8.9e-199;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 34 TCTTCTGTAAGAACCCATTGGTCTCAGAGACAGATGGGCAATGGTGTGCGTTGC 93
DB 256 TCTTCTGTAAGAACCCATTGGTCTCAGAGACAGATGGGCAATGGTGTGCGTTGC 315
QY 94 TTCCCTCTCTGAGGAGAGCGGCGCAAGACAGCTGGGCACTTCTGAGACCAAGCAGCAGC 153
DB 316 TTCCCTCTCTGAGGAGAGCGGCGCAAGACAGCTGGGCACTTCTGAGACCAAGCAGCAGC 375
QY 154 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGCGGCACTGCTTCCCTGCG 213
DB 376 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGCGGCACTGCTTCCCTGCG 435
QY 214 TGCAGGGGAGTGGCAGAGACAGCTGGGCGCTTCTGAGACCAAGCAGACTGCTATG 273
DB 436 TGCAGGGGAGTGGCAGAGACAGCTGGGCGCTTCTGAGACCAAGCAGACTGCTATG 495
QY 274 AAGACACTCAGAGACACATGGGCAAGTGGTGTCTCCACTGCTTCCCTGCTGCAAGGGG 333
DB 496 AAGACACTCAGAGACACATGGGCAAGTGGTGTCTCCACTGCTTCCCTGCTGCAAGGGG 555
QY 334 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTGACATGACAGTCCCTTCAATGGAGCC 393
DB 556 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTGACATGACAGTCCCTTCAATGGAGCC 615
QY 394 AGTACACAGCTCCGTGGAAGATCTGACAACTCCAGAGCTGCGCTGTTGGGTTAA 453
DB 616 AGTACACAGCTCCGTGGAAGATCTGACAACTCCAGAGCTGCGCTGTTGGGTTAA 675
QY 454 GTCCCAAGAAAGATCTATGCTCATGCTCAGGACACTGACGTACACAGAGAGCAAG 513
DB 676 GTCCCAAGAAAGATCTATGCTCATGCTCAGGACACTGACGTACACAGAGAGCAAG 735
QY 514 CAAAAGAGAGCTCTCATCTGTGCGCTGTGCAATGGGAATTCGAAGTATAAATC 573
DB 736 CAAAAGAGAGCTCTCATCTGTGCGCTGTGCAATGGGAATTCGAAGTATAAATC 795
QY 574 CTGCTGACAGACGATGTCAACTTATGTCTTGCACAAACAAAGAGACAGCTGTGATA 633
DB 796 STGCTGACAGACGATGTCAACTTATGTCTTGCACAAACAAAGAGACAGCTGTGATA 855
QY 634 AAGCCGCTACAAATGCCAGAGAGATGTGCGTTAATGTGCTGGAACATGGCACTGAT 693
DB 856 AAGCCGCTACAAATGCCAGAGAGATGTGCGTTAATGTGCTGGAACATGGCACTGAT 915
QY 694 CCAATATTCAGATGATGGAATACCACTCT 728
DB 916 CCAATATTCAGATGATGGAATACCACTCT 950

RESULT 12

US-09-062-451-294

Sequence 294, Application US/09062451

Patent No. 6344550

GENERAL INFORMATION:

APPLICANT: Fridakis, Tony N.

APPLICANT: Smith, John M.

APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

NUMBER OF SEQUENCES: 297 TREATMENT AND DIAGNOSIS OF BREAST CANCER

CORRESPONDENCE ADDRESS:

ADDRESS: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,451
FILING DATE: 04-APR-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mark, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.419C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 294:
SEQUENCE CHARACTERISTICS:
LENGTH: 1512 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-062-451-294

Query Match 24.1%; Score 491; DB 4; Length 1512;
Best Local Similarity 99.4%; Pred. No. 8.9e-199;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 34 TCTTCTGTAAGAACCCATTGGTCTCAGAGACAGATGGGCAAGTGGTGTGCGTTGC 93
DB 256 TCTTCTGTAAGAACCCATTGGTCTCAGAGACAGATGGGCAAGTGGTGTGCGTTGC 315
QY 94 TTCCCTCTCTGAGGAGAGCGGCGCAAGACAGCTGGGCACTTCTGAGACCAAGCAGCAGC 153
DB 316 TTCCCTCTCTGAGGAGAGCGGCGCAAGACAGCTGGGCACTTCTGAGACCAAGCAGCAGC 375
QY 154 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGGCACTGCTTCCCTGCG 213
DB 376 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGGCACTGCTTCCCTGCG 435
QY 214 TGCAGGGGAGTGGCAGAGACAGCTGGGCGCTTCTGAGACCAAGCAGACTGCTATG 273
DB 436 TGCAGGGGAGTGGCAGAGACAGCTGGGCGCTTCTGAGACCAAGCAGACTGCTATG 495
QY 274 AAGACACTCAGAGACACATGGGCAAGTGGTGTCTCCACTGCTTCCCTGCTGCAAGGGG 333
DB 496 AAGACACTCAGAGACACATGGGCAAGTGGTGTCTCCACTGCTTCCCTGCTGCAAGGGG 555
QY 334 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTGACATGACAGTCCCTTCAATGGAGCC 393
DB 556 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTGACATGACAGTCCCTTCAATGGAGCC 615
QY 394 AGTACACAGCTCCGTGGAAGATCTGACAACTCCAGAGCTGCGCTGTTGGGTTAA 453
DB 616 AGTACACAGCTCCGTGGAAGATCTGACAACTCCAGAGCTGCGCTGTTGGGTTAA 675
QY 454 GTCCCAAGAAAGATCTATGCTCATGCTCAGGACACTGACGTACACAGAGAGCAAG 513
DB 676 GTCCCAAGAAAGATCTATGCTCATGCTCAGGACACTGACGTACACAGAGAGCAAG 735
QY 514 CAAAAGAGAGCTCTCATCTGTGCGCTGTGCAATGGGAATTCGAAGTATAAATC 573
DB 736 CAAAAGAGAGCTCTCATCTGTGCGCTGTGCAATGGGAATTCGAAGTATAAATC 795
QY 574 CTGCTGACAGACGATGTCAACTTATGTCTTGCACAAACAAAGAGACAGCTGTGATA 633
DB 796 STGCTGACAGACGATGTCAACTTATGTCTTGCACAAACAAAGAGACAGCTGTGATA 855

Db 556 AGC 558

RESULT 15
US-09-439-313-369
; Sequence 369, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqul
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 369
; LENGTH: 1853
; TYPE: DNA
; ORGANISM: Homo sapien.
US-09-439-313-369

Query Match 12.4%; Score 252; DB 4; Length 1853;
Best Local Similarity 99.7%; Pred. No. 3.6e-97;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAAGCCATTGGTCTCAGAGCAAGATGGGCAAGTGTGCTGCCGTTGC 93
DB 256 TCTTCTGTGAAGAAGCCATTGGTCTCAGAGCAAGATGGGCAAGTGTGCTGCCGTTGC 315
QY 94 TTCCCTGCTGCAGGAGAGCGGCAAGACAGCAAGTGGGCACTTCTGGAGACCAAGACGAC 153
DB 316 TTCCCTGCTGCAGGAGAGCGGCAAGACAGCAAGTGGGCACTTCTGGAGACCAAGACGAC 375
QY 154 TGTGATGAAGACACTCTGAGAGCAAGATGGGCAAGTGGGCACTTCTGGAGACCAAGACGAC 213
DB 376 TGTGATGAAGACACTCTGAGAGCAAGATGGGCAAGTGGGCACTTCTGGAGACCAAGACGAC 435
QY 214 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGAGCAAGACGACGACTCTGCTATG 273
DB 436 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGAGCAAGACGACGACTCTGCTATG 495
QY 274 AAGACACTCAGGAACAAGATGGGCAAGTGGGCGCTTCTGAGAGCAAGACGACTCTGCTATG 333
DB 496 AAGACACTCAGGAACAAGATGGGCAAGTGGGCGCTTCTGAGAGCAAGACGACTCTGCTATG 555
QY 334 AGC 336
DB 556 AGC 558

RESULT 16
US-09-062-451-295
; Sequence 295, Application US/09062451
; Patent No. 6344350
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
; NUMBER OF SEQUENCES: 297
; CORRESPONDENCE ADDRESS:

ADDRESSER: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,451
FILING DATE: 04-APR-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.419C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 295:
SEQUENCE CHARACTERISTICS:
LENGTH: 1853 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-062-451-295

Query Match 12.4%; Score 252; DB 4; Length 1853;
Best Local Similarity 99.7%; Pred. No. 3.6e-97;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAAGCCATTGGTCTCAGAGCAAGATGGGCAAGTGTGCTGCCGTTGC 93
DB 256 TCTTCTGTGAAGAAGCCATTGGTCTCAGAGCAAGATGGGCAAGTGTGCTGCCGTTGC 315
QY 94 TTCCCTGCTGCAGGAGAGCGGCAAGACAGCAAGTGGGCACTTCTGGAGACCAAGACGAC 153
DB 316 TTCCCTGCTGCAGGAGAGCGGCAAGACAGCAAGTGGGCACTTCTGGAGACCAAGACGAC 375
QY 154 TGTGATGAAGACACTCTGAGAGCAAGATGGGCAAGTGGGCACTTCTGGAGACCAAGACGAC 213
DB 376 TGTGATGAAGACACTCTGAGAGCAAGATGGGCAAGTGGGCACTTCTGGAGACCAAGACGAC 435
QY 214 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGAGCAAGACGACGACTCTGCTATG 273
DB 436 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGAGCAAGACGACGACTCTGCTATG 495
QY 274 AAGACACTCAGGAACAAGATGGGCAAGTGGGCGCTTCTGAGAGCAAGACGACTCTGCTATG 333
DB 496 AAGACACTCAGGAACAAGATGGGCAAGTGGGCGCTTCTGAGAGCAAGACGACTCTGCTATG 555
QY 334 AGC 336
DB 556 AGC 558

RESULT 17
US-09-352-616A-369
; Sequence 369, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqul
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A

;; CURRENT FILING DATE: 1999-07-13
;; NUMBER OF SEQ ID NOS: 472
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 369
;; LENGTH: 1853
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-352-616a-369

Query Match 12.4%; Score 252; DB 4; Length 1853;
Best Local Similarity 99.7%; Pred. No. 3.6e-97;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 TCTTCTGTAAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGCTGCGCTTGC 93
DB 256 TCTCTGTGAAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGCTGCGCTTGC 315
QY 94 TTCCCTGTCGAGGAGGAGCGGCAAGAGCAAGTGGGCAAGTGGGCAAGTGGGCAAG 153
DB 316 TTCCCTGTCGAGGAGGAGCGGCAAGAGCAAGTGGGCAAGTGGGCAAGTGGGCAAG 375
QY 154 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGGCAAGTGGGCAAGTGGGCA 213
DB 376 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGGCAAGTGGGCAAGTGGGCA 435
QY 214 TGCAGGGGGAGTGCGCAAGCAAGCTGGGCGCTTCTGAGACACAGAGACTGTCTATG 273
DB 436 TGCAGGGGGAGTGCGCAAGCAAGCTGGGCGCTTCTGAGACACAGAGACTGTCTATG 495
QY 274 AAGCACTCAGGAACAAGATGGGCAAGTGGGCAAGTGGGCAAGTGGGCAAGTGGGCA 333
DB 496 AAGCACTCAGGAACAAGATGGGCAAGTGGGCAAGTGGGCAAGTGGGCAAGTGGGCA 555
QY 334 AGC 336
DB 556 AGC 558

RESULT 18
US-09-605-785-531
; Sequence 531, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, JIangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 531
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-605-785-531

Query Match 5.9%; Score 120; DB 4; Length 879;
Best Local Similarity 99.1%; Pred. No. 1.4e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAAAGAGAGCTGCTACATCTGGCCCTGCGCAATGGGAATTCAGAACTAGT 566
DB 333 GGACAGCAAAAGAGAGCTGCTACATCTGGCCCTGCGCAATGGGAATTCAGAACTAGT 392
QY 567 AAAAATCTGCTGAGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAGAGAGCAGC 626
DB 393 AAAAATCTGCTGAGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAGAGAGCAGC 452
QY 627 TCTGATTAAGGCGCTACAAATGCCAGGAAGATGAATGTGCTTAATGTGCTGGAACATGG 686
DB 453 TCTGATTAAGGCGCTACAAATGCCAGGAAGATGAATGTGCTTAATGTGCTGGAACATGG 512
QY 687 CACTGATCCAAATATTCAGATGATGGAATATACACTCT 728
DB 513 CACTGATCCAAATATTCAGATGATGGAATATACACTCT 554

RESULT 19
US-09-439-313-531
; Sequence 531, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, JIangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Stolk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 531
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-313-531

Query Match 5.9%; Score 120; DB 4; Length 879;
Best Local Similarity 99.1%; Pred. No. 1.4e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAAAGAGAGCTGCTACATCTGGCCCTGCGCAATGGGAATTCAGAACTAGT 566
DB 333 GGACAGCAAAAGAGAGCTGCTACATCTGGCCCTGCGCAATGGGAATTCAGAACTAGT 392
QY 567 AAAAATCTGCTGAGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAGAGAGCAGC 626
DB 393 AAAAATCTGCTGAGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAGAGAGCAGC 452
QY 627 TCTGATTAAGGCGCTACAAATGCCAGGAAGATGAATGTGCTTAATGTGCTGGAACATGG 686
DB 453 TCTGATTAAGGCGCTACAAATGCCAGGAAGATGAATGTGCTTAATGTGCTGGAACATGG 512
QY 687 CACTGATCCAAATATTCAGATGATGGAATATACACTCT 728
DB 513 CACTGATCCAAATATTCAGATGATGGAATATACACTCT 554

RESULT 20
US-09-605-785-372

```
; Sequence 372, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vegdick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 372
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-605-785-372
```

```
Query Match          5.9%; Score 120; DB 4; Length 1059;
Best Local Similarity 99.1%; Pred. No. 1.4e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAGCAAAAAGAGACTGCTCTACATCTGGCCCTCGCCATGGGAATTGAGAAGTACT 566
DB 276 GGACAAGCAAAAAGAGAGACTGCTCTACATCTGGCCCTCGCCATGGGAATTGAGAAGTACT 335
QY 567 AAAACTCTGCTGCGAGACAGATGTCACCTTAATGTCCTTGACAACAAAAAGAGACAGC 626
DB 336 AAAACTCTGCTGCGAGACAGATGTCACCTTAATGTCCTTGACAACAAAAAGAGACAGC 395
QY 627 TCTGATTAAGGCCGTACATATGCCAGAGATGAATGTGGTTAATGTTGCTGGAACATGG 686
DB 396 TCTGATTAAGGCCGTACATATGCCAGAGATGAATGTGGTTAATGTTGCTGGAACATGG 455
QY 687 CACTGATCCAAATATTCCAGATGAGTATGGAATAACCACTCT 728
DB 456 CACTGATCCAAATATTCCAGATGAGTATGGAATAACCACTCT 497
```

```
RESULT 21
US-09-439-313-372
; Sequence 372, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
```

```
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 372
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-372
```

```
Query Match          5.9%; Score 120; DB 4; Length 1059;
Best Local Similarity 99.1%; Pred. No. 1.4e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAGCAAAAAGAGACTGCTCTACATCTGGCCCTCGCCATGGGAATTGAGAAGTACT 566
DB 276 GGACAAGCAAAAAGAGAGACTGCTCTACATCTGGCCCTCGCCATGGGAATTGAGAAGTACT 335
QY 567 AAAACTCTGCTGCGAGACAGATGTCACCTTAATGTCCTTGACAACAAAAAGAGACAGC 626
DB 336 AAAACTCTGCTGCGAGACAGATGTCACCTTAATGTCCTTGACAACAAAAAGAGACAGC 395
QY 627 TCTGATTAAGGCCGTACATATGCCAGAGATGAATGTGGTTAATGTTGCTGGAACATGG 686
DB 396 TCTGATTAAGGCCGTACATATGCCAGAGATGAATGTGGTTAATGTTGCTGGAACATGG 455
QY 687 CACTGATCCAAATATTCCAGATGAGTATGGAATAACCACTCT 728
DB 456 CACTGATCCAAATATTCCAGATGAGTATGGAATAACCACTCT 497
```

```
RESULT 22
US-09-352-616A-372
; Sequence 372, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 372
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-372
```

```
Query Match          5.9%; Score 120; DB 4; Length 1059;
Best Local Similarity 99.1%; Pred. No. 1.4e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAGCAAAAAGAGACTGCTCTACATCTGGCCCTCGCCATGGGAATTGAGAAGTACT 566
DB 276 GGACAAGCAAAAAGAGAGACTGCTCTACATCTGGCCCTCGCCATGGGAATTGAGAAGTACT 335
QY 567 AAAACTCTGCTGCGAGACAGATGTCACCTTAATGTCCTTGACAACAAAAAGAGACAGC 626
DB 336 AAAACTCTGCTGCGAGACAGATGTCACCTTAATGTCCTTGACAACAAAAAGAGACAGC 395
QY 627 TCTGATTAAGGCCGTACATATGCCAGAGATGAATGTGGTTAATGTTGCTGGAACATGG 686
DB 396 TCTGATTAAGGCCGTACATATGCCAGAGATGAATGTGGTTAATGTTGCTGGAACATGG 455
QY 687 CACTGATCCAAATATTCCAGATGAGTATGGAATAACCACTCT 728
DB 456 CACTGATCCAAATATTCCAGATGAGTATGGAATAACCACTCT 497
```


LENGTH: 1851
TYPE: DNA
ORGANISM: Homo sapien
US-09-439-313-366

Query Match 5.9%; Score 120; DB 4; Length 1851;
Best Local Similarity 99.1%; Pred. No. 1.3e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAAAAGAGAGACTGCTCTACATCTGGCCCTCTGCCAATGGGAATTGGAAGTACT 566
DB 791 GGACAGCAAAAAGAGAGAGACTGCTCTACATCTGGCCCTCTGCCAATGGGAATTGGAAGTACT 732
QY 567 AAAACTCTGCTGGACAGACGATGTCACCTTAATGCTTGACAAACAAAAAGAGACAGC 626
DB 731 AAAACTCTGCTGGACAGACGATGTCACCTTAATGCTTGACAAACAAAAAGAGACAGC 672
QY 627 TCTGATAAAGGCCGTCACATGCGCAGAGATGATGCGTTAATGTTGCTGGAACATGG 686
DB 671 TCTGACAAAGGCCGTCACATGCGCAGAGATGATGCGTTAATGTTGCTGGAACATGG 612
QY 687 CACTGATCCCAATATTCCAGATGATGATGGAATACCACTCT 728
DB 611 CACTGATCCCAATATTCCAGATGATGATGGAATACCACTCT 570

RESULT 26

US-09-062-451-291/c
Sequence 291, Application US/09062451
Patent No. 6344550
GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
NUMBER OF SEQUENCES: 297
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,451
FILING DATE: 04-APR-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.419C2
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 291:
SEQUENCE CHARACTERISTICS:
LENGTH: 1851 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-062-451-291

Query Match 5.9%; Score 120; DB 4; Length 1851;
Best Local Similarity 99.1%; Pred. No. 1.3e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAAAAGAGAGACTGCTCTACATCTGGCCCTCTGCCAATGGGAATTGGAAGTACT 566

DB 791 GGACAGCAAAAAGAGAGACTGCTCTACATCTGGCCCTCTGCCAATGGGAATTGGAAGTACT 732
QY 567 AAAACTCTGCTGGACAGACGATGTCACCTTAATGCTTGACAAACAAAAAGAGACAGC 626
DB 731 AAAACTCTGCTGGACAGACGATGTCACCTTAATGCTTGACAAACAAAAAGAGACAGC 672
QY 627 TCTGATAAAGGCCGTCACATGCGCAGAGATGATGCGTTAATGTTGCTGGAACATGG 686
DB 671 TCTGACAAAGGCCGTCACATGCGCAGAGATGATGCGTTAATGTTGCTGGAACATGG 612
QY 687 CACTGATCCCAATATTCCAGATGATGATGGAATACCACTCT 728
DB 611 CACTGATCCCAATATTCCAGATGATGATGGAATACCACTCT 570

RESULT 27

US-09-062-451-292/c
Sequence 292, Application US/09062451
Patent No. 6344550
GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
NUMBER OF SEQUENCES: 297
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,451
FILING DATE: 04-APR-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.419C2
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 292:
SEQUENCE CHARACTERISTICS:
LENGTH: 1851 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-062-451-292

Query Match 5.9%; Score 120; DB 4; Length 1851;
Best Local Similarity 99.1%; Pred. No. 1.3e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAAAAGAGAGACTGCTCTACATCTGGCCCTCTGCCAATGGGAATTGGAAGTACT 566
DB 791 GGACAGCAAAAAGAGAGACTGCTCTACATCTGGCCCTCTGCCAATGGGAATTGGAAGTACT 732
QY 567 AAAACTCTGCTGGACAGACGATGTCACCTTAATGCTTGACAAACAAAAAGAGACAGC 626
DB 731 AAAACTCTGCTGGACAGACGATGTCACCTTAATGCTTGACAAACAAAAAGAGACAGC 672
QY 627 TCTGATAAAGGCCGTCACATGCGCAGAGATGATGCGTTAATGTTGCTGGAACATGG 686
DB 671 TCTGACAAAGGCCGTCACATGCGCAGAGATGATGCGTTAATGTTGCTGGAACATGG 612

```
QY 687 CACTGATCCAAATATTCAGATGATGGAATACCACTCT 728
|||||
Db 611 CACTGATCCAAATATTCAGATGATGGAATACCACTCT 570

RESULT 28
US-09-352-616A-366/C
; Sequence 366, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 366
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-366

Query Match 5.9%; Score 120; DB 4; Length 1851;
Best Local Similarity 99.1%; Pred. No. 1.3e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAGCAAAAGAGAGCTCTACATCTGGCCTCGCCAAATGGAAATTCAGAACTAGT 566
|||||
Db 791 GGACAAGCAAAAGAGAGCTCTACATCTGGCCTCGCCAAATGGAAATTCAGAACTAGT 732

QY 567 AAAATCTCTGCTGGACAGAGATGTCACTTAATGTCTTGACAAACAAAAAGAGACAGC 626
|||||
Db 731 AAAATCTCTGCTGGACAGAGATGTCACTTAATGTCTTGACAAACAAAAAGAGACAGC 672

QY 627 TCTGATTAAGCCGTACATGCGCAGGAAGATGATGTGCTTATGTCTGGAACATGG 686
|||||
Db 671 TCTGATTAAGCCGTACATGCGCAGGAAGATGATGTGCTTATGTCTGGAACATGG 612

QY 687 CACTGATCCAAATATTCAGATGATGGAATACCACTCT 728
|||||
Db 611 CACTGATCCAAATATTCAGATGATGGAATACCACTCT 570

RESULT 29
US-09-605-785-530
; Sequence 530, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
```

```
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 530
; LENGTH: 1852
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-605-785-530

Query Match 5.9%; Score 120; DB 4; Length 1852;
Best Local Similarity 99.1%; Pred. No. 1.3e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAGCAAAAGAGAGCTCTACATCTGGCCTCGCCAAATGGAAATTCAGAACTAGT 566
|||||
Db 1062 GGACAAGCAAAAGAGAGCTCTACATCTGGCCTCGCCAAATGGAAATTCAGAACTAGT 1121

QY 567 AAAATCTCTGCTGGACAGAGATGTCACTTAATGTCTTGACAAACAAAAAGAGACAGC 626
|||||
Db 1122 AAAATCTCTGCTGGACAGAGATGTCACTTAATGTCTTGACAAACAAAAAGAGACAGC 1181

QY 627 TCTGATTAAGCCGTACATGCGCAGGAAGATGATGTGCTTATGTCTGGAACATGG 686
|||||
Db 1182 TCTGATTAAGCCGTACATGCGCAGGAAGATGATGTGCTTATGTCTGGAACATGG 1241

QY 687 CACTGATCCAAATATTCAGATGATGGAATACCACTCT 728
|||||
Db 1242 CACTGATCCAAATATTCAGATGATGGAATACCACTCT 1283

RESULT 30
US-09-439-313-530
; Sequence 530, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 530
; LENGTH: 1852
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-313-530

Query Match 5.9%; Score 120; DB 4; Length 1852;
Best Local Similarity 99.1%; Pred. No. 1.3e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAGCAAAAGAGAGCTCTACATCTGGCCTCGCCAAATGGAAATTCAGAACTAGT 566
|||||
Db 1062 GGACAAGCAAAAGAGAGCTCTACATCTGGCCTCGCCAAATGGAAATTCAGAACTAGT 1121

QY 567 AAAATCTCTGCTGGACAGAGATGTCACTTAATGTCTTGACAAACAAAAAGAGACAGC 626
|||||
Db 1122 AAAATCTCTGCTGGACAGAGATGTCACTTAATGTCTTGACAAACAAAAAGAGACAGC 1181
```

[illegible]

RESULT 31
US-09-605-785-371
; Sequence 371, Application US/09605785
; Patent No. 6321716

```

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: JIANG, YUQI
APPLICANT: Henderson, Robert A.
APPLICANT: Kaios, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darlick
APPLICANT: Li, Samuel
APPLICANT: Wang, Ajun
APPLICANT: Skelky, Vasil A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: PasteSeq for Windows Version 3.0
SEQ ID NO 371
LENGTH: 1855
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1855)
OTHER INFORMATION: n = A,T,C or G
US-09-605-785-371

```

Query Match	5.98; Score 120; DB 4; Length 1855;
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Matches	220;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
---------	------	--------------	----	------------	----	--------	----	------	----

QY	507	GGACAAACCAAAAGGAGCTCTCTACATCTGGGCTCTGGCANTGGGAATTCGAAGTGT	566
Db	1072	GGACAGACCAAAAGGAGCTCTCTACATCTGGCCTCTGGCAATGGGAATTCGAAGTGT	1131
QY	567	AAAACCTCTCTGGACAGACAGTGTCAACTTAATGTCTTGACAACAAAAAAGAGCAGC	626
Db	1132	AAAACCTGTCTGTGACAGACAGATGTCACTTAATGTCTTGACACAAAAAAGAGCAGC	1191
QY	627	TCCTGATTAAGGCGGTACATATGCCAGGAAGATGANTGTGCGTTAATGTTGCTGGAACATGG	686
Db	1192	TCCTGACAAAGGCGGTACAAATGCCAGGAAGATGANTGTGCGTTAATGTTGCTGGAACATGG	1251
QY	687	CACGTATCCAAATTAATTCACATAGATATGGAATTAACACTCT	728
Db	1252	CACGTATCCAAATTAATTCACATAGATATGGAATTAACACTCT	1293

RESULT 32
US-09-439-313-371
; Sequence 371, Application US/09439313

```

; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121,42709
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 371
; LENGTH: 1855
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1855)
; OTHER INFORMATION: n = A,T,C or G
; US-09/439-313-371

```

Query Match	Score	DB 4	Length
5.9%	120		1855

```
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY	507	GGAAACCAAAAAGAGCGCTCTACATCGGGCGCTGGCAATGGGAATTCAGAACTAGT	566
QY <td>1072</td> <td>GGACACCAAAAAGACGCTCTACATCTGGCCCTTGGCAATGGGAATTCAGAACTAGT</td> <td>1133</td>	1072	GGACACCAAAAAGACGCTCTACATCTGGCCCTTGGCAATGGGAATTCAGAACTAGT	1133
QY <td>567</td> <td>AAAACCTCTCTGGACGAGCATGTCACTTAATGTCTTGCACCAACAAAAGAGCAGC</td> <td>626</td>	567	AAAACCTCTCTGGACGAGCATGTCACTTAATGTCTTGCACCAACAAAAGAGCAGC	626
QY <td>1132</td> <td>AAAACCTCTCTGGACGAGCATGTCACTTAATGTCTTGCACCAACAAAAGAGCAGC</td> <td>1191</td>	1132	AAAACCTCTCTGGACGAGCATGTCACTTAATGTCTTGCACCAACAAAAGAGCAGC	1191
QY <td>627</td> <td>TCGTATTAAGGCCGTACATGCCAGGAAGTGAATGCGCTTAATGTCTTGGAAACATGG</td> <td>686</td>	627	TCGTATTAAGGCCGTACATGCCAGGAAGTGAATGCGCTTAATGTCTTGGAAACATGG	686
QY <td>1192</td> <td>TCGTACCAAAAGCCGTACAAATGCCAGGAAGTGAATGCGCTTAATGTCTTGGAAACATGG</td> <td>1251</td>	1192	TCGTACCAAAAGCCGTACAAATGCCAGGAAGTGAATGCGCTTAATGTCTTGGAAACATGG	1251
QY <td>687</td> <td>CACGTATCCAAATATTCCAGATGAGTATGGAAATACCACCTCT</td> <td>728</td>	687	CACGTATCCAAATATTCCAGATGAGTATGGAAATACCACCTCT	728
QY <td>1252</td> <td>CACGTATCCAAATATTCCAGATGAGTATGGAAATACCACCTCT</td> <td>1293</td>	1252	CACGTATCCAAATATTCCAGATGAGTATGGAAATACCACCTCT	1293

RESULT 33
US-09-062-451-297

Patent No. 6344550

GENERAL INFORMATION.

APPLICANT: Frudakis, Tony N.

APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED AND FEED BUL
STREET: 6300 Columbia Center, 701 Fifth Avenue

STATE: Washington

ZIP: 98104-7092

MEDIUM TYPE: Floppy

OPERATING SYSTEM: PC-DOS/MS-DOS

```

1 SOFTWARE: PatentIn Release #1.0, Version #1.30
2
3 CURRENT APPLICATION DATA:
4 APPLICATION NUMBER: US/09/062,451
5 FILING DATE: 04-APR-1997
6
7 CLASSIFICATION:
8
9 ATTORNEY/AGENT INFORMATION:
10 NAME: MakI, David J.
11 REGISTRATION NUMBER: 31,392
12 REFERENCE/DOCKET NUMBER: 210121.419C2
13 TELECOMMUNICATION INFORMATION:
14 TELEPHONE: (206) 622-4900
15 TELEFAX: (206) 682-6031
16
17 INFORMATION FOR SEQ ID NO: 297:
18 SEQUENCE CHARACTERISTICS:
19 LENGTH: 1855 base pairs
20 TYPE: nucleic acid
21 STRANDEDNESS: single
22 TOPOLOGY: linear
23
24 US-09-062-451-297

```

Query Match	5.9%	Score 120	DB 4	Length 1855
Best Local Similarity	99.18%	Pred. No. 1.3e-41		
Matches 220	Conservative 0	Mismatches 2	Indels 0	Gaps 0
QY	507	GGACAAGCAAAAGAGAGACTGCTCTACATCTGTGGCCTCTGTGCCAATYGGGAATTCCAGAAGTACT	566	
Db	1072	GGACAAGCAAAAGAGAGACTGCTCTACATCTGTGGCCTCTGTGCCAATYGGGAATTCCAGAAGTACT	1131	
QY	567	AAAATCTCGTGGAGACACATGTCACTTAATCTCCTGACAAACAAAAGAGACAGC	626	
Db	1132	AAAATCTCGTGGAGACACATGTCACTTAATCTCCTGACAAACAAAAGAGACAGC	1191	
QY	627	TCTGATAAAGGCCGTACATGCCAGGAAGATGAATGTGGCTTAATGTGCTCGAACATGG	686	
Db	1192	TCTGACAAAGGCCGTACATGCCAGGAAGATGAATGTGGCTTAATGTGCTCGAACATGG	1251	
QY	687	CACGTATCCAAATATATCCAGATGATATAGGAATACCACTCT	728	
Db	1252	CACGTATCCAAATATATCCAGATGATATAGGAATACCACTCT	1293	

```

RESULT 34
US-09-352-616A-371
Sequence 371, Application US/09352616A
Patent No. 6595278
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuguai
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ. ID NOS: 472
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 371
LENGTH: 1855
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1855)
OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-371

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Query Match	5.98;	Score 120;	DB 4;	Length 1855;
Best Local Similarity	99.1%;	Pred. No. 1.3e-41;		
Matches 220;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;

07 GGACAGCAAAAGAGGAGTGCCTCTACATCTGGCCCTCTGCCAATGGGAATTCGAAGTACT 566

Db	1072	GGACAAAGCAAAAGGAGCTGCTTACATCTGGGCTTGCCAATGGGAATTCAGAACTACT	1133
Qy	567	AAACCTCCTGCTGGACAGACGATGTCAACTTAATGTCTTGACAAACAAAAGAGCACAC	626
Db	1132	AAAACCTGCTGTGGACAGACAGATGTCAACTTAATGTCTTGACAAACAAAAGAGCACAC	1199
Qy	627	TCTGATAAAGCCGCTACAAATGCCAGGAAGATGTAATGCGTTAATGTTCTCTGGAACATGG	686
Db	1192	TCTGACAAAGCCCTACAATGCCAGGAAGATGTAATGCGTTAATGTTCTCTGGAACATGG	1251
Qy	687	CACATGATCCAAATATTTCACAGATGATGTGGAATACCACTCT	728
Db	1252	CACATGATCCAAATATTTCACAGATGATGTGGAATACCACTCT	1293

```
US-09-605-785-370  
Sequence 370, Application US/09605785  
Patent No. 6321716  
GENERAL INFORMATION:  
APPLICANT: Xu, JiangChun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yuqi  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel  
APPLICANT: Wang, Ajjun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
FILE REFERENCE: 210121.427c16  
CURRENT APPLICATION NUMBER: US/09/605,785  
CURRENT FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 835  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 370  
LENGTH: 2184  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-605-785-370
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	Query Match	Best Local Similarity	5.9%;	Score 120;	DB 4;	Length 2184;			
	Matches	220;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps
Qy	507	GGACAGCAAAAGAGCACTGCTTACATCTGCGCTTCCCAATGGCAATTCAGAAAGTAGT	566						
Db	1061	GGACAAGCAAAAGAGCACTCTTACATCTGCGCTTCCCAATGGCAATTCAGAAAGTAGT	1120						
Qy	567	AAAACCTCGTGGACAGAGAGATGCAACTTAATGTCGTGACAAACAAAAAGCAGAC	626						
Db	1121	AAAACCTGCTGGACAGAGAGATGCAACTTAATGTCGTGACAAACAAAAAGCAGAC	1180						
Qy	627	TCTGATAAAGCCGTACAAATGCCAGAAAGTAATGCGTTAATGTTCTGGAACATGG	686						
Db	1181	TCTGACAAAGCCGTACAAATGCCAGAAAGTAATGCGTTAATGTTCTGGAACATGG	1240						
Qy	687	CACATGATCCAAATATTCACAATGAGTAGTGAAATACCACCTCT	728						
Db	1241	CACATGATCCAAATATTCACAATGAGTAGTGAAATACCACCTCT	1282						

RESULT 36

US-09-439-313-370
; Sequence 370, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiongchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Relfer, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439, 313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 370
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-370

Query Match 5.9%; Score 120; DB 4; Length 2184;
Best Local Similarity 99.1%; Pred. No. 1.3e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 507 GGACAGCAAAAGAGACTGCTCTACATCTGCGCTCCCAATGGGAATTCAGAGTAGT 566
DB 1061 GGACAGCAAAAGAGACTGCTCTACATCTGCGCTCCCAATGGGAATTCAGAGTAGT 1120
OY 567 AAACTCGTGTGGACAGACGATGTCACCTTAATGCTCTTGACACAAACAAAGAGACAGC 626
DB 1121 AAACTCGTGTGGACAGACGATGTCACCTTAATGCTCTTGACACAAACAAAGAGACAGC 1180
OY 627 TCTGATAAGCGCCGTACATCCAGAGATGATGTCGTTAATGTTGCTGGAAACATGG 686
DB 1181 TCTGATAAGCGCCGTACATCCAGAGATGATGTCGTTAATGTTGCTGGAAACATGG 1240
OY 687 CACTGATCCAAATATTCAGATGATGAAATACCACTCT 728
DB 1241 CACTGATCCAAATATTCAGATGATGAAATACCACTCT 1282

RESULT 37
US-09-062-451-296
; Sequence 296, Application US/09062451
; Patent No. 6344550
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
; NUMBER OF SEQUENCES: 297
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/062,451
FILING DATE: 04-APR-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.419C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 296:
SEQUENCE CHARACTERISTICS:
LENGTH: 2184 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-062-451-296

Query Match 5.9%; Score 120; DB 4; Length 2184;
Best Local Similarity 99.1%; Pred. No. 1.3e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 507 GGACAGCAAAAGAGACTGCTCTACATCTGCGCTCCCAATGGGAATTCAGAGTAGT 566
DB 1061 GGACAGCAAAAGAGACTGCTCTACATCTGCGCTCCCAATGGGAATTCAGAGTAGT 1120
OY 567 AAACTCGTGTGGACAGACGATGTCACCTTAATGCTCTTGACACAAACAAAGAGACAGC 626
DB 1121 AAACTCGTGTGGACAGACGATGTCACCTTAATGCTCTTGACACAAACAAAGAGACAGC 1180
OY 627 TCTGATAAGCGCCGTACATCCAGAGATGATGTCGTTAATGTTGCTGGAAACATGG 686
DB 1181 TCTGATAAGCGCCGTACATCCAGAGATGATGTCGTTAATGTTGCTGGAAACATGG 1240
OY 687 CACTGATCCAAATATTCAGATGATGAAATACCACTCT 728
DB 1241 CACTGATCCAAATATTCAGATGATGAAATACCACTCT 1282

RESULT 38
US-09-352-616A-370
; Sequence 370, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Xu, Jiongchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352, 616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 370
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-370

Query Match 5.9%; Score 120; DB 4; Length 2184;
Best Local Similarity 99.1%; Pred. No. 1.3e-41;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 507 GGACAGCAAAAGAGACTGCTCTACATCTGCGCTCCCAATGGGAATTCAGAGTAGT 566
DB 1061 GGACAGCAAAAGAGACTGCTCTACATCTGCGCTCCCAATGGGAATTCAGAGTAGT 1120
OY 567 AAACTCGTGTGGACAGACGATGTCACCTTAATGCTCTTGACACAAACAAAGAGACAGC 626
DB 1121 AAACTCGTGTGGACAGACGATGTCACCTTAATGCTCTTGACACAAACAAAGAGACAGC 1180

QY 627 TCGATTAAGGCGGTACATGCGCAGAGATGATGCGTTATGCTGCGACATGG 686
DB 1181 TCTGACAAAGCGGTACATGCGCAGAGATGATGCGTTATGCTGCGACATGG 1240
QY 687 CACTGATCCAAATATTCGAGATGATGATGAAATACCACTCT 728
DB 1241 CACTGATCCAAATATTCGAGATGATGATGAAATACCACTCT 1282

RESULT 39

US-09-605-785-367/C
Sequence 367, Application US/09605785
Patent No. 6321716

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqul
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 367
LENGTH: 668
TYPE: DNA
ORGANISM: Homo sapien
US-09-605-785-367

Query Match 5.8%; Score 118; DB 4; Length 668;
Best Local Similarity 100.0%; Pred. No. 9.7e-41;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 520 AGGACTGCTCTACATCTGGCCTTGCCTGCAATGGGAATTCAGAACTAGTAAACTCTGCTG 579
DB 548 AGGACTGCTCTACATCTGGCCTTGCCTGCAATGGGAATTCAGAACTAGTAAACTCTGCTG 489
QY 580 GACAGACGATGCACTTATGCTCTTGACACAAAAAGAGACAGCTCTGATTAAGG 637
DB 488 GACAGACGATGCACTTATGCTCTTGACACAAAAAGAGAGACAGCTCTGATTAAGG 431

RESULT 40

US-09-439-313-367/C
Sequence 367, Application US/09439313
Patent No. 6329505

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqul
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John

APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 367
LENGTH: 668
TYPE: DNA
ORGANISM: Homo sapien
US-09-439-313-367

Query Match 5.8%; Score 118; DB 4; Length 668;
Best Local Similarity 100.0%; Pred. No. 9.7e-41;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 520 AGGACTGCTCTACATCTGGCCTTGCCTGCAATGGGAATTCAGAACTAGTAAACTCTGCTG 579
DB 548 AGGACTGCTCTACATCTGGCCTTGCCTGCAATGGGAATTCAGAACTAGTAAACTCTGCTG 489
QY 580 GACAGACGATGCACTTATGCTCTTGACACAAAAAGAGACAGCTCTGATTAAGG 637
DB 488 GACAGACGATGCACTTATGCTCTTGACACAAAAAGAGACAGCTCTGATTAAGG 431

RESULT 41

US-09-062-451-293/C
Sequence 293, Application US/09062451
Patent No. 6344550

GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
NUMBER OF SEQUENCES: 297
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,451
FILING DATE: 04-APR-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.419C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 293:
SEQUENCE CHARACTERISTICS:
LENGTH: 668 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-062-451-293

Query Match 5.8%; Score 118; DB 4; Length 668;
Best Local Similarity 100.0%; Pred. No. 9.7e-41;
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-062-451-211

Query Match 5.38; Score 109; DB 4; Length 454;
Best Local Similarity 99.18; Pred. No. 6.1e-37;
Matches 209; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAAAGAGGAGCTGCTACATCTGGCCCTGCGCAATGGGAATTGAGAAGTAGT 566
DB 418 GGACAGCAAAAGAGGAGCTGCTACATCTGGCCCTGCGCAATGGGAATTGAGAAGTAGT 359
QY 567 AAACTCCTGCTGGACAGACGATGTCAACTTAATGCTTGTGACAAACAAAAGAGACAGC 626
DB 358 AAACTCCTGCTGGACAGACGATGTCAACTTAATGCTTGTGACAAACAAAAGAGACAGC 299
QY 627 TCTGATTAAGGCGCTACATGCCAGAAAGATGAATGTGCTTAATGTTGCTGGAACATGG 686
DB 298 TCTGATTAAGGCGCTACATGCCAGAAAGATGAATGTGCTTAATGTTGCTGGAACATGG 239
QY 687 CACTGATCCAATAATATCCAGATGAGTATGA 717
DB 238 CACTGATCCAATAATATCCAGATGAGTATGA 208

RESULT 45

US-09-598-326-211/C
Sequence 211, Application US/09598326
Patent No. 6423496

GENERAL INFORMATION:

APPLICANT: Frudakis, Tony N.
Reed, Steven G.
Smith, John M.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER

NUMBER OF SEQUENCES: 247

CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group PLLC

STREET: 701 Fifth Avenue, Suite 6300

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentlin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/598,326

FILING DATE: 20-Jun-2000

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Potter, Jane E.R.

REGISTRATION NUMBER: 33,332

REFERENCE/DOCKET NUMBER: 210121.41901

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4800

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 211:

SEQUENCE CHARACTERISTICS:

LENGTH: 454 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 211:

US-09-598-326-211

QY 507 GGACAGCAAAAGAGGAGCTGCTACATCTGGCCCTGCGCAATGGGAATTGAGAAGTAGT 566
DB 418 GGACAGCAAAAGAGGAGCTGCTACATCTGGCCCTGCGCAATGGGAATTGAGAAGTAGT 359
QY 567 AAACTCCTGCTGGACAGACGATGTCAACTTAATGCTTGTGACAAACAAAAGAGACAGC 626
DB 358 AAACTCCTGCTGGACAGACGATGTCAACTTAATGCTTGTGACAAACAAAAGAGACAGC 299
QY 627 TCTGATTAAGGCGCTACATGCCAGAAAGATGAATGTGCTTAATGTTGCTGGAACATGG 686
DB 298 TCTGATTAAGGCGCTACATGCCAGAAAGATGAATGTGCTTAATGTTGCTGGAACATGG 239
QY 687 CACTGATCCAATAATATCCAGATGAGTATGA 717
DB 238 CACTGATCCAATAATATCCAGATGAGTATGA 208

Search completed: November 8, 2002, 13:36:08
Job time: 110.703 secs

Query Match 5.38; Score 109; DB 4; Length 454;

Best Local Similarity 99.18; Pred. No. 6.1e-37;

Matches 209; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2002, 06:30:33 ; Search time 379.723 Seconds
(without alignments)
12098.502 Million cell updates/sec

Title: US-09-924-400-303

Perfect score: 2040

Sequence: 1 atggtgtgtgtgtgtgtgtc.....aaaaaaaaaaaaaaaaaaaaa 2040

Scoring table:

OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 15

Total number of hits satisfying chosen parameters: 113580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
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17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2040	100.0	2040	21 AAC81013	Human B1Agl antiig
2	2040	100.0	2040	22 AA167213	B305D Isoform C sp
3	2040	100.0	2040	22 AAS63809	Human prostate CDN
4	2040	100.0	2040	22 AAH93716	Human prostate-spe
5	2040	100.0	2040	22 AAH85030	Human prostate-spe
6	2040	100.0	2040	22 AAH02781	Prostate tumour an
7	2040	100.0	2040	24 ABL95180	Human B305D splice
8	2040	100.0	2040	24 AAS99859	Breast tumour-spec
9	1989	97.5	2040	21 AAA06600	Human immunogenic

10	1551	76.0	2000	21 AAC81012	Human B1Agl antiig
11	1551	76.0	2000	22 AA167212	B305D Isoform C sp
12	1551	76.0	2000	22 AAS63808	Human prostate CDN
13	1551	76.0	2000	22 AAH93715	Human prostate-spe
14	1551	76.0	2000	22 AAH85029	Human prostate-spe
15	1551	76.0	2000	22 AAH02780	Prostate tumour an
16	1551	76.0	2000	24 ABL95179	Human B305D splice
17	1551	76.0	2000	24 AAS99857	Breast tumour-spec
18	1500	73.5	2000	21 AAA06599	Human immunogenic
19	1128	55.3	1155	21 AAC81011	Human B1Agl antiig
20	1128	55.3	1155	21 AAA06598	Human immunogenic
21	1128	55.3	1155	22 AA167211	B305D Isoform C sp
22	1128	55.3	1155	22 AAS63807	Human prostate CDN
23	1128	55.3	1155	22 AAH93714	Human prostate-spe
24	1128	55.3	1155	22 AAH85028	Human prostate-spe
25	1128	55.3	1155	22 AAH02779	Prostate tumour an
26	1128	55.3	1155	24 ABL95178	Human B305D splice
27	1128	55.3	1155	24 AAS99857	Breast tumour-spec
28	1044	51.2	1590	24 AAS99869	Breast tumour-spec
29	975	47.8	1155	24 AAS99872	Breast tumour-spec
30	491	24.1	1512	19 AAV68995	DNA molecule encod
31	491	24.1	1512	21 AAC81006	Human B1Agl antiig
32	491	24.1	1512	21 AAA06593	Human immunogenic
33	491	24.1	1512	22 AAS63802	Human prostate CDN
34	491	24.1	1512	22 AAH93709	Human prostate-spe
35	491	24.1	1512	22 AAH85023	Human prostate-spe
36	491	24.1	1512	22 AAH02774	Prostate tumour an
37	491	24.1	1512	24 ABL95173	Human B305D splice
38	491	24.1	1512	24 ABR46896	Human breast tumou
39	491	24.1	1512	24 AAS99852	Breast tumour-spec
40	252	12.4	1853	19 AAV68996	DNA molecule encod
41	252	12.4	1853	21 AAC81007	Human B1Agl antiig
42	252	12.4	1853	21 AAA06594	Human immunogenic
43	252	12.4	1853	22 AAS63803	Human prostate CDN
44	252	12.4	1853	22 AAH93710	Human prostate-spe
45	252	12.4	1853	22 AAH85024	Human prostate-spe

ALIGNMENTS

RESULT 1	
AAC81013	
ID	AAC81013 strand: cDNA: 2040 BP.
AC	AAC81013:
XX	
DT	13-FEB-2001 (first entry)
XX	
DE	Human B1Agl antigen splice isoform B1C-9-16 cDNA.
XX	
KW	Human; breast tumour-specific antigen; cytosolic; vaccine;
KW	breast cancer; B1Agl; B1Agl; B1Agl; ss.
OS	Homo sapiens.
XX	
PN	WO200061753-A2.
XX	
PD	19-OCT-2000.
XX	
PF	07-APR-2000; 2000WO-US09312.
XX	
PR	09-APR-1999; 99US-0288198.
XX	
PR	28-OCT-1999; 99US-0428735.
XX	
PR	23-MAR-2000; 2000US-0534825.
XX	
PA	(CORI-) CORIXA CORP.
XX	
PI	Frudakis TN, Smith JM, Reed SG, Misher LE, Retter MW, Dillon DC;
XX	
DR	WPI; 2000-628403/60.
XX	
DR	P-PSDB; AAB28630.
XX	

PT An isolated polypeptide comprising an immunogenic portion of a breast
PT tumor protein used for inhibiting the development of cancer, especially
PT breast cancer, and monitoring cancer progression in a patient -
XX
PS Claim 4; Page 178; 187pp; English.
XX The present sequence is given in a specification relating to compositions
CC and methods for the treatment and diagnosis of breast cancer. Nucleotide
CC sequences that are preferentially expressed in breast tumour tissue, and
CC the polypeptides encoded by such nucleotide sequences, are used in
CC compositions and vaccines to inhibit the development of cancer,
CC especially breast cancer. The progression of a cancer may be monitored by
CC carrying out detection of tumour-specific antigens at subsequent time
CC points and comparing the results from the different time points.
CC CD4+ and/or CD8+ T-Cells isolated from the cancer patient may be treated
CC with tumour-specific polypeptides, polynucleotides encoding the
CC polypeptides or antigen presenting cells expressing the polypeptides. The
CC cells are then administered to the patient to inhibit development of
CC cancer.
XX
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 other;.
Query Match 100.0%; Score 2040; DB 21; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 ATGTGGTGTGAGTGAATTCATCCGCGCTCTCTCTGTGAAGAGCATTTGGTCTC 60
DB 1 ATGTGGTGTGAGTGAATTCATCCGCGCTCTCTCTGTGAAGAGCATTTGGTCTC 60
QY 61 AGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCTGAGGAGCGGCAAG 120
DB 61 AGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCTGAGGAGCGGCAAG 120
QY 121 AGCAACCTGGGCAATTTCTGGAGACACAGAGACTCTGCTATGAAGAACTATGAGCAAG 180
DB 121 AGCAACCTGGGCAATTTCTGGAGACACAGAGACTCTGCTATGAAGAACTATGAGCAAG 180
QY 181 ATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCTGAGGAGGAGTGGCAAGAGCAAGT 240
DB 181 ATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCTGAGGAGGAGTGGCAAGAGCAAGT 240
QY 241 GGGCTTCTGGAGACACAGAGACTCTGCTATGAAGAACTATGAGCAAGAGCAAGT 300
DB 241 GGGCTTCTGGAGACACAGAGACTCTGCTATGAAGAACTATGAGCAAGAGCAAGT 300
QY 301 TGGTGGTGGCACTGCTGCTGCTGCTGAGGAGGAGCGCAAGAGCAAGTGGGCTGG 360
DB 301 TGGTGGTGGCACTGCTGCTGCTGCTGAGGAGGAGCGCAAGAGCAAGTGGGCTGG 360
QY 361 GGAAGCTACGATGACATGCTTCTGATGAGGCCAGGTACCACTGCTGGAGAGATCTG 420
DB 361 GGAAGCTACGATGACATGCTTCTGATGAGGCCAGGTACCACTGCTGGAGAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGCTGAGGAGCCAGGTACCACTGCTGAGAGATCTG 480
DB 421 GACAAGCTCCACAGAGCTGCTGCTGAGGAGCCAGGTACCACTGCTGAGAGATCTG 480
QY 481 CTGAGGAGACAGTGAAGCAAGAGCAAGAGCAAGAGAGTCTCTATCATCTGGCC 540
DB 481 CTGAGGAGACAGTGAAGCAAGAGCAAGAGCAAGAGAGTCTCTATCATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGGACACAGATGCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGGACACAGATGCAACTTAAT 600
QY 601 GTCTTGAACAACAAAAGAGAGAGCTCTGATTAAGGCCGATCAATGCGAAGAGATGAA 660
DB 601 GTCTTGAACAACAAAAGAGAGAGCTCTGATTAAGGCCGATCAATGCGAAGAGATGAA 660
QY 661 TGTGCGTGAATGTGTGAGAACATGGCATGTATCAATATTTCCAGATGATGAAAT 720
DB 661 TGTGCGTGAATGTGTGAGAACATGGCATGTATCAATATTTCCAGATGATGAAAT 720

QY 721 ACCACTGACACTACGCTATCTATATGAAGATTAATTAAGCCAAAGCACTGCTCTTA 780
DB 721 ACCACTGACACTACGCTATCTATATGAAGATTAATTAATTAAGCCAAAGCACTGCTCTTA 780
QY 781 TATGTCCTGATATGCAATCAAAAAACAGAGGCTCCACACCACTGTTTGGTGA 840
DB 781 TATGTCCTGATATGCAATCAAAAAACAGAGGCTCCACACCACTGTTTGGTGA 840
QY 841 CATAGCAAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
DB 841 CATAGCAAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATGATATGGAAGAGAGCTGCTCATATCTGCTATGTTGGATGACAGCAATATA 960
DB 901 CTGATGATATGGAAGAGAGCTGCTCATATCTGCTATGTTGGATGACAGCAATATA 960
QY 961 GTGACCTTCTACTTGAACCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAC 1020
DB 961 GTGACCTTCTACTTGAACCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAC 1020
QY 1021 GCCAGAGATATGCTGTTCTAGTCAATCATCATGATTAATTTGCCAGTACTTGCAGTAC 1080
DB 1021 GCCAGAGATATGCTGTTCTAGTCAATCATCATGATTAATTTGCCAGTACTTGCAGTAC 1080
QY 1081 AAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAAACAGACTTAAG 1140
DB 1081 AAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCACAAAAGTTCAAGGCGAGTAAATATGACGACAGAA 1200
DB 1141 CTGACATCAGAGAGAGAGTCACAAAAGTTCAAGGCGAGTAAATATGACGACAGAA 1200
QY 1201 ATGTCTCAAGACCAAAATTAATTAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGACCAAAATTAATTAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
DB 1261 AAGCATGAAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
QY 1321 AATGCTGATTAATGATTAATCTCTCAAAAGAGAGCAAGACCTGAAATATGACAAATTT 1380
DB 1321 AATGCTGATTAATGATTAATCTCTCAAAAGAGAGCAAGACCTGAAATATGACAAATTT 1380
QY 1381 CTTGACAAAGAGATGAGATATCACAGATTTGCGAATAGTTTGTGACTACAAAGAA 1440
DB 1381 CTTGACAAAGAGATGAGATATCACAGATTTGCGAATAGTTTGTGACTACAAAGAA 1440
QY 1441 AAGAGATGCCAAATATCTTCTGAAAAACAGCAACCCAGAACAAAGACTTAAGCTGACA 1500
DB 1441 AAGAGATGCCAAATATCTTCTGAAAAACAGCAACCCAGAACAAAGACTTAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGTACAAAGGCTTGAAGGCGAGTAAAAATGGCCAGCCAGAGAAAAATCT 1560
DB 1501 TCAGAGAGAGAGTACAAAGGCTTGAAGGCGAGTAAAAATGGCCAGCCAGAGAAAAATCT 1560
QY 1561 CAAGAACAGAAATTAATTAAGATGATGATGATGATGATGATGATGATGATGATGATG 1620
DB 1561 CAAGAACAGAAATTAATTAAGATGATGATGATGATGATGATGATGATGATGATGATG 1620
QY 1621 GAAATGAAGAGAGAGAGTACTCATGCGGATTTCCAGAAAACTGACTAATGATGCC 1680
DB 1621 GAAATGAAGAGAGAGAGTACTCATGCGGATTTCCAGAAAACTGACTAATGATGCC 1680
QY 1681 ACTGCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
DB 1681 ACTGCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
QY 1741 CAGCAATTTCTGACACTGAGAAATGAAGAGATATCACAGTACGACAAATATGATCTAC 1800
DB 1741 CAGCAATTTCTGACACTGAGAAATGAAGAGATATCACAGTACGACAAATATGATCTAC 1800

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OY 1801 AAGCAATTTTGTGAAGACAGACACTGGAATATTACAGCATGAGATTCTGATTTCATGAA 1860
    |||
DB 1801 AAGCAATTTTGTGAAGACAGACACTGGAATATTACAGCATGAGATTCTGATTTCATGAA 1860
OY 1861 GAAAAGCAGATGAAAGTGGTTGAAAAATGAATTCGACCTTCTCTTGTGTTAAGAAA 1920
    |||
DB 1861 GAAAAGCAGATGAAAGTGGTTGAAAAATGAATTCGACCTTCTCTTGTGTTAAGAAA 1920
OY 1921 GAAAAAGACATCTTCGATGAAAAATAGTAGCTTGGCGGGAAGAAATGCCATGCTAGACATG 1980
    |||
DB 1921 GAAAAAGACATCTTCGATGAAAAATAGTAGCTTGGCGGGAAGAAATGCCATGCTAGACATG 1980
OY 1981 GAGCTAGACACATGAATGAACATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAAATGAAAA 2040
    |||
DB 1981 GAGCTAGACACATGAATGAACATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAAATGAAAA 2040

RESULT 2
AA167213 standard; cDNA: 2040 BP.
ID AA167213;
AC AA167213;
XX
XX 11-FEB-2002 (first entry)
XX
XX B305D isoform C splice variant 3 encoding cDNA.
XX
XX Genetic subtraction; DNA microarray analysis; polymerase chain reaction;
XX cancer: B305D; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1.2016
XX /tag= a
XX /product= "B305D isoform C splice variant"
XX
XX WO200175171-A2.
XX
XX 11-OCT-2001.
XX
XX 02-APR-2001; 2001WO-US10631.
XX
XX 03-APR-2000; 2000US-194241P.
XX 20-JUL-2000; 2000US-219862P.
XX 27-JUL-2000; 2000US-221300P.
XX 18-DEC-2000; 2000US-256592P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Houghton RL, Dillon DC, Molesh DA, Xu J, Zehentner B, Persing DH;
XX WPI: 2001-626449/72.
XX P-PSDB; AAG65978.
XX
XX Identifying tissue (tumour)-specific polynucleotides overexpressed in
XX cells in patient, comprises DNA microarray analysis or quantitative
XX polymerase chain reaction -
XX
XX Claim 4; Page 94-95; 127pp; English.
XX
XX The invention relates to identifying tissue-specific polynucleotides (P)
XX that involves performing a genetic subtraction to identify pool of (P)
XX from tissue of interest (TI), performing DNA microarray analysis to
XX identify first subset of polynucleotides (SP1) at least 2-fold over
XX expressed in TI, and performing quantitative polymerase chain reaction
XX (PCR) analysis on SP1 to identify second subset of (P). The method is
XX useful for determining the presence or absence of a cancer cell in a
XX patient, monitoring the progression of cancer in a patient using a
XX biological sample such as blood, serum, lymph nodes, bone marrow, sputum,
XX urine or a tumour biopsy sample. The methods are useful for determining
XX the presence or absence of or monitoring progression of prostate, breast,

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CC colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver,
CC gastric, kidney, bladder, pancreatic or endometrial cancer. The present
CC sequence represents a cDNA encoding a B305D isoform C splice variant.
XX
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 other;
Query Match 100.0%; Score 2040; DB 22; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATGTGGTTGAGGTGATTCCATGCCGCGCTCTCTTGTGAAGAACCATTTGGTCTC 60
DB 1 ATGTGGTTGAGGTGATTCCATGCCGCGCTCTCTTGTGAAGAACCATTTGGTCTC 60
OY 61 AGAGCAGATGAGGCAAGTGGTGGTCTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
DB 61 AGAGCAGATGAGGCAAGTGGTGGTCTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
OY 121 ACCAAGTGGGACCTTCTGAGACACGACGACTGCTATGAAGACACTCAGAGCAAG 180
DB 121 ACCAAGTGGGACCTTCTGAGACACGACGACTGCTATGAAGACACTCAGAGCAAG 180
OY 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTCAGGAGGAGTGGCAAGCAACGTG 240
DB 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTCAGGAGGAGTGGCAAGCAACGTG 240
OY 241 GGGCGTTCTGGAGACGACGACGACTCTGCTATGAAGACACTAGAACAAATGGGCAAG 300
DB 241 GGGCGTTCTGGAGACGACGACGACTCTGCTATGAAGACACTAGAACAAATGGGCAAG 300
OY 301 TGGTCTGCGCACTGCTTCCCTGCTGCAAGGAGGAGCGGCAAGAGTGGGCGCTGG 360
DB 301 TGGTCTGCGCACTGCTTCCCTGCTGCAAGGAGGAGCGGCAAGAGTGGGCGCTGG 360
OY 361 GGAGACTAGATGACAGTGCCTTTCATGAGCCAGGACCAAGTCCCTGGAGCAAGATCTG 420
DB 361 GGAGACTAGATGACAGTGCCTTTCATGAGCCAGGACCAAGTCCCTGGAGCAAGATCTG 420
OY 421 GACAAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATGTG 480
DB 421 GACAAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATGTG 480
OY 481 CTCGAGGACACTGAGCTGAGCAAGAGCAAGAGAGGAGCTCTACATTTGGCC 540
DB 481 CTCGAGGACACTGAGCTGAGCAAGAGCAAGAGAGGAGCTCTACATTTGGCC 540
OY 541 TCTGCCAATGGGAATTCAGAAATAGTAATAAATCTGCTGAGACAGATGTCACCTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAATAGTAATAAATCTGCTGAGACAGATGTCACCTTAAT 600
OY 601 GTCTTTGACACAAAAGAGACAGCTGTGATAAGCCGCTACATTCAGAGAGATGAA 660
DB 601 GTCTTTGACACAAAAGAGAGACAGCTGTGATAAGCCGCTACATTCAGAGAGATGAA 660
OY 661 TGTGGTTAATGTTGCTGTAACATGGCACTGATCCAAATTTCCAGATGAGTGAAT 720
DB 661 TGTGGTTAATGTTGCTGTAACATGGCACTGATCCAAATTTCCAGATGAGTGAAT 720
OY 721 ACCACTGACACTAGCTATCTATATGAAGATAAATTAATGGCCAAAGCACTGCTTGA 780
DB 721 ACCACTGACACTAGCTATCTATATGAAGATAAATTAATGGCCAAAGCACTGCTTGA 780
OY 781 TATGTTGCTGATATGATTCAAAAAACAAGCATGGCTTCACACCTTTACTTGGTGA 840
DB 781 TATGTTGCTGATATGATTCAAAAAACAAGCATGGCTTCACACCTTTACTTGGTGA 840
OY 841 CATGAGCAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCAATTTAAATCA 900
DB 841 CATGAGCAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCAATTTAAATCA 900
OY 901 CTGATAGATATGGAAGAGCTCTCTCATCTTGGTGTATGATGATGATGATGATGATGAT 960
DB 901 CTGATAGATATGGAAGAGCTCTCTCATCTTGGTGTATGATGATGATGATGATGATGAT 960

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OY	121	AGCACTGGGACACTTCTTGAAAGCACAGACACTCGCTATATAAAGCACTCAGAGACAAG	180
Dp	121	AGCAAGCTGGGACACTTCTTGGAAGCACAGACACTCGCTATATAAAGCACTCAGAGACAAG	180
OY	181	ATTGGCAAGTGTGGCCGCCACTGCTTCCTCCGTGTGAGGGGAGTGGCAAGCAACTGTG	240
Dp	181	ATTGGGCAAGTGTGTCCGCCACTGCTTCCTCCGTGTGAGGGGAGTGGCAAGCAACTGTG	240
OY	241	GCGGCTTCTGAGAACCAAGCACTGCTGTATGAACACTCAGGAACAAGATGGGCAGA	300
Dp	241	GCGGCTTCTGGAAGACCAGCACTGCTGTATGAACACTCAGGAACAAGATGGGCAGA	300
OY	301	TGGTGCTGCCACATGCTTTCCCCCTGCTCAGGGGAGGGGCAAGAGTGGGCGCTTGG	360
Dp	301	TGGTGCTGCCACTGCTTCCCCTGCTCAGGGGAGGGGCAAGAGTGGGCGCTTGG	360
OY	361	GGAGACTACGATGACAGTAGTGCCCTTCATGAGACCAGGTACACGTCCGTGGAGAAAGATG	420
Dp	361	GGAGACTACGATGACAGTAGTGCCCTTCATGAGACCAGGTACACGTCCGTGGAGAAAGATG	420
OY	421	GACAACTCCACAGAGCTGCTGTGGGGTAAAGTCCCAGAAAGATCTCATGCTCATG	480
Dp	421	GACAACTCCACAGAGCTGCTGTGGGGTAAAGTCCCAGAAAGATCTCATGCTCATG	480
OY	481	CTCAGGACACTGACGTGAACAAGAGGACCAAGCAAAGACATGCTCATATGACC	540
Dp	481	CTCAGGACACTGACGTGAACAAGAGGACCAAGCAAAGAGCTGCTCATATGACC	540
OY	541	TCGCGCAATGGGAATTCAGAAATGTAATAACTCTGCTGGACAGACGATGTCACCTTAAT	600
Dp	541	TCGCGCAATGGGAATTCAGAAATGTAATAACTCTGCTGGACAGACGATGTCACCTTAAT	600
OY	601	GTCCTTACACAACAAAAGAGACAGTCTGATPAAGGGCCGTACATGGCAGGAAGATGA	660
Dp	601	GTCCTTACACAACAAAAGAGACAGTCTGATPAAGGGCCGTACATGGCAGGAAGATGA	660
OY	661	TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCCAAGATGATGGAAT	720
Dp	661	TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCCAAGATGATGGAAT	720
OY	721	ACCACTGTGACATACGCTATCTTAATGAAGATTAATTAATGGCCAAAGCACTGCTTA	780
Dp	721	ACCACTGTGACATACGCTATCTTAATGAAGATTAATTAATGGCCAAAGCACTGCTTA	780
OY	781	TATGCTCTGATATCGAATCAAAAAACAAGCAATGGCGCTCACACCACTGTACTTGGTGA	840
Dp	781	TATGCTCTGATATCGAATCAAAAAACAAGCAATGGCGCTCACACCACTGTACTTGGTGA	840
OY	841	CATAGCAAAAACAGCAAGTCTGGAATTTTTTAATCAGAAAAAAGCGAATTTAAATGCA	900
Dp	841	CATAGCAAAAACAGCAAGTCTGGAATTTTTTAATCAGAAAAAAGCGAATTTAAATGCA	900
OY	901	CTGATATGATATGGAAGGACTGCTCATATCTTGGCTGTATGTTGGATCGACAGATTA	960
Dp	901	CTGATATGATATGGAAGGACTGCTCATATCTTGGCTGTATGTTGGATCGACAGATTA	960
OY	961	GTCAGCTTACTTGAAGCAAAATATTTGATGATCTTCAAGATCTATCTGGACAGAG	1020
Dp	961	GTCAGCTTACTTGAAGCAAAATATTTGATGATCTTCAAGATCTATCTGGACAGAG	1020
OY	1021	GCGAGATGATGCTGTTCTATCATATCATATGATTAATTTGGCACTTACTTTCGACATC	1080
Dp	1021	GCGAGATGATGCTGTTCTATCATATCATATGATTAATTTGGCACTTACTTTCGACATC	1080
OY	1081	AAAGAAACAGATGCTAAAAAATCTTCTGAAAACAGCAATCCAGAACAGACTTAAG	1140
Dp	1081	AAAGAAACAGATGCTAAAAAATCTTCTGAAAACAGCAATCCAGAACAGACTTAAG	1140
OY	1141	CTGACATCAAGGAAGTGCACAAAGGTTCAAAGGAGTGAATAATGGCAGCAGAGAA	1200
Dp	1141	CTGACATCAAGGAAGTGCACAAAGGTTCAAAGGAGTGAATAATGGCAGCAGAGAA	1200

Qy	1201	ATGTCTCAAGAACCCAGAAATTAATTAAGATAGTGATGATAGAGAGTTGAGAGAAATTAAG	1280
Db	1201	ATGTCTCAAGAACCCAGAAATTAATTAAGATAGTGATAGAGAGTTGAGAGAAATTAAG	1260
Qy	1261	AAGCATGAAGATTAATTAATGTGGGATTTCTTGAAACCTGACTAATGTGTCACTGTGGC	1320
Db	1261	AAGCATGAAGATTAATTAATGTGGGATTTCTTGAAACCTGACTAATGTGTCACTGTGGC	1320
Qy	1321	AATGGTGAATTAATGGATTAATTTCTTCAAGAGAGAGAGAAACCTGAAATTCAGCAATTT	1380
Db	1321	AATGGTGAATTAATGGATTAATTTCTTCAAGAGAGAGAGAAACCTGAAATTCAGCAATTT	1380
Qy	1381	CCTGACAACGAAAGTGAAGAGTATCACAGAAATTTGCCAAATTAAGTTTCTGACTACAAAGA	1440
Db	1381	CCTGACAACGAAAGTGAAGAGTATCACAGAAATTTGCCAAATTAAGTTTCTGACTACAAAGA	1440
Qy	1441	AAACGATGCCAAATTAATCTCTTCTGAAACAGCAACCCAGAACCAAGACTTAAGCTGACA	1500
Db	1441	AAACGATGCCAAATTAATCTCTTCTGAAACAGCAACCCAGAACCAAGACTTAAGCTGACA	1500
Qy	1501	TCAGAGGAAGAGTACACAAAGGCTTGAAGGACAGTGAATAATGGCAGCAGAGAAAGATCT	1560
Db	1501	TCAGAGGAAGAGTACACAAAGGCTTGAAGGACAGTGAATAATGGCAGCAGAGAAAGATCT	1560
Qy	1561	CAGAACCCAGAAATTAATTAAGAGATGATAGAGAGCTAGAAAAATTTTAATGGCTATCGAA	1620
Db	1561	CAGAACCCAGAAATTAATTAAGAGATGATAGAGAGCTAGAAAAATTTTAATGGCTATCGAA	1620
Qy	1621	GAAATGAAGAGACACGGAATGATCTCATGTCTGGATTTCCCAAGAAACCTGACTAATGTGCC	1680
Db	1621	GAAATGAAGAGACACGGAATGATCTCATGTCTGGATTTCCCAAGAAACCTGACTAATGTGCC	1680
Qy	1681	ACTGCTGGCAATGGTGAATGATGATTAATTTCTTCAAGAGAGAGCAACACTGAAAGC	1740
Db	1681	ACTGCTGGCAATGGTGAATGATGATTAATTTCTTCAAGAGAGAGCAACACTGAAAGC	1740
Qy	1741	CAGCAATTTCTTGAACACTGAGAAATGAAGAGTATCACAGTACAGAACAAATTAATCTCAG	1800
Db	1741	CAGCAATTTCTTGAACACTGAGAAATGAAGAGTATCACAGTACAGAACAAATTAATCTCAG	1800
Qy	1801	AAGCAATTTTGTGAAGAACAGAACACTGGAATTTTACAGATGAGATCTGTATTCATGAA	1860
Db	1801	AAGCAATTTTGTGAAGAACAGAACACTGGAATTTTACAGATGAGATCTGTATTCATGAA	1860
Qy	1861	GAAAGCAGATAGAGAGTGTGAATAAATGAATTCAGACTTTCTTAGTGTAAAGAA	1920
Db	1861	GAAAGCAGATAGAGAGTGTGAATAAATGAATTCAGACTTTCTTAGTGTAAAGAA	1920
Qy	1921	GAAAAAGACATTTGATGAAAAATAGTACGTTGCGGGAAGAAATTTGCCATGTAAGACTG	1980
Db	1921	GAAAAAGACATTTGATGAAAAATAGTACGTTGCGGGAAGAAATTTGCCATGTAAGACTG	1980
Qy	1981	GAGCTAGACACAAATGAAGAAATCAGAGCAGCTAAAAAATTTTAAAAAATTTTAAAAA	2040
Db	1981	GAGCTAGACACAAATGAAGAAATCAGAGCAGCTAAAAAATTTTAAAAAATTTTAAAAA	2040
RESULT 4			
AAH93716			
ID	AAH93716 standard; cDNA; 2040 BP.		
XX	AAH93716;		
XX	04-Oct-2001 (first entry)		
DE	Human prostate-specific cDNA sequence B305D splice variant #10.		
XX	Human; prostate cancer; prostate-specific; diagnosis; vaccine;		
KW	cytostatic; gene therapy; metastasis; ss.		
XX	Homo sapiens.		
OS	Homo sapiens.		
XX	MO200151633-A2.		

XX 19-JUL-2001.
PD
XX 16-JAN-2001; 2001MO-US01574.
PF
XX 14-JAN-2000; 2000US-0483672.
PR
XX (CORI-) CORIXA CORP.
PA
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kholo MD, Fanger GR, Day CH, Retter MM, Stolk JA, Skeiky YAM,
PI Wang A, Mesgher MJ;
XX WPI; 2001-425873/45.
DR
XX
XX New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -
PS
XX Claim 1; Page 348; 543pp; English.
XX
CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 other;

Query Match 100.0%; Score 2040; DB 22; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGTTGATTCATCGCGGCTGCTCTTCTGTGAAGAAAGCCATTGGTCTC 60
DB 1 ATGGTGGTTGAGTTGATTCATCGCGGCTGCTCTTCTGTGAAGAAAGCCATTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
DB 61 AGGAGCAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
QY 121 AGCAAGCTGGGCACTTGTGAGACACGACGACTCTGTATGAAGACACTGAGGACAAG 180
DB 121 AGCAAGCTGGGCACTTGTGAGACACGACGACTCTGTATGAAGACACTGAGGACAAG 180
QY 181 ATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
DB 181 ATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
QY 241 GGGCCCTTGTGAGACACGACGACTCTGTATGAAGACACTGAGGACAAGTGGGCAAG 300
DB 241 GGGCCCTTGTGAGACACGACGACTCTGTATGAAGACACTGAGGACAAGTGGGCAAG 300
QY 301 TGGTGGTGGCACTGCTCCCTGCTGCGAGGGGAGCGGCAAGAGAGTGGGCGCTTGG 360
DB 301 TGGTGGTGGCACTGCTCCCTGCTGCGAGGGGAGCGGCAAGAGAGTGGGCGCTTGG 360
QY 361 GGAAGTACTGATGACGAGTGGCTTATGAGAGCCAGTACCAACGTCGCGGGAAGATCTG 420
DB 361 GGAAGTACTGATGACGAGTGGCTTATGAGAGCCAGTACCAACGTCGCGGGAAGATCTG 420
QY 421 GACAAGCTCCACAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
DB 421 GACAAGCTCCACAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480

QY 481 CTCAGGACACTGACGTGAACAAGAGACAAAGAGAGACTGCTTACATCTGGCC 540
DB 481 CTCAGGACACTGACGTGAACAAGAGACAAAGAGAGACTGCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAATGTAATAAATCTGCTGGACAGACATGTAATTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAATGTAATAAATCTGCTGGACAGACATGTAATTAAT 600
QY 601 GTCTTGAACAACAAAAGAGAGACGCTGTGTAAGGCCGACACATGCTCAGAGATGAA 660
DB 601 GTCTTGAACAACAAAAGAGAGACGCTGTGTAAGGCCGACACATGCTCAGAGATGAA 660
QY 661 TGTGCGTTAAATGTTGCTGGAACATGGCAGTATCCAAATATTCAGATGATGAAAT 720
DB 661 TGTGCGTTAAATGTTGCTGGAACATGGCAGTATCCAAATATTCAGATGATGAAAT 720
QY 721 ACCACTGTGCACCTACGCTATCTATTAATGAATTAATGATGATGATGATGATGATGAT 780
DB 721 ACCACTGTGCACCTACGCTATCTATTAATGAATTAATGATGATGATGATGATGATGAT 780
QY 781 TATGCTGCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 781 TATGCTGCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAATAATTTTATCAAGAAAAGGAAATTTAATGCA 900
DB 841 CATGAGCAAAAACAGCAAGTGTGAATAATTTTATCAAGAAAAGGAAATTTAATGCA 900
QY 901 CTGATGATATGAGAGAGTCTCTCATACCTGCTGATGCTGATGATGATGATGATGATGAT 960
DB 901 CTGATGATATGAGAGAGTCTCTCATACCTGCTGATGCTGATGATGATGATGATGATGAT 960
QY 961 GTGAGCTTCTACTGTGAGCAAAATATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
DB 961 GTGAGCTTCTACTGTGAGCAAAATATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1021 GCCAGAGATGATGCTGTTTCTAGTATCATCATGTAATTTGCCAGTACTTTCGATAC 1080
DB 1021 GCCAGAGATGATGCTGTTTCTAGTATCATCATGTAATTTGCCAGTACTTTCGATAC 1080
QY 1081 AAAGAAAAACAGATGCTAAATAATCTCTTCTGAAAACAGCAATTCAGAAAGACTTAAAG 1140
DB 1081 AAAGAAAAACAGATGCTAAATAATCTCTTCTGAAAACAGCAATTCAGAAAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGTCAAAAGGTCAAAAGGCAAGTGAATTAATGACCCAGAGAAA 1200
DB 1141 CTGACATCAGAGAGAGTCAAAAGGTCAAAAGGCAAGTGAATTAATGACCCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGATGATGATGATGATGATGATGATGATGAT 1260
DB 1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 1261 AAGCATGAAGTAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
DB 1261 AAGCATGAAGTAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
QY 1321 AATGCTATATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1380
DB 1321 AATGCTATATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1380
QY 1381 CTTGACACAGAAATGAAAGTATCACAGAAATTTGCAATTAATTAATTAATTAATTAATTAAT 1440
DB 1381 CTTGACACAGAAATGAAAGTATCACAGAAATTTGCAATTAATTAATTAATTAATTAATTAAT 1440
QY 1441 AAACAGATGCCAAATAATCTCTTCTGAAAACAGCAACCCAGAACAGCTTAAAGCTGACA 1500
DB 1441 AAACAGATGCCAAATAATCTCTTCTGAAAACAGCAACCCAGAACAGCTTAAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGTACAAAGGCTTGAAGGAGAGTGAATAATGAGGAGGAGGAGGAGGAGGAGGAG 1560
DB 1501 TCAGAGAGAGAGTACAAAGGCTTGAAGGAGAGTGAATAATGAGGAGGAGGAGGAGGAGGAGGAG 1560


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QY 841 CATGACCAAAAAACGACAGTCTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
   |||
Db 841 CATGACCAAAAAACGACAGTCTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
QY 901 CTGGATAGATATGGAAGGACTGCTCATCTCTGCTGATGTTGTGTGATAGACAAGTATA 960
   |||
Db 901 CTGGATAGATATGGAAGGACTGCTCATCTCTGCTGATGTTGTGTGATAGACAAGTATA 960
QY 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTCTCAAGATCATCTGAGACAGAG 1020
   |||
Db 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTCTCTCAAGATCATCTGAGACAGAG 1020
QY 1021 GCCAGAGATGATGCTGTTCTAGTCATCATGATTAATTTGCCAGTACTTCTGACTAC 1080
   |||
Db 1021 GCCAGAGATGATGCTGTTCTAGTCATCATGATTAATTTGCCAGTACTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAAAATCTCTGAAAAACAGCAATCGACAAACAGCTPAAAG 1140
   |||
Db 1081 AAGAAAAACAGATGCTAAAAATCTCTGAAAAACAGCAATCGACAAACAGCTPAAAG 1140
QY 1141 CTGACATCAGAGGAGAGTGCACAAAGGTTCAAGGCGAGTAAATAGCCAGAGAGAA 1200
   |||
Db 1141 CTGACATCAGAGGAGAGTGCACAAAGGTTCAAGGCGAGTAAATAGCCAGAGAGAA 1200
QY 1201 ATGCTCAAGAACCCAGAAATAAATAGAGATGATAGAGAGTTGAAGAAATGAAG 1260
   |||
Db 1201 ATGCTCAAGAACCCAGAAATAAATAGAGATGATAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AACGATGAAGATATATGTTGGGATTAATGAAAAACCTGCTAATGGTGTCACTGCGGC 1320
   |||
Db 1261 AACGATGAAGATATATGTTGGGATTAATGAAAAACCTGCTAATGGTGTCACTGCGGC 1320
QY 1321 AATGCTGATTAATGATTAATCTCTCAAGAGAGAGCAACCTGAAATACAGCAATTT 1380
   |||
Db 1321 AATGCTGATTAATGATTAATCTCTCAAGAGAGAGCAACCTGAAATACAGCAATTT 1380
QY 1381 CCGACACAGCAAGAGTGAAGAGTATCACAGAAATTTGCGAATTTCTGACTACAAAGAA 1440
   |||
Db 1381 CCGACACAGCAAGAGTGAAGAGTATCACAGAAATTTGCGAATTTCTGACTACAAAGAA 1440
QY 1441 AAACATATGCCAAATATCTTCTGAAAAACAGCAACCCCAAAACAGCTTAAGCTGACA 1500
   |||
Db 1441 AAACATATGCCAAATATCTTCTGAAAAACAGCAACCCCAAAACAGCTTAAGCTGACA 1500
QY 1501 TCAGAGGAGAGTGCACAAAGGCTTGAAGGCGACGTAAGATGGCCAGAGAAAGATCT 1560
   |||
Db 1501 TCAGAGGAGAGTGCACAAAGGCTTGAAGGCGACGTAAGATGGCCAGAGAAAGATCT 1560
QY 1561 CAAGAACCCAGAAATAAATAGATGTTGATAGAGCTAGAAAAATTTTATGGCTATCGAA 1620
   |||
Db 1561 CAAGAACCCAGAAATAAATAGATGTTGATAGAGCTAGAAAAATTTTATGGCTATCGAA 1620
QY 1621 GAATATGAAGAGACGGAATCTACTCATGTGGGATTCGCCAATAACCGATTAATGGTCC 1680
   |||
Db 1621 GAATATGAAGAGACGGAATCTACTCATGTGGGATTCGCCAATAACCGATTAATGGTCC 1680
QY 1681 ACTGCTGGCAATGATGATGATTAATCTCTCAAGAGAGAGCAACCTGAAAGC 1740
   |||
Db 1681 ACTGCTGGCAATGATGATGATTAATCTCTCAAGAGAGAGCAACCTGAAAGC 1740
QY 1741 CAGCAATTTCTTGACACTGAGAAATGAAGAGTATCACAGTACAGCAACAAATGATCTACG 1800
   |||
Db 1741 CAGCAATTTCTTGACACTGAGAAATGAAGAGTATCACAGTACAGCAACAAATGATCTACG 1800
QY 1801 AACCAATTTTGTGAAGAACGAACTGGAATTTACACATGAGATTCGATTCATGAA 1860
   |||
Db 1801 AACCAATTTTGTGAAGAACGAACTGGAATTTACACATGAGATTCGATTCATGAA 1860
QY 1861 GAAAAAGAGATAGAGTGTGAAAAAATGAATTCAGCTTCTCTTAACTTGAAGAA 1920
   |||
Db 1861 GAAAAAGAGATAGAGTGTGAAAAAATGAATTCAGCTTCTCTTAACTTGAAGAA 1920
QY 1921 GAAAAAGACATCTTGATGAAAAATAGTACGTTGCGGGAAGAAATTGCCATGCTAAGACTG 1980

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Db 1921 GAAAAAGACATCTTGCTGAAAAATAGTACCTTCGGGAATAAATTTGCCATGCTAAGACTG 1980
QY 1981 GAGCTAGACACAAATGAAACATCAGAGCCAGCTAAAAAAGAGAGAGAGAGAGAGAGAGAG 2040
   |||
Db 1981 GAGCTAGACACAAATGAAACATCAGAGCCAGCTAAAAAAGAGAGAGAGAGAGAGAGAGAG 2040

RESULT 6
AAH02781
ID AAH02781 standard; cDNA; 2040 BP.
XX
AC AAH02781;
XX
DT 14-JUN-2001 (first entry)
XX
DE Prostate tumour antigen determined cDNA splice variant of B305D #10.
XX
KW Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
KW prostate cancer; immunogenic; cytostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200125272-A2.
XX
PD 12-APR-2001.
XX
PF 04-OCT-2000; 2000MO-US27464.
XX
PR 04-OCT-1999; 99US-0157455.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Skelky YAW, Reed SG, Cheever MA;
XX
DR WPI; 2001-245062/25.
XX
DR P-PSDB; AAB74817.
XX
PT Prostate specific protein and its encoding polynucleotide, useful for
PT the treatment and diagnosis of prostate cancer -
XX
PS Claim 50; Page 233; 276pp; English.
XX
CC The present invention describes an isolated polypeptide (I) comprising
CC at least an immunogenic portion of a prostate tumour antigen protein or
CC its variant. (I) have cytostatic activity and can be used in vaccine
CC production. (I), prostate tumour antigen polynucleotides, an antigen
CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
CC pharmaceutical composition containing (I) are useful for inhibiting the
CC development of cancer in a patient. Antibodies specific for prostate
CC specific proteins and oligonucleotides that hybridise to a
CC polynucleotide that encodes a prostate specific protein are useful
CC for detecting the presence or absence of a cancer or monitoring the
CC progression the progression of a cancer, especially prostate cancer.
CC AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences
CC used in the exemplification of the present invention.
XX
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 other;

Query Match 100.0%; Score 2040; DB 22; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGTTGAGTTGATTCATGCGGCGTCCCTCTGTAAGAAAGCCATTTGGTCTC 60
   |||
Db 1 ATGCTGTTGAGTTGATTCATGCGGCGTCCCTCTCTTCTGTAAGAAAGCCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTCTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
   |||
Db 61 AGGAGCAAGATGGGCAAGTGGTCTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
QY 121 AGCAAGCTGGCACTTCTGAGACACGACGACTCTGCTGTGAAGACATCTCAGAGAGCAAG 180
   |||

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Db 121 AGCAACGTGGGCACTTGTGAGACACGACGACTGCTGATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAATGGTGGCGCCACTGCTCCCTGCTGAGGGGAGGTGCAAGCAACGCTG 240
Db 181 ATGGGCAATGGTGGCGCCACTGCTCCCTGCTGAGGGGAGGTGCAAGCAACGCTG 240
QY 241 GCGGCTTGTGAGACACGACACTGCTGATGAAGACACTCAGAAAGATGGGCAAG 300
Db 241 GCGGCTTGTGAGACACGACACTGCTGATGAAGACACTCAGAAAGATGGGCAAG 300
QY 301 TGGTGTGCTGCTGCTCCCTGCTGCTGAGGGGAGCGGCAAGCAAGGTGGGCGCTGG 360
Db 301 TGGTGTGCTGCTGCTCCCTGCTGCTGAGGGGAGCGGCAAGCAAGGTGGGCGCTGG 360
QY 361 GGAGACTAGATGACAGTCCCTTCATGAGCCAGGTACCAGTCCGCTGAGAAAGATCTG 420
Db 361 GGAGACTAGATGACAGTCCCTTCATGAGCCAGGTACCAGTCCGCTGAGAAAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGTTGGGGTAAAGTCCCGAAGAAAGATCTCATGCTATG 480
Db 421 GACAAGCTCCACAGAGCTGCTGTTGGGGTAAAGTCCCGAAGAAAGATCTCATGCTATG 480
QY 481 CTCAGGAGACACTGACGTGAACAAGAAAGCAAGCAAGAGAGACTGCTTACATCTGGCC 540
Db 481 CTCAGGAGACACTGACGTGAACAAGAAAGCAAGCAAGAGAGACTGCTTACATCTGGCC 540
QY 541 TGTGCCAATGGGAATTCACAAGTACTAAACATCTGCTGAGACAGACGATGCTAACTAAT 600
Db 541 TGTGCCAATGGGAATTCACAAGTACTAAACATCTGCTGAGACAGACGATGCTAACTAAT 600
QY 601 GTCTCTTGACAAACAAAAGAGAGACAGCTGATTAAGCGCGTACAAATGCCAGAAATGAA 660
Db 601 GTCTCTTGACAAACAAAAGAGAGACAGCTGATTAAGCGCGTACAAATGCCAGAAATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGGGACTGATCCAAATATTCACAGATGATGGAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGGGACTGATCCAAATATTCACAGATGATGGAAT 720
QY 721 ACCACTCTGACACTGACGCTATCTATATGAAGATTAATTAAGGCCAAAGCAGCTGCTTA 780
Db 721 ACCACTCTGACACTGACGCTATCTATATGAAGATTAATTAAGGCCAAAGCAGCTGCTTA 780
QY 781 TATGCTGCTGATATCGAATCAAAAAACAAGCATGGCTCACAACGCTGTTACTTGGTGA 840
Db 781 TATGCTGCTGATATCGAATCAAAAAACAAGCATGGCTCACAACGCTGTTACTTGGTGA 840
QY 841 CATGAGCAAAAAACAGCAAGTCTGGAATTTTATATCAAGAAAAAGCGAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTCTGGAATTTTATATCAAGAAAAAGCGAATTTAAATGCA 900
QY 901 CTGGAATAGATATGAAGAGCTGCTCATACTTGTGATGTTGTGGATCAGCAAGTATA 960
Db 901 CTGGAATAGATATGAAGAGCTGCTCATACTTGTGATGTTGTGGATCAGCAAGTATA 960
QY 961 GTACAGCTTCTACTTGAGCAAAAAATATGATGATCTTCAAGATCTATCTGGACAGAG 1020
Db 961 GTACAGCTTCTACTTGAGCAAAAAATATGATGATCTTCAAGATCTATCTGGACAGAG 1020
QY 1021 GCCAGAGAGTATGCTGTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGAGTATGCTGTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
QY 1081 AAAAGAAAAACAGATGCTAAAAATCTTCTGAAACAGCAATCCAGAACAGACTTAAAG 1140
Db 1081 AAAAGAAAAACAGATGCTAAAAATCTTCTGAAACAGCAATCCAGAACAGACTTAAAG 1140
QY 1141 CTGACATCTAGAGAAAGTCCACAAAGGTTCAAAAGCGAGTGAAGAAATGCCAGAGAAA 1200
Db 1141 CTGACATCTAGAGAAAGTCCACAAAGGTTCAAAAGCGAGTGAAGAAATGCCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATAAGATGATGATAGAGAGGTTGAAGAAAGATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAGAAATTAATAAGATGATGATAGAGAGGTTGAAGAAAGATGAAG 1260

QY 1261 AAGCATGAAAGTAAATATGNGGGATTACTAGAAAACCTGACTAATGTTGCTACTGCTGGC 1320
Db 1261 AAGCATGAAAGTAAATATGNGGGATTACTAGAAAACCTGACTAATGTTGCTACTGCTGGC 1320
QY 1321 AATGCTGATTAATGATTAATTTCTTCAAGGAAAGAGCAGAAACACCTGAAATACGAATTT 1380
Db 1321 AATGCTGATTAATGATTAATTTCTTCAAGGAAAGAGCAGAAACACCTGAAATACGAATTT 1380
QY 1381 CCTGACACGAAAGTAAAGATATCACAGAAATTTGCGAATTTAGTTCTGACTACAAAGAA 1440
Db 1381 CCTGACACGAAAGTAAAGATATCACAGAAATTTGCGAATTTAGTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAATATGCTTCTGAAAACAGCAACCCAGAAACAAACTTAAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATATGCTTCTGAAAACAGCAACCCAGAAACAAACTTAAAGCTGACA 1500
QY 1501 TCAGAGGAAGAGTCCACAAAGGCTTGAAGGCGAGTGAAGAAATGGCCAGAGAAAGATCT 1560
Db 1501 TCAGAGGAAGAGTCCACAAAGGCTTGAAGGCGAGTGAAGAAATGGCCAGAGAAAGATCT 1560
QY 1561 CAAGAACCGAAATTAATAAGATGATGATAGAGACTAGAAAATTTTATGCTATCGAA 1620
Db 1561 CAAGAACCGAAATTAATAAGATGATGATAGAGACTAGAAAATTTTATGCTATCGAA 1620
QY 1621 GAAATGAAGACGAGGAGTACTCATGTCGGATTGCCGAAAACCTGACTAATGGTGGC 1680
Db 1621 GAAATGAAGACGAGGAGTACTCATGTCGGATTGCCGAAAACCTGACTAATGGTGGC 1680
QY 1681 ACTGCTGGCAATGATGATGATGATTAATTTCCCAAGGAAAGAGCAACCTGAAAGC 1740
Db 1681 ACTGCTGGCAATGATGATGATGATTAATTTCCCAAGGAAAGAGCAACCTGAAAGC 1740
QY 1741 CAGCAATTTCTGACACTGGAATGAAGATATCACAGTGCAGAACAAATGATACTCAG 1800
Db 1741 CAGCAATTTCTGACACTGGAATGAAGATATCACAGTGCAGAACAAATGATACTCAG 1800
QY 1801 AAGCAATTTTGTGAACACGAACACTGGAAATTTACAGATGATGATGATGATGATGAA 1860
Db 1801 AAGCAATTTTGTGAACACGAACACTGGAAATTTACAGATGATGATGATGATGATGAA 1860
QY 1861 GAAAGCAGATGAAAGTGTGTAAGAAAAATGAAATTTCTGAGCTTCTCTAGTTGAAGAA 1920
Db 1861 GAAAGCAGATGAAAGTGTGTAAGAAAAATGAAATTTCTGAGCTTCTCTAGTTGAAGAA 1920
QY 1921 GAAAAAGACATCTTGCATGAAATTAATGATGATGATGATGATGATGATGATGATGATG 1980
Db 1921 GAAAAAGACATCTTGCATGAAATTAATGATGATGATGATGATGATGATGATGATGATG 1980
QY 1981 GAGCTAGACCAATGAAGCAATCTGAGCCAGCTAAAAAAGAAAAAAGAAAAA 2040
Db 1981 GAGCTAGACCAATGAAGCAATCTGAGCCAGCTAAAAAAGAAAAAAGAAAAA 2040

RESULT 7
ID ABL95180 standard; cDNA; 2040 BP.
XX
AC ABL95180;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human B305D splice variant cDNA sequence SBO ID NO 375.
XX
KW Human; cancer; prostate cancer; vaccine; cytosolic; immunostimulant;
XX gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US200202248-A1.
XX
PD 21-FEB-2002.
XX

PF 12-JAN-2001; 200105-0759143.
XX 25-FEB-1997; 9705-0806099.
PR 01-AUG-1997; 9705-0904804.
PR 09-FEB-1998; 9805-0020956.
PR 25-FEB-1998; 9805-0030607.
PR 14-JUL-1998; 9805-0115453.
PR 23-SEP-1998; 9805-0159812.
PR 15-JAN-1999; 9905-0232149.
PR 09-APR-1999; 9905-0288946.
PR 13-JUL-1999; 9905-0352616.
PR 12-NOV-1999; 9905-0439313.
PR 18-NOV-1999; 9905-0443686.
PR 14-JAN-2000; 200005-0483672.
PR 27-MAR-2000; 200005-0536857.
PR 09-MAY-2000; 200005-0568100.
PR 12-MAY-2000; 200005-0570737.
PR 13-JUN-2000; 200005-0593793.
PR 27-JUN-2000; 200005-0605783.
PR 10-AUG-2000; 200005-0636215.
PR 29-AUG-2000; 200005-0651236.
PR 06-SEP-2000; 200005-0657279.
PR 02-OCT-2000; 200005-0679426.
PR 10-OCT-2000; 200005-0685166.
XX (XUJ/) XU J.
PA (DIL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX WPI; 2002-255649/30.
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer -
XX
PS Claim 1; SEQ ID NO 375; 87bp; English.
XX The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a CDNA
CC described in the invention.
XX
SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 other;
Query Match 100.0%; Score 2040; DB 24; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 AGCAAGTGGGCACTTCTGGAGACGACGACTCTGTATGAAGACTCAGGACAAG 180
DB 121 AGCAACGCGGGCACTTCTGGAGACGACGACACTCTGTATGAAGACTCAGGACAAG 180
QY 181 ATGGGCAAGTGGTCCCGCACTGCTTCCCTGCTGACAGGGGAGTGGCAAGCACTG 240
DB 181 ATGGGCAAGTGGTCCCGCACTGCTTCCCTGCTGACAGGGGAGTGGCAAGCACTG 240
QY 241 GGGCTTCTGGAGACCAAGACGACTCTGTATGAAGACTCAGGACAAGTGGGACAAG 300
DB 241 GGGCTTCTGGAGACCAAGACGACTCTGTATGAAGACTCAGGACAAGTGGGACAAG 300
QY 301 TGGTGTGCGCACTCTTCCCTGCTGACAGGGGAGCGGCAAGAGTGGCGCTTGG 360
DB 301 TGGTGTGCGCACTCTTCCCTGCTGACAGGGGAGCGGCAAGAGTGGCGCTTGG 360
QY 361 GGAGACTACGATGACAGTGCCTTCATGAGGCCAGTACACGCTCCGTGGAAGATCTG 420
DB 361 GGAGACTACGATGACAGTGCCTTCATGAGGCCAGTACACGCTCCGTGGAAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGGTGGGTAAATGCCCAAGAAAGATCTCATGTCATG 480
DB 421 GACAAGCTCCACAGAGCTGCTGGTGGGTAAATGCCCAAGAAAGATCTCATGTCATG 480
QY 481 CTCAGGCACTGACGTGACAAAGAGGACAAAGCAAGAAAGAGACTGCTTACATCTGGCC 540
DB 481 CTCAGGCACTGACGTGACAAAGAGGACAAAGCAAGAAAGAGACTGCTTACATCTGGCC 540
QY 541 TGTGCCAATGGGAATTCAGAAATAGTAAACTCTGCTGACAGAGATGCAACTTAAT 600
DB 541 TGTGCCAATGGGAATTCAGAAATAGTAAACTCTGCTGACAGAGATGCAACTTAAT 600
QY 601 GTCTTGAACAACAAAGAGGACGCTGTATGAAGGCCGTACATGCGAGGAAGATGAA 660
DB 601 GTCTTGAACAACAAAGAGGACGCTGTATGAAGGCCGTACATGCGAGGAAGATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGACGACTGATCCAAATATTCAGATGATGAAAT 720
DB 661 TGTGCGTTAATGTTGCTGGAACATGACGACTGATCCAAATATTCAGATGATGAAAT 720
QY 721 ACCACTGTGACACTACGCTATCTATATGAAGATTAATGATGATGATGATGATGAT 780
DB 721 ACCACTGTGACACTACGCTATCTATATGAAGATTAATGATGATGATGATGATGAT 780
QY 781 TATGCTGCTGATATGCAATCAAAAACAGCATGGCCCTCACACCACTGTATGATGTA 840
DB 781 TATGCTGCTGATATGCAATCAAAAACAGCATGGCCCTCACACCACTGTATGATGTA 840
QY 841 CATGAGCAAAAACAGCAAGTCTGTAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
DB 841 CATGAGCAAAAACAGCAAGTCTGTAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATATGATATGGAAGAGCTGCTCATACTCTGTATGTTGGATCGCAAGATTA 960
DB 901 CTGATATGATATGGAAGAGCTGCTCATACTCTGTATGTTGGATCGCAAGATTA 960
QY 961 GTGAGCTTCTACTTGAACAAATATGATGATCTTCTCAAGATCTATCTGGACAGCG 1020
DB 961 GTGAGCTTCTACTTGAACAAATATGATGATCTTCTCAAGATCTATCTGGACAGCG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCAATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCAATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
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DB 1081 AAAGAAAAACAGATGCTTAAATATCTTCTGAAAAACGCAATCCAGAAAGACTTAAAG 1140
QY 1141 CTGACATCAAGAGGAAGTCAAAAGTTCAGAAAGCGAGTGAATATGACGCGCAGAGAAA 1200
DB 1141 CTGACATCAAGAGGAAGTCAAAAGTTCAGAAAGCGAGTGAATATGACGCGCAGAGAAA 1200

QY 481 CTCAGGACACTGACGTGAACAGAGACAAAGAGAGACTGCTCTACATCTGGCC 540
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Db 481 CTCAGGACACTGACGTGAACAGAGACAAAGAGAGACTGCTCTACATCTGGCC 540
QY 541 TCTCCCAATGGGAATTGAGAAGTGTAAACTCTGCTGGACAGACGATGTCAACTTAAT 600
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Db 541 TCTCCCAATGGGAATTGAGAAGTGTAAACTCTGCTGGACAGACGATGTCAACTTAAT 600
QY 601 GTCTTGCACAAACAAAGAGACAGCTGTGTAAGGCGCCGACAAATGCCAGGAATGAA 660
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Db 601 GTCTTGCACAAACAAAGAGAGACAGCTGTGTAAGGCGCCGACAAATGCCAGGAATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAAACATGGCATGATCCAAATATTTCCAGATGATGAAAT 720
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Db 661 TGTGCGTTAATGTTGCTGGAAACATGGCATGATCCAAATATTTCCAGATGATGAAAT 720
QY 721 ACCACTCTGCACCTACGCTATCTATATGAGATTAATTAATGGCCAAAGCACTGCTTA 780
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Db 721 ACCACTCTGCACCTACGCTATCTATATGAGATTAATTAATGGCCAAAGCACTGCTTA 780
QY 781 TATGCTGCTGATTCGAATCAAAAACAGCATGGCCCTCACACCACTGTACTTGCTTA 840
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Db 781 TATGCTGCTGATTCGAATCAAAAACAGCATGGCCCTCACACCACTGTACTTGCTTA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
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Db 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
QY 901 CTGATATGATATGGAAGACGCTCTCATCTTCTGTATGTGTGGATCGACAGATTA 960
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QY 1081 AAAAAGAAAAAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAAACAGACTTAAG 1140
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Db 1081 AAAAAGAAAAAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGAAAGTCTCAAAAGTTCAAGAGCAGTGAATATAGCCAGCCAGAGAA 1200
|||||
Db 1141 CTGACATCAGAGAAAGTCTCAAAAGTTCAAGAGCAGTGAATATAGCCAGCCAGAGAA 1200
QY 1201 ATGTCTCAGAACCAAGAAATTAATTAAGATGTGATAGAGAGTTGAAGAAATGAG 1260
|||||
Db 1201 ATGTCTCAGAACCAAGAAATTAATTAAGATGTGATAGAGAGTTGAAGAAATGAG 1260
QY 1261 AAGCATGAAGTATATATGTTGGGATTAATGAAAACTGACTAATGGTGTACTGCTGGC 1320
|||||
Db 1261 AAGCATGAAGTATATATGTTGGGATTAATGAAAACTGACTAATGGTGTACTGCTGGC 1320
QY 1321 AATGCTATATATGATTAATTTCTCTCAAGAGAGACAGAACCTGGAATAATCAGCAATTT 1380
|||||
Db 1321 AATGCTATATATGATTAATTTCTCTCAAGAGAGACAGAACCTGGAATAATCAGCAATTT 1380
QY 1381 CTTGACAAACGAAGTGAAGACTATCAGAAATTTGCGAATTAAGTTTCTGACTACAAAGAA 1440
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Db 1381 CTTGACAAACGAAGTGAAGACTATCAGAAATTTGCGAATTAAGTTTCTGACTACAAAGAA 1440
QY 1441 AAAACAGATGCCAAATACTCTTCTGAAAAACGCAACCCAGACAGACTTAAGCTGACA 1500
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Db 1441 AAAACAGATGCCAAATACTCTTCTGAAAAACGCAACCCAGACAGACTTAAGCTGACA 1500
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Db 1501 TCAGAGGAAGATGCACAAAGGCTTGAGGCGAGTAAAAATGGCCAGCAGAGAAAAAGATCT 1560

QY 1561 CAAAGACCAGAAATTAATTAAGATGTGATAGAGAGCTAGAAAAATTTTATGGCTATCGAA 1620
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Db 1561 CAAAGACCAGAAATTAATTAAGATGTGATAGAGAGCTAGAAAAATTTTATGGCTATCGAA 1620
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Db 1621 GAATTAAGAAAGCAGGAAAGTCTCATGTGCGATTTCCAGAAACCTGACTAATAGTGCC 1680
QY 1681 ACTGCTGGCAATGGTATGATGATTAATTCCTCAAGAGAGACAGAACACTGAAAGC 1740
|||||
Db 1681 ACTGCTGGCAATGGTATGATGATTAATTCCTCAAGAGAGAGACAGAACACTGAAAGC 1740
QY 1741 CAGCAATTTCTCTGACACTGAGATGAAGATATACAGTGAAGCAAAATGATATCTAG 1800
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Db 1741 CAGCAATTTCTCTGACACTGAGATGAAGATATACAGTGAAGCAAAATGATATCTAG 1800
QY 1801 AAGCAATTTTGTGAAGAACACAGACACTGGAATATTACAGATGAGATTCGATCATGAA 1860
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Db 1801 AAGCAATTTTGTGAAGAACACAGACACTGGAATATTACAGATGAGATTCGATCATGAA 1860
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Db 1861 GAAAGCAGATAGAAGTGTGAAAAATGAATCTGAGCTTCTCTTACTGTTAGAGAA 1920
QY 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTGCGGAGAGAAATTCGATCTAAGACTG 1980
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Db 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTGCGGAGAGAAATTCGATCTAAGACTG 1980
QY 1981 GAGCTAGACAAATGAAGAACATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAA 2040
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Db 1981 GAGCTAGACAAATGAAGAACATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAA 2040

RESULT 9

AAA06600

ID AAA06600 standard; cDNA: 2040 BP.

AC AAA06600;

DT 13-JUN-2000 (first entry)

XX

DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:375.

XX

KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;

XX

KW immunogenic; cyostatic; vaccine; ss.

XX

OS Homo sapiens.

XX

FN W0200004149-A2.

XX

PD 27-JAN-2000.

XX

PF 14-JUL-1999; 99WO-US15838.

XX

PR 14-JUL-1998; 98US-0115453.

XX

PR 14-JUL-1998; 98US-0116134.

XX

PR 23-SEP-1998; 98US-0159812.

XX

PR 15-JAN-1999; 99US-0232149.

XX

PR 09-APR-1999; 99US-0288946.

XX

PA (CORI-) CORIXA CORP.

XX

PI Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;

XX

DR WPL; 2000-171268/15.

XX

PT New polypeptide useful for treating and diagnosing prostate cancer

XX

PS Claim 50; Page 223-224; 263pp; English.

CC The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumour protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC the polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AA06241 to AA06591 and
CC AA08200 to AA08202 represent sequences used in the exemplification of
CC the present invention.

xx Sequence 2040 BP: 716 A; 393 C; 500 G; 431 T; 0 other:

Query Match 97.5%; Score 1989; DB 21; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2039; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 ATGGGTGTTGAGGTGATTCATGCGGCTGCTCTCTGTGAAGAAGCATTTGGTCTC 60
Db 1 ATGGGTGTTGAGGTGATTCATGCGGCTGCTCTCTGTGAAGAAGCATTTGGTCTC 60
OY 61 AGGAGCAAGATGGGCAAGTGTGTCGCGTCTCCCTGCTGAGGAGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGTGTCGCGTCTCCCTGCTGAGGAGAGCGGCAAG 120
OY 121 AGCAACGTGGGCACTTCTGGAGACCAAGACGACTGCTGTAGAAGACACTGAGGCAAG 180
Db 121 AGCAACGTGGGCACTTCTGGAGACCAAGACGACTGCTGTAGAAGACACTGAGGCAAG 180
OY 181 ATGGCAAGTGTGCGCGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAACGTG 240
Db 181 ATGGCAAGTGTGCGCGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAACGTG 240
OY 241 GCGCGTCTGGAGACCAAGCACTGCTGTATGAAGACACTGAGAACCAAGATGGGCAAG 300
Db 241 GCGCGTCTGGAGACCAAGCACTGCTGTATGAAGACACTGAGAACCAAGATGGGCAAG 300
OY 301 TGGTCTGCTGCTGCTTCCCTGCTGAGGGGAGCGGCAAGCAAGTGGCGCTTGG 360
Db 301 TGGTCTGCTGCTGCTTCCCTGCTGAGGGGAGCGGCAAGCAAGTGGCGCTTGG 360
OY 361 GGAGACTGAGATGACAGTGCCTTTCATGAGGCCAGGTACCAAGTCCGTTGAGAAAGTCTG 420
Db 361 GGAGACTGAGATGACAGTGCCTTTCATGAGGCCAGGTACCAAGTCCGTTGAGAAAGTCTG 420
OY 421 GACAAAGTCCACAGAGTGCCTGCTGAGGTAAGTCCCGAAGAAAGATCTCATCTCATG 480
Db 421 GACAAAGTCCACAGAGTGCCTGCTGAGGTAAGTCCCGAAGAAAGATCTCATCTCATG 480
OY 481 CTCAGGAGACTGACGTGTAACAAGAACAAAGAGAGAGTCTCTACATCTGGCC 540
Db 481 CTCAGGAGACTGACGTGTAACAAGAACAAAGAGAGAGTCTCTACATCTGGCC 540
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Db 541 TCTGCAATGGGAATTCAGAAAGTAAACCTCCTGAGAGAGAGATGCAACTTAT 600
OY 601 GTCTCTGACAAACAAAAGAGACAGCTGTATGAAGGCGGTACATGCGCAGGAAGATGA 660
Db 601 GTCTCTGACAAACAAAAGAGAGACAGCTGTATGAAGGCGGTACATGCGCAGGAAGATGA 660
OY 661 TGTGCGTTAATGTCTGAGACATGGCACTGATCCAATATTCCAGATGAGTGAAT 720
Db 661 TGTGCGTTAATGTCTGAGACATGGCACTGATCCAATATTCCAGATGAGTGAAT 720
OY 721 ACCACTCTGCACTAGCTATCTATATGAAGATTAATTAATGGCAAGCACTGCTCTTA 780
Db 721 ACCACTCTGCACTAGCTATCTATATGAAGATTAATTAATGGCAAGCACTGCTCTTA 780
OY 781 TATGCTGCTGATATGAATCAAAAAAACAAGCATGGCCTCACACCACTGTTACTTGTGTA 840
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Db 781 TATGCTGCTGATATGAATCAAAAAAACAAGCATGGCCTCACACCACTGTTACTTGTGTA 840
OY 841 CATGAGCAAAAACACAGAGTGTGAATTTTATATCAAGAAAAAGCGAATTTAATGCA 900
Db 841 CATGAGCAAAAACACAGAGTGTGAATTTTATATCAAGAAAAAGCGAATTTAATGCA 900
OY 901 CTGATATGATATGAAGAGCTGCTCATCTGCTGTATGTTGATCAGCAAGTATA 960
Db 901 CTGATATGATATGAAGAGCTGCTCATCTGCTGTATGTTGATCAGCAAGTATA 960
OY 961 GTGACCTTCTACTTGTAGCAAAATATGATATCTTCAAGATCTATCTGAGACAGC 1020
Db 961 GTGACCTTCTACTTGTAGCAAAATATGATATCTTCAAGATCTATCTGAGACAGC 1020
OY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATATGTAATTTGCCAGTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATATGTAATTTGCCAGTACTTCTGACTAC 1080
OY 1081 AAGAAAAACAGATGCTAAATATCTCTGAAACAGCAATCCGAACCAAGACTTAAG 1140
Db 1081 AAGAAAAACAGATGCTAAATATCTCTGAAACAGCAATCCGAACCAAGACTTAAG 1140
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Db 1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAAGCAGTGAATAAGCCAGCCAGAGAA 1200
OY 1201 ATGCTCAAGAACCAAAATTAATTAAGAGTGTATAGAGAGCTTGAAAGAAATGAAG 1260
Db 1201 ATGCTCAAGAACCAAAATTAATTAAGAGTGTATAGAGAGCTTGAAAGAAATGAAG 1260
OY 1261 AAGCATGAAGATTAATATGTTGGATTACTAGAAACCTGATTAAGTGTGCTGCTGGC 1320
Db 1261 AAGCATGAAGATTAATATGTTGGATTACTAGAAACCTGATTAAGTGTGCTGCTGGC 1320
OY 1321 AATGCTGATTAATGATTAATTCCTCAAAAGAGAGCAAGCACTGAAATACAGCAATT 1380
Db 1321 AATGCTGATTAATGATTAATTCCTCAAAAGAGAGCAAGCACTGAAATACAGCAATT 1380
OY 1381 CCTGACAAACGAAGTGAAGAGTATCACAGATTTGCGAATTAGTTTCTGACATCAAGAA 1440
Db 1381 CCTGACAAACGAAGTGAAGAGTATCACAGATTTGCGAATTAGTTTCTGACATCAAGAA 1440
OY 1441 AAACAGATCCAAATATCTCTGAAACACCAACCCGAACAAGACTTAAGCTGACA 1500
Db 1441 AAACAGATCCAAATATCTCTGAAACACCAACCCGAACAAGACTTAAGCTGACA 1500
OY 1501 TCAGAGAAAGACTCAACAAAGGCTTGAGGCACTGAAATATGCGCAGAGAGAAAGATCT 1560
Db 1501 TCAGAGAAAGACTCAACAAAGGCTTGAGGCACTGAAATATGCGCAGAGAGAAAGATCT 1560
OY 1561 CAAGAACCAAAATTAATTAAGAGTGTATAGAGCTTAGAAATTTTATGCTATCGAA 1620
Db 1561 CAAGAACCAAAATTAATTAAGAGTGTATAGAGCTTAGAAATTTTATGCTATCGAA 1620
OY 1621 GAAATGAAGAAACAGGAAGTCTCATGCGGATTCGCAAGAAACCTGACTAATGGTGC 1680
Db 1621 GAAATGAAGAAACAGGAAGTCTCATGCGGATTCGCAAGAAACCTGACTAATGGTGC 1680
OY 1681 ACTGCTGGCAATGCTGATGATGATTAATTCCTCCAAAGAGAGAGAGACACCTGAAGC 1740
Db 1681 ACTGCTGGCAATGCTGATGATGATTAATTCCTCCAAAGAGAGAGAGACACCTGAAGC 1740
OY 1741 CAGCAATTTCTGACACTGAGATGAGAGTATCACAGTGAACCAAAATATATCTCAG 1800
Db 1741 CAGCAATTTCTGACACTGAGATGAGAGTATCACAGTGAACCAAAATATATCTCAG 1800
OY 1801 AAGCAATTTTGAAGAACAGAACTGGAAATTAACAGATGAGATTCGATTCATGAA 1860
Db 1801 AAGCAATTTTGAAGAACAGAACTGGAAATTAACAGATGAGATTCGATTCATGAA 1860
OY 1861 GAAAGCAGATGAAGTGGTTGAAAAAATGAATTCGAGCTTCTTCTAGTTGAAGAA 1920
Db 1861 GAAAGCAGATGAAGTGGTTGAAAAAATGAATTCGAGCTTCTTCTAGTTGAAGAA 1920
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Db 1861 GAAAAGCAGATAGAGTGGTTGAAAAAATGTAATCTGAGCTTTCTTACTGTAGAAA 1920
QY 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTCGGGAGAAATTTGCCATGCTAAGACTG 1980
Db 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTCGGGAGAAATTTGCCATGCTAAGACTG 1980
QY 1981 GAGCTAGACACAATGAAACATCAGAGCCAGCTAATAAAAAAAAAAAAAAAAAAAAAA 2040
Db 1981 GAGCTAGACACAATGAAACATCAGAGCCAGCTAATAAAAAAAAAAAAAAAAAAAAAA 2040
RESULT 10
AAC81012
ID AAC81012 standard; cDNA; 2000 BP.
XX AAC81012;
AC
XX
DT 13-FEB-2001 (first entry)
XX
DE Human B1Agl antigen splice isoform B1Lc-8 cDNA.
XX
XX Human; breast tumour-specific antigen; cytostatic; vaccine;
KM breast cancer; B1Bgl; B1Agl; B15Agl; ss.
XX
OS Homo sapiens.
XX
PN W020061753-A2.
XX
PD 19-OCT-2000.
XX
PE 07-APR-2000; 2000MO-US09312.
XX
XX 09-APR-1999; 9905-0289198.
PR 28-OCT-1999; 9905-0429755.
PR 23-MAR-2000; 2000US-0534825.
XX
PA (CORI-) CORIXA CORP.
XX
PI Frudakis TN, Smith JM, Reed SG, Misher LE, Retter MW, Dillon DC;
XX
DR MPI: 2000-628403/60.
XX
P-PSDB: AAB28629.
XX
PT An isolated polypeptide comprising an immunogenic portion of a breast
PT tumor protein used for inhibiting the development of cancer, especially
PT breast cancer, and monitoring cancer progression in a patient -
XX
XX
PS Claim 4; Page 177-178; 187pp; English.
XX
XX The present sequence is given in a specification relating to compositions
CC and methods for the treatment and diagnosis of breast cancer. Nucleotide
CC sequences that are preferentially expressed in breast tumour tissue, and
CC the polypeptides encoded by such nucleotide sequences, are used in
CC compositions and vaccines to inhibit the development of cancer,
CC especially breast cancer. The progression of a cancer may be monitored by
CC carrying out detection of tumour-specific antigens at subsequent time
CC points and comparing the results from the different time points.
CC CD4+ and/or CD8+ T-Cells isolated from the cancer patient may be treated
CC with tumour-specific polypeptides, polynucleotides encoding the
CC polypeptides or antigen presenting cells expressing the polypeptides. The
CC cells are then administered to the patient to inhibit development of
CC cancer.
CC
XX
SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 other;

Query Match 76.0%; Score 1551; DB 21; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTAGGTTGATTCATGCGGCTCTCTGTGAAGAGCCATTGGCTC 60
Db 1 ATGGTGGTTAGGTTGATTCATGCGGCTCTCTGTGAAGAGCCATTGGCTC 60

QY 61 AGGAGCAAGATGGGCAAGTGGTCTGCCGTTCTTCCCTGCTGCAGGAGGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGGTCTGCCGTTCTTCCCTGCTGCAGGAGGAGCGGCAAG 120
QY 121 AGCAAGCTGGGCACTTGTGAGACCAAGAGACCTGCTGTGAAGACATCAGAGCAAG 180
Db 121 AGCAAGCTGGGCACTTGTGAGACCAAGAGACCTGCTGTGAAGACATCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGCAGGAGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGCAGGAGGAGTGGCAAGCAAGCTG 240
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Db 241 GGGCTTCTTGAGACCAAGAGCACTGCTGTATGAGACACTCAGAAACAAGATGGCAAG 300
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Db 301 TGGTGGTCCAGCTGCTTCCCTGCTGCAGGAGGAGGAGGAGCAAGATGGGCGCTGG 360
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Db 361 GGAGACTACGATGACAGATGCTTCATGAGAGCCAGGATACCGCTCGTGAGAGAAATCTG 420
QY 421 GACAAAGCTCCACAGAGCTGCTGCTGGTGGGTAAGTCCCAAGAAAGATCTCATCTCATG 480
Db 421 GACAAAGCTCCACAGAGCTGCTGCTGGTGGGTAAGTCCCAAGAAAGATCTCATCTCATG 480
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Db 541 TCTGCCAATGGGAATTCAGAAATGTAATGAAATCTGCTGAGACAGATGCTCAACTTAAT 600
QY 601 GTCCCTTGACACAAAAAGAGAGACAGCTGTATTAAGAGCCCTACAGAGCAAGATGAA 660
Db 601 GTCCCTTGACACAAAAAGAGAGAGAGCTGTATTAAGAGCCCTACAGAGCAAGATGAA 660
QY 661 TGTGCGTAAATGTTGCTGGAACATGGCATGATCCAAATTTCCAGATGATGGAAT 720
Db 661 TGTGCGTAAATGTTGCTGGAACATGGCATGATCCAAATTTCCAGATGATGGAAT 720
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Db 721 ACCACTGTGACACTACGCTATCTATTAATGAAGATTAATTAAGCAAGCAAGCTCTTA 780
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Db 781 TATGCTGCTGATATCGAATCAAAAAACACATGCGCTCACACCACTGTTACTTGGTGA 840
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Db 841 CATGAGCAAAAAACAGCAAGTCGTGAATTTTATATCAAGAAAAAGGAATTTAATGCA 900
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Db 961 GTACAGCTTCTACTTGAGCAAAATATTTGATGATCTTCTCAAGATCTATGTCAGAGAG 1020
QY 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTGTGACTAC 1080
Db 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTGTGACTAC 1080
QY 1081 AAGGAAAAACAGATGCTAAATAATCTCTTGAAGAACAGCAATCCAGAACAGACTTAAG 1140
Db 1081 AAGGAAAAACAGATGCTAAATAATCTCTTGAAGAACAGCAATCCAGAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCAAAAAGGTTCAAAAGCAGTAGTAATAATGCCCAGAGAGAA 1200

QY 781 TATGCTCTGATATCGAATCAAAAACAGCAGCGCTCACACAGCTGTTACTTGCTGTA 840
 DB 781 TATGCTCTGATATCGAATCAAAAACAGCAGCGCTCACACAGCTGTTACTTGCTGTA 840
 QY 841 CATGAGCAAAAACAGCAGCTGTAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
 DB 841 CATGAGCAAAAACAGCAGCTGTAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
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 DB 901 CTGATAGATATGAGAGAGCTGCTCTCATCTTCTGATGTTGTGATCAGCAAGTATA 960
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 DB 961 GTGAGCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATGCAAGAGC 1020
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 DB 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGCGGATCTTCTGACTAC 1080
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 DB 1141 CTGACATCAGAGAGAGCTCAAAAAGGTTCAAAAGCAGTGAATAATGACCCAGAGAAA 1200
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 DB 1261 AAGCATGAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
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 DB 1381 CCTGACAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
 QY 1441 AAACAGATGCAAAATCTCTTCTGAAAAACAGCAACCCAGAAAGACTTAAAGCTGACA 1500
 DB 1441 AAACAGATGCAAAATCTCTTCTGAAAAACAGCAACCCAGAAAGACTTAAAGCTGACA 1500
 QY 1501 TCAG 1551
 DB 1501 TCAG 1551

RESULT 12
 AAS63808
 ID AAS63808 standard; cDNA; 2000 BP.
 XX
 AC AAS63808;
 XX
 DT 29-JAN-2002 (first entry)
 XX
 DE Human prostate cDNA clone B305D splice variant #9.
 XX
 KM Human; prostate cancer; ss; cytosolic; immunostimulant; tumour.
 XX
 OS Homo sapiens.
 XX
 PN WO200173032-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001MO-US09919.

PR 27-MAR-2000; 2000US-0536857.
 PR 09-MAY-2000; 2000US-0568100.
 PR 12-MAY-2000; 2000US-0570737.
 PR 13-JUN-2000; 2000US-0593793.
 PR 27-JUN-2000; 2000US-0605783.
 PR 10-AUG-2000; 2000US-0636215.
 PR 29-AUG-2000; 2000US-0651236.
 PR 06-SEP-2000; 2000US-0657279.
 PR 02-OCT-2000; 2000US-0679426.
 PR 10-OCT-2000; 2000US-0685166.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
 DR WPI; 2001-639232/73.
 DR P-PSDB; AA069778.
 XX
 PT New human prostate-specific polypeptides and polynucleotides useful for
 PT the diagnosis and treatment of cancer, especially prostate cancer -
 PS Claim 1; Page 349-350; 579pp; English.
 XX
 PS The invention relates to isolated prostate-specific
 CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
 CC antibodies raised against the polypeptides (or antigenic epitopes
 CC derived from them) and antigen-presenting cells expressing the
 CC polypeptides. The antibodies are useful for detecting the presence of
 CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
 CC the antigen-presenting cells are useful for stimulating and/or expanding
 CC T cells specific for a tumour protein, and for inhibiting the development
 CC of cancer especially prostate cancer. Compositions comprising the
 CC polynucleotide and/or polypeptide are useful for stimulating an immune
 CC response, and for treating cancer. The oligonucleotide is useful for
 CC detecting cancer. The present sequence is a prostate specific
 CC polynucleotide of the invention.
 XX
 SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 other;

Query Match 76.0%; Score 1551; DB 22; Length 2000;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60
 DB 1 ATGCTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60
 QY 61 AGGAGCAAGATGAGCAAGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
 DB 61 AGGAGCAAGATGAGCAAGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
 QY 121 AGCAAGCTGGGCACTTCTGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
 DB 121 AGCAAGCTGGGCACTTCTGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
 QY 181 ATGAGCAAGTGGGCACTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 DB 181 ATGAGCAAGTGGGCACTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
 QY 241 GCGCTTCTGAGAGACAG 300
 DB 241 GCGCTTCTGAGAGACAG 300
 QY 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
 DB 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
 QY 361 GGAGACTAGAGATGAG 420
 DB 361 GGAGACTAGAGATGAG 420

OY	421	GACAGCTCCACAGAGCTGCTGGTGGGTTAAAGTCCCGAAGAGATCTATGCTCATG	480
Db	421	GACAGCTCCACAGAGCTGCTGGTGGGTTAAAGTCCCGAAGAGATCTATGCTCATG	480
OY	481	CTCAGGGACACTGACGTAACAAGAGGACCAAGGACGACGCTCTCATCTG	540
Db	481	CTCAGGGACACTGACGTAACAAGAGGACCAAGGACGACGCTCTCATCTG	540
OY	541	TCGCGCAATGGGAATTCAGAAAGTACTCTGCTGGAGACAGATGTCACCTTAAT	600
Db	541	TCGCGCAATGGGAATTCAGAAAGTACTCTGCTGGAGACAGATGTCACCTTAAT	600
OY	601	GTCTTACACACAAAAGAGGACGCTCTGATPAAGGCCGTACAAATGCCAGGAAGTAA	660
Db	601	GTCTTACACACAAAAGAGGACGCTCTGATPAAGGCCGTACAAATGCCAGGAAGTAA	660
OY	661	TGTGCGTTAATGTTGCGGAAACAATGGCACTGATCCAAATATCCAGATGATGGAAT	720
Db	661	TGTGCGTTAATGTTGCGGAAACAATGGCACTGATCCAAATATCCAGATGATGGAAT	720
OY	721	ACGACCTGTGCACTACGCTATCTATATGAAGATTAATTAATGGCCAAAGCACTGCTTA	780
Db	721	ACGACCTGTGCACTACGCTATCTATATGAAGATTAATTAATGGCCAAAGCACTGCTTA	780
OY	781	TATGGTCTGATATCGAATCAAAAACAAGCATGGCCTCACACCACTGTACTTGGTGA	840
Db	781	TATGGTCTGATATCGAATCAAAAACAAGCATGGCCTCACACCACTGTACTTGGTGA	840
OY	841	CATAGCAAAAACAGCAAGTCGTGAATTTTATATCAGAAAAAGCCAAATTTAAATGCA	900
Db	841	CATAGCAAAAACAGCAAGTCGTGAATTTTATATCAGAAAAAGCCAAATTTAAATGCA	900
OY	901	CTGAGATGATATGGAAGAGTGCCTCATACTGCTGTATGTTGGAATCAGCAAGTATA	960
Db	901	CTGAGATGATATGGAAGAGTGCCTCATACTGCTGTATGTTGGAATCAGCAAGTATA	960
OY	961	GTCAGCCTTACTTGAGCAAAATATTTGATGTATCTTCAAGATCTATCTGGACAGCG	1020
Db	961	GTCAGCCTTACTTGAGCAAAATATTTGATGTATCTTCAAGATCTATCTGGACAGCG	1020
OY	1021	GCCAGAGATAGCTGTTTCTTACTCATCATGTAATTTGGCAATTACTTTCTGACATC	1080
Db	1021	GCCAGAGATAGCTGTTTCTTACTCATCATGTAATTTGGCAATTACTTTCTGACATC	1080
OY	1081	AAAAAAAACAGATGCTAAAAATCTCTTCTGAAAACAGCAATCCAGAAAGCAACTTAAG	1140
Db	1081	AAAAAAAACAGATGCTAAAAATCTCTTCTGAAAACAGCAATCCAGAAAGCAACTTAAG	1140
OY	1141	CTGACATCAGAGGAAGATCACAAAGGTTCAAAAGGCAGTGAATAATAGCAGCCAGAGAA	1200
Db	1141	CTGACATCAGAGGAAGATCACAAAGGTTCAAAAGGCAGTGAATAATAGCAGCCAGAGAA	1200
OY	1201	ATGTCCTCAAGAACCAAAATTAATTAAGGATGGTGATAGAGAGTTGAAAGAAATGAG	1260
Db	1201	ATGTCCTCAAGAACCAAAATTAATTAAGGATGGTGATAGAGAGTTGAAAGAAATGAG	1260
OY	1261	AAGCATGAAGTAAATATGTGGGATTAAGTAAAGAAACCTGACATTAAGGTGCTACGCTGGC	1320
Db	1261	AAGCATGAAGTAAATATGTGGGATTAAGTAAAGAAACCTGACATTAAGGTGCTACGCTGGC	1320
OY	1321	AATGGTATATATGATTAATTTCTTCCAAAGGAGAGCAGAAACCTGAAATATCAGCAATTT	1380
Db	1321	AATGGTATATATGATTAATTTCTTCCAAAGGAGAGCAGAAACCTGAAATATCAGCAATTT	1380
OY	1381	CCTGACACAGAAAGTGAAGATATCACAAGATTTGGCAATTTAGTTCTGACACAAAGAA	1440
Db	1381	CCTGACACAGAAAGTGAAGATATCACAAGATTTGGCAATTTAGTTCTGACACAAAGAA	1440
OY	1441	AAACAGATGCCAAATATCTCTTCTGAAAACAGCAACCCGAGCAAGACTTAAAGTGACA	1500
Db	1441	AAACAGATGCCAAATATCTCTTCTGAAAACAGCAACCCGAGCAAGACTTAAAGTGACA	1500
OY	1501	TCACAGGAAGAGTCCACAAAGCTTTGAGGGCAGTGAATAATGGCCAGCCAGAG	1551

DB	1501	TGAGGAGGAAGATCTCACAAAGGCTTGAGGGCGACATGAAAAATGCCAGCCAGAG	1551
<p> </p>			
RESULT 13			
ID	AAH93715	standard; cDNA; 2000 BP.	
XX	AAH93715;		
XX	04-OCT-2001	(first entry)	
DE	Human prostate-specific cDNA sequence B305D splice variant #9.		
XX	Human; prostate cancer; prostate-specific; diagnosis; vaccine;		
KM	cytostatic; gene therapy; metastasis; ss.		
XX	Homo sapiens.		
OS	WO200151633-A2.		
XX	PN		
XX	PD		
XX	19-JUL-2001.		
PX	16-JAN-2001; 2001WO-US01574.		
PR	14-JAN-2000; 2000US-0483672.		
PA	(CORI-) CORIXA CORP.		
PI	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG,		
PI	Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skelly YAW;		
PI	Wang A, Meagher MJ;		
DR	WPI; 2001-425873/45.		
XX	New polynucleotide encoding a prostate-specific protein, for		
PT	diagnosing, monitoring and treating prostate cancer in a patient and		
PT	for use in vaccines -		
PS	Claim 1; Page 347-348; 543pp; English.		
XX	The present invention describes polynucleotide sequences (I) which encode		
CC	prostate-specific proteins (II). (I) and (II) have cytostatic activity,		
CC	and can be used in vaccine production and gene therapy. (I), (II),		
CC	antibodies to (II), fusion proteins comprising (II), and isolated		
CC	T cells prepared using (I) or (II) are used treat cancer in a patient.		
CC	(I) and the antibodies are also used in the detection of cancer in a		
CC	patient. The cancer that is diagnosed or treated is particularly		
CC	prostate cancer. (I) and (II) can be used in vaccines. The antibodies or		
CC	(I) can be used for monitoring the progression of cancer in a patient.		
CC	(I) and (II) can also be used to improve diagnostic and therapeutic		
CC	methods for prostate cancer. They can indicate the level of metastasis		
CC	as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to		
CC	AAH01318 represent polynucleotide and amino acid sequences used in the		
CC	exemplification of the present invention.		
XX	Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 other:		
SQ			
Query Match	76.0%; Score 1551; DB 22; Length 2000;		
Best Local Similarity	100.0%; Pred. No. 0;		
Matches 1551; Conservative	0; Mismatches 0; Indels 0; Gaps 0.0;		
OY	1 AAGGCGGTGAGTGCATTCATGCGCGGTGCTCTGTGAAGAAGCATTTGGTCTC	60	
DB	1 AAGGCGGTGAGTGCATTCATGCGCGGTGCTCTGTGAAGAAGCATTTGGTCTC	60	
OY	61 AGAGCAAGATGGCAAGTGATGCTCCCTTCCCTGCTGCAGAGACGGCAAG	120	
DB	61 AGAGCAAGATGGCAAGTGATGCTCCCTTCCCTGCTGCAGAGACGGCAAG	120	
OY	121 AGCAAAGTGGGACATTCTTGAGACCAGCAGACTCTGTATGAAGACACTCAGAGCAAG	180	
DB	121 AGCAAAGTGGGACATTCTTGAGACCAGCAGACTCTGTATGAAGACACTCAGAGCAAG	180	

OY	181	ATGGGCAAGTGTGTCCGCCCACTGCTTCCCTGCTGCAAGGGGAGTGTGCAGACGACGTG	240
Dp	181	ATGGGCAAGTGTGTCCGCCCACTGCTTCCCTGCTGCAAGGGGAGTGTGCAGACGACGTG	240
OY	241	GGCGCTTCTGGAGCCACGACGACTCGTGGTATGGAACACCTCAGGAACAAGTGTGGCGAG	300
Dp	241	GGCGCTTCTGGAGCCACGACGACTCGTGGTATGGAACACCTCAGGAACAAGTGTGGCGAG	300
OY	301	TGGTGTCCCACTGTCTTCCCTGCTGCAAGGGGAGGGGCAAGCAAGTGTGGCGCTTGG	360
Dp	301	TGGTGTCCCACTGTCTTCCCTGCTGCAAGGGGAGGGGCAAGCAAGTGTGGCGCTTGG	360
OY	361	GGAGACTACGATGTACACTGTCTTCATGTGAGCCCGAGTACCACTGCTGGAGAAAGATGTG	420
Dp	361	GGAGACTACGATGTACACTGTCTTCATGTGAGCCCGAGTACCACTGCTGGAGAAAGATGTG	420
OY	421	GACAAAGCCACAGAGCTGTGCTGGTGGGGTAAAGTCCCGAAGAAAGATCTATGCTCATG	480
Dp	421	GACAAAGCCACAGAGCTGTGCTGGTGGGGTAAAGTCCCGAAGAAAGATCTATGCTCATG	480
OY	481	CTCAGGGGCACTGTGACGTAACAAGAGGACAAAGCAAAAGAGGACTGTCTACATCTGGCC	540
Dp	481	CTCAGGGGCACTGTGACGTAACAAGAGGACAAAGCAAAAGAGGACTGTCTACATCTGGCC	540
OY	541	TCTGTCCATGTGGGAATTTCAGATGATGTAATACTCTGTGTGACAGACGATGTCACTTAAT	600
Dp	541	TCTGTCCATGTGGGAATTTCAGATGATGTAATACTCTGTGTGACAGACGATGTCACTTAAT	600
OY	601	GTCCTGTGACAAACAAAAGAGACAGCTGTGATTAAGGGCCGTCAATGGCAGGAAGATGAA	660
Dp	601	GTCCTGTGACAAACAAAAGAGACAGCTGTGATTAAGGGCCGTCAATGGCAGGAAGATGAA	660
OY	661	TGTGCGTTAATGTTGCTGTGGAACATGTGCACGTATCCAAATATTCAGATGATGGAAT	720
Dp	661	TGTGCGTTAATGTTGCTGTGGAACATGTGCACGTATCCAAATATTCAGATGATGGAAT	720
OY	721	ACCACTGTGCACATACGCTATCTTAATGAAGATTAATGATGGCCAAAGCACTGCTCTTA	780
Dp	721	ACCACTGTGCACATACGCTATCTTAATGAAGATTAATGATGGCCAAAGCACTGCTCTTA	780
OY	781	TATGCTGTGATTCGAAATCAAAAAACAAGCATGGGCTCACACCACTGTACTGGGTGTA	840
Dp	781	TATGCTGTGATTCGAAATCAAAAAACAAGCATGGGCTCACACCACTGTACTGGGTGTA	840
OY	841	CATGAGCAAAAAACGCAAGTCTGGAATTTTTTAATCAAGAAAAAAGCGAATTTAAATGCA	900
Dp	841	CATGAGCAAAAAACGCAAGTCTGGAATTTTTTAATCAAGAAAAAAGCGAATTTAAATGCA	900
OY	901	CTGATATGATATGGAAGAGCTGCTGTCAATCTTGTGTGATGATGACAGATATA	960
Dp	901	CTGATATGATATGGAAGAGCTGCTGTCAATCTTGTGTGATGATGACAGATATA	960
OY	961	GTCAGCCCTTACTGTGACAAATATTGATGATCTTCCAGATCTATCTGAGACAGCG	1020
Dp	961	GTCAGCCCTTACTGTGACAAATATTGATGATCTTCCAGATCTATCTGAGACAGCG	1020
OY	1021	GCCAGAGATATGCTGTTTCTTACATCAATCATATGTAATTTGCCAGTATCTTCTGACATAC	1080
Dp	1021	GCCAGAGATATGCTGTTTCTTACATCAATCATATGTAATTTGCCAGTATCTTCTGACATAC	1080
OY	1081	AAAGAAAAACAGATGCTAAAAATCTCTTGAAACAGCAATTCAGAACAGACTTTAAAG	1140
Dp	1081	AAAGAAAAACAGATGCTAAAAATCTCTTGAAACAGCAATTCAGAACAGACTTTAAAG	1140
OY	1141	CTGACATCAGAGAAAGGTACAAAGGTTCCAAAGGACGTGAAAAAATGACGACGACAGAAA	1200
Dp	1141	CTGACATCAGAGAAAGGTACAAAGGTTCCAAAGGACGTGAAAAAATGACGACGACAGAAA	1200
OY	1201	ATGTCTCAAGAACACGAAATTAATTAAGATGTGTATGAGAGGTTGAAGAAAGAAATGAAG	1260
Dp	1201	ATGTCTCAAGAACACGAAATTAATTAAGATGTGTATGAGAGGTTGAAGAAAGAAATGAAG	1260

QY	1261	AAGCATGAAACTAATAATATGTCGGATTTCTAGAAAACCTGACTAATGCTGCACTGCTGGC	1320
Db	1261	AAGCATGAAACTAATAATATGTCGGATTTCTAGAAAACCTGACTAATGCTGCACTGCTGGC	1320
QY	1321	AATGCTGATTAATGATTAATTCCTCAAGAAGAGCAGAACACCTGATAATCAATGACAAATTT	1380
Db	1321	AATGCTGATTAATGATTAATTCCTCAAGAAGAGCAGAACACCTGATAATCAATGACAAATTT	1380
QY	1381	CCTGCAACGAAAGTGAAGAGTATCACAGAAATTTGCGAATTTAGTTTCTGACTACAAAGAA	1440
Db	1381	CCTGCAACGAAAGTGAAGAGTATCACAGAAATTTGCGAATTTAGTTTCTGACTACAAAGAA	1440
QY	1441	AAACGATGCCCAAAATTAATCTCTTGGAAAACAGCAACCCACAAACAACTTAAAGCTGACA	1500
Db	1441	AAACGATGCCCAAAATTAATCTCTTGGAAAACAGCAACCCACAAACAACTTAAAGCTGACA	1500
QY	1501	TCAGAGGAAGAGTCACAAAGGCTTGAGGCGCAGTGAAATGGCCAGCCAGAG	1551
Db	1501	TCAGAGGAAGAGTCACAAAGGCTTGAGGCGCAGTGAAATGGCCAGCCAGAG	1551
RESULT 14			
AAH85029			
ID	AAH85029 standard; cDNA; 2000 BP.		
XX	AAH85029;		
XX	25-SEP-2001 (first entry)		
DE	Human prostate-specific cDNA sequence B305D splice variant #9.		
XX	Human; prostate cancer; therapy; diagnosis; cat eye syndrome;		
KM	chromosome 22q11.2; prostate-specific protein; chromosome 1;		
KM	prostate specific antigen; PSA; ss.		
OS	Homo sapiens.		
XX	Wo200134802-A2.		
PN	17-MAY-2001.		
PD	09-NOV-2000; 2000MO-US30904.		
PF	12-NOV-1999; 99US-0439313.		
PR	18-NOV-1999; 99US-0443686.		
XX	(CORI-) CORIXA CORP.		
PA	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;		
PI	Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;		
DR	WPI; 2001-308785/32.		
XX	Isolated polypeptide comprising at least an immunogenic portion of a		
PT	prostate-specific protein, useful in the diagnosis and therapy of		
PT	prostate cancer -		
PS	Claim 31; Page 247-248; 325pp; English.		
XX	The present invention describes an isolated polypeptide (P1) comprising		
CC	at least an immunogenic portion of a prostate-specific protein, or its		
CC	variant. Also described are polynucleotides (N1) encoding (P1). (P1) and		
CC	(N1) have cytostatic activity and can be used in vaccine production.		
CC	The polypeptides, nucleic acids and antibodies from the present		
CC	invention are useful in the diagnosis and therapy of prostate cancer.		
CC	Prostate specific genes P704P, F712P, P774P, P775P and B305D are located		
CC	in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome		
CC	region. Prostate specific antigen (PSA) P501S was located on		
CC	chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent		
CC	polynucleotide and polypeptide sequences used in the exemplification		
CC	of the present invention.		
XX	Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 other;		

Query Match 76.0%; Score 1551; DB 22; Length 2000;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1 ATGGTGGTTGAGGTGATTCCATGCGCGCTGCTTCTTGTAAGAGCCATTGGTCTC 60
Db 1 ATGGTGGTTGAGGTGATTCCATGCGCGCTGCTTCTTGTAAGAGCCATTGGTCTC 60
Oy 61 AGGACAGATGAGGCAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
Db 61 AGGACAGATGAGGCAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
Oy 121 AGCAAGTGGGCACTTCTGAGACGACGACGACGACGACGACGACGACGACGACG 180
Db 121 AGCAAGTGGGCACTTCTGAGACGACGACGACGACGACGACGACGACGACGACG 180
Oy 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGAACG 240
Db 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGAACG 240
Oy 241 GGGCGTTTGTGAGACGACGACGACGACGACGACGACGACGACGACGACGACG 300
Db 241 GGGCGTTTGTGAGACGACGACGACGACGACGACGACGACGACGACGACGACG 300
Oy 301 TGGTCTGCGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGTGGCGCTTGG 360
Db 301 TGGTCTGCGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGTGGCGCTTGG 360
Oy 361 GGAGACTAGATGACAGTGGCTTCTGAGAGCCAGTACACGCTCGTGGAGAGATCTG 420
Db 361 GGAGACTAGATGACAGTGGCTTCTGAGAGCCAGTACACGCTCGTGGAGAGATCTG 420
Oy 421 GACAAAGTCCACAGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
Db 421 GACAAAGTCCACAGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
Oy 481 CTCAGGACACTGACGCTGACGACGACGACGACGACGACGACGACGACGACGAC 540
Db 481 CTCAGGACACTGACGCTGACGACGACGACGACGACGACGACGACGACGACGAC 540
Oy 541 TCTGCAATGGGAATTCAGAGTAGTAAACTCTGCTGAGACAGATGTCACCTTAAT 600
Db 541 TCTGCAATGGGAATTCAGAGTAGTAAACTCTGCTGAGACAGATGTCACCTTAAT 600
Oy 601 GTCTTGACACAAAAAAGAGACGCTGATAAAGCCGCTACATGCCAGAGATGAA 660
Db 601 GTCTTGACACAAAAAAGAGACGCTGATAAAGCCGCTACATGCCAGAGATGAA 660
Oy 661 TGTGGCTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGGCTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
Oy 721 ACCACTGCACTAGCTATCTATATGAGATTAATTAATGAGCAAGCACTGCTTTA 780
Db 721 ACCACTGCACTAGCTATCTATATGAGATTAATTAATGAGCAAGCACTGCTTTA 780
Oy 781 TATGGTGTGATATGATCAAAAAAAGCAATGGCTCACACCACTGTTACTTGTGTA 840
Db 781 TATGGTGTGATATGATCAAAAAAAGCAATGGCTCACACCACTGTTACTTGTGTA 840
Oy 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAAGCAATTAATGA 900
Db 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAAGCAATTAATGA 900
Oy 901 CTGATATAGATGGAAGAGCTGCTCATCTGCTGATGTTGTTGATCAGCAAGTATA 960
Db 901 CTGATATAGATGGAAGAGCTGCTCATCTGCTGATGTTGTTGATCAGCAAGTATA 960
Oy 961 GTCAGCCCTTCTACTGAGCAAAAAATTTGATGATCTTCTCAAGATCTATCTGGACAG 1020
Db 961 GTCAGCCCTTCTACTGAGCAAAAAATTTGATGATCTTCTCAAGATCTATCTGGACAG 1020

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Oy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
Oy 1081 AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACGCAATCCAGAACAGCTTAAAG 1140
Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACGCAATCCAGAACAGCTTAAAG 1140
Oy 1141 CTGACATCAGAGAGAGCACAAGTTCACAAGGCTCAAGGCAAGTAATGACGACAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGCACAAGTTCACAAGGCTCAAGGCAAGTAATGACGACAGAGAA 1200
Oy 1201 ATGCTCAAGAACCAAGTAATTAATGAAGTGTGATAGAGAGTTGAAGAAATAATGAAG 1260
Db 1201 ATGCTCAAGAACCAAGTAATTAATGAAGTGTGATAGAGAGTTGAAGAAATAATGAAG 1260
Oy 1261 AAGCATGAAAGTAATTAATGTTGGATTACTAGAAAACTGACTAATGTTGCTCCTGCGC 1320
Db 1261 AAGCATGAAAGTAATTAATGTTGGATTACTAGAAAACTGACTAATGTTGCTCCTGCGC 1320
Oy 1321 AATGTTGATTAATGATTAATTCCTCAAGAGAGACGACAGAACCTGGAATAATGACAAATT 1380
Db 1321 AATGTTGATTAATGATTAATTCCTCAAGAGAGACGACAGAACCTGGAATAATGACAAATT 1380
Oy 1381 CCTGACACGAAGTAAGATGATCAGAGATTTGGAAATTTGTTCTGACTACAAAGAA 1440
Db 1381 CCTGACACGAAGTAAGATGATCAGAGATTTGGAAATTTGTTCTGACTACAAAGAA 1440
Oy 1441 AAACAGATGCCAAATTAATCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATTAATCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Oy 1501 TCAGAGGAAGATTCACAAAGGCTTGAAGGCACTGAGGCAATGAAATGGCCAGCAGAG 1551
Db 1501 TCAGAGGAAGATTCACAAAGGCTTGAAGGCACTGAGGCAATGAAATGGCCAGCAGAG 1551

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RESULT 15
 ID AAH02780 standard; cDNA; 2000 BP.
 XX AAH02780;
 XX
 AC
 XX
 DT 14-JUN-2001 (first entry)
 XX
 XX prostate tumour antigen determined cDNA splice variant of B305D #9.
 DE Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
 KW prostate cancer; immunogenic; cytostatic; vaccine; ss.
 KM
 XX
 OS Homo sapiens.
 PN WO200125272-A2.
 PD 12-APR-2001.
 PF 04-OCT-2000; 2000WO-US27464.
 PR 04-OCT-1999; 99US-0157455.
 PA (CORI-) CORIXA CORP.
 PI Xu J, Skelky YAM, Reed SC, Cheever MA.
 DR WPI; 2001-245062/25.
 DR P-PSDB; AAB74816.
 PT prostate specific protein and its encoding polynucleotide, useful for
 the treatment and diagnosis of prostate cancer -
 PS Claim 50; Page 232; 276pp; English.
 CC The present invention describes an isolated polypeptide (I) comprising

CC at least an immunogenic portion of a prostate tumour antigen protein or
CC its variant. (i), prostate tumour antigen polynucleotides, an antigen
CC production. (ii), prostate tumour antigen polynucleotides, an antigen
CC presenting cell (APC e.g. a dendritic cell) that expresses (i), and a
CC pharmaceutical composition containing (i) are useful for inhibiting the
CC development of cancer in a patient. Antibodies specific for prostate
CC specific proteins and oligonucleotides that hybridise to a
CC polynucleotide that encodes a prostate specific protein are useful
CC for detecting the presence or absence of a cancer or monitoring the
CC progression the progression of a cancer, especially prostate cancer.
CC AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences
CC used in the exemplification of the present invention.

XX Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 other;

Query Match 76.0%; Score 1551; DB 22; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ATGGTGTTGAGTGTGATTCATGCGCGCTCTCTCTGTAAGAACCATTTGGCTC 60
DB 1 ATGGTGTTGAGTGTGATTCATGCGCGCTCTCTCTGTAAGAACCATTTGGCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGCAAGCGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGCAAGCGCAAG 120
QY 121 AGCAAGTGGGCACTTGTGAGACACAGAGACTGCTTGAAGACACACAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTGTGAGACACAGAGACTGCTTGAAGACACACAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGGAGTGGCAAGCAAGCTG 240
DB 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGGAGTGGCAAGCAAGCTG 240
QY 241 GGGGCTTCTGGAACCAACAGAGCTGCTTGAAGACACTCAGGAACAGATGGGCAAG 300
DB 241 GGGGCTTCTGGAACCAACAGAGCTGCTTGAAGACACTCAGGAACAGATGGGCAAG 300
QY 301 TGGTGTGACACTGCTTCCCTGCTGCAAGGGAGCGGCAAGAGTGGGCGCTTGG 360
DB 301 TGGTGTGACACTGCTTCCCTGCTGCAAGGGAGCGGCAAGAGTGGGCGCTTGG 360
QY 361 GGAAGTACAGATGACAGTGTCTTCAAGAGCCAGTACAGCTCCGTGGAAGATCTG 420
DB 361 GGAAGTACAGATGACAGTGTCTTCAAGAGCCAGTACAGCTCCGTGGAAGATCTG 420
QY 421 GACAAGCTCCACAGAGTGTCTGCTGAGGGAAGTCCCGAAGAAAGATCTCATG 480
DB 421 GACAAGCTCCACAGAGTGTCTGCTGAGGGAAGTCCCGAAGAAAGATCTCATG 480
QY 481 CTCAGGAGACGTGACGTAAGCAAGAGGACAAAGAGGAGTGTCTCATCTGCGCC 540
DB 481 CTCAGGAGACGTGACGTAAGCAAGAGGACAAAGAGGAGTGTCTCATCTGCGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAATGTAATAAATCTGCTGAGACAGAGTCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAATGTAATAAATCTGCTGAGACAGAGTCAACTTAAT 600
QY 601 GTCTCTTGACACAAAAAGAGGACAGCTGTGATTAAGGCGCTACAGTCCAGGAAGTAA 660
DB 601 GTCTCTTGACACAAAAAGAGGACAGCTGTGATTAAGGCGCTACAGTCCAGGAAGTAA 660
QY 661 TGTGCGTATATGTTGCGGAACATGGCAGTCAATATTCACAGATGAGTAAAT 720
DB 661 TGTGCGTATATGTTGCGGAACATGGCAGTCAATATTCACAGATGAGTAAAT 720
QY 721 ACCACTCTGCATACGCTATCTATTAATGAAGATAAATTAAGGCCAAGCAGCTCTTA 780
DB 721 ACCACTCTGCATACGCTATCTATTAATGAAGATAAATTAAGGCCAAGCAGCTCTTA 780
QY 781 TATGTGCTGATATCGAATCAAAAAACAGCATGGCTCAACACACTGTTACTTGGTGA 840
DB 781 TATGTGCTGATATCGAATCAAAAAACAGCATGGCTCAACACACTGTTACTTGGTGA 840
```

```
DB 781 TATGTGCTGATATCGAATCAAAAAACAGCATGGCTCAACACACTGTTACTTGGTGA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAATTTTATATCAGAAAAAGCAATTTAAATGCA 900
DB 841 CATGAGCAAAAACAGCAAGTGTGAATTTTATATCAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATATGATATGGAAGAGAGTGTCTTCAATCTTCTGATATGTTGTGATCAGCAATGA 960
DB 901 CTGATATGATATGGAAGAGAGTGTCTTCAATCTTCTGATATGTTGTGATCAGCAATGA 960
QY 961 GTACAGCTTCTACTTGAGCAAAATATGATGATCTTCTCAACATCATATCGACAGAG 1020
DB 961 GTACAGCTTCTACTTGAGCAAAATATGATGATCTTCTCAACATCATATCGACAGAG 1020
QY 1021 GCCAGAGATGATGCTGTTTATGATCATCATGATTAATTTGCCAGTACTTGTGACTAC 1080
DB 1021 GCCAGAGATGATGCTGTTTATGATCATCATGATTAATTTGCCAGTACTTGTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTTAAATCTCTTGAAGAACAGCAATCCAGAACAGACTTAAG 1140
DB 1081 AAAGAAAAACAGATGCTTAAATCTCTTGAAGAACAGCAATCCAGAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCAAAAGTTCAAAAGGCGAGTAAATAGCCAGAGAAA 1200
DB 1141 CTGACATCAGAGAGAGAGTCAAAAGTTCAAAAGGCGAGTAAATAGCCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTAAATATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
DB 1261 AAGCATGAAAGTAAATATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
QY 1321 AATGTGATATATGATTAATTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB 1321 AATGTGATATATGATTAATTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 CTTGACACAGAAAGTGAAGAGATACAGAGATTTGCAATTAATTTCTGACTACAGAGAA 1440
DB 1381 CTTGACACAGAAAGTGAAGAGATACAGAGATTTGCAATTAATTTCTGACTACAGAGAA 1440
QY 1441 AAACAGATGCCAAATATCTTTCTGAAGACAGACCCAGACAACTTAAAGCTGACA 1500
DB 1441 AAACAGATGCCAAATATCTTTCTGAAGACAGACCCAGACAACTTAAAGCTGACA 1500
QY 1501 TCAGAGGAGAGAGTCAAAAGGCTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAG 1551
DB 1501 TCAGAGGAGAGAGTCAAAAGGCTTGAAGGAGAGAGAGAGAGAGAGAGAGAGAG 1551

RESULT 16
ABL95179
ID ABL95179 standard; cDNA; 2000 BP.
XX
AC ABL95179;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human B305D splice variant cDNA sequence SEQ ID NO 374.
XX
EX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002022248-A1.
XX
PD 21-FEB-2002.
XX
PF 12-JAN-2001; 2001US-0759143.
XX
PR 25-FEB-1997; 97US-0806099.
```

PR 01-AUG-1997; 97US-0904804.
 PR 09-FEB-1998; 98US-0020956.
 PR 25-FEB-1998; 98US-0030607.
 PR 14-JUL-1998; 98US-0115453.
 PR 23-SEP-1998; 98US-0159812.
 PR 15-JAN-1999; 99US-0232149.
 PR 09-APR-1999; 99US-0288946.
 PR 13-JUL-1999; 99US-0352616.
 PR 12-NOV-1999; 99US-0439313.
 PR 18-NOV-1999; 99US-0443686.
 PR 14-JAN-2000; 2000US-0483672.
 PR 27-MAR-2000; 2000US-0536857.
 PR 09-MAY-2000; 2000US-0568100.
 PR 12-MAY-2000; 2000US-0570737.
 PR 13-JUN-2000; 2000US-0593793.
 PR 27-JUN-2000; 2000US-0605783.
 PR 10-AUG-2000; 2000US-0636215.
 PR 29-AUG-2000; 2000US-0651236.
 PR 06-SEP-2000; 2000US-0657279.
 PR 02-OCT-2000; 2000US-0679426.
 PR 10-OCT-2000; 2000US-0685166.

PA (XUJ/) XU J.
 PA (DILL/) DILLON D C.
 PA (MIRC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISX/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.

PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
 XX WPI: 2002-255649/30.

PT New prostate-specific polynucleotides for diagnosing and treating
 PT diseases, in particular prostate cancer, and as markers for the
 PT progression of cancer -

PS Claim 1: SEQ ID NO 374; 87pp; English.

CC The present invention provides prostate-specific coding sequences and
 CC their encoded proteins. These can be used in the diagnosis and treatment
 CC of cancers, particularly prostate cancer. The present sequence is a cDNA
 CC described in the invention.

XX Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 other;

Query Match 76.0%; Score 1551; DB 24; Length 2000;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGCTGAGTGATTCATGCGCGGCTGCTTCTTGTAAGAAGCCATTGGCTTC 60
 DB 1 ATGGTGCTGAGTGATTCATGCGCGGCTGCTTCTTGTAAGAAGCCATTGGCTTC 60
 QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCGGAGGAGGAGGCAAG 120
 DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCGGAGGAGGAGGCAAG 120
 QY 121 AGCAAGCTGGGCACTTCTGAGAGCAAGAGCACTGCTATGAAGCACTCAGAGCAAG 180
 DB 121 ATGCTCTAAGAACCAAGAAATTAATTAAGATGTGATAGAGGTTGAAGAAATGAAG 1260

DB 121 AGCAAGCTGGGCACTTCTGAGAGCAAGAGCACTGCTATGAAGCACTCAGAGCAAG 180
 QY 181 ATGGCAAGTGTGGCCGACCTGCTCCCTGTGAGGGGAGTGGCAAGACCAAGTGTG 240
 DB 181 ATGGCAAGTGTGGCCGACCTGCTCCCTGTGAGGGGAGTGGCAAGACCAAGTGTG 240
 QY 241 GGGCTTCTGAGAGCAGCAGCAGCTGCTATGAAGACACTCAGAAAGATGGGCAAG 300
 DB 241 GGGCTTCTGAGAGCAGCAGCAGCTGCTATGAAGACACTCAGAAAGATGGGCAAG 300
 QY 301 TGGTGTGCTGCTGCTTCCCTGCTGAGGGGAGGCGCAAGCAAGTGGGCTTGG 360
 DB 301 TGGTGTGCTGCTGCTTCCCTGCTGAGGGGAGGCGCAAGCAAGTGGGCTTGG 360
 QY 361 GGAGACTAGATGACAGTGCCTTCATGAGGCCAGGTACACGCTCCGTGGAGAAATCG 420
 DB 361 GGAGACTAGATGACAGTGCCTTCATGAGGCCAGGTACACGCTCCGTGGAGAAATCG 420
 QY 421 GACAACTCCACAGAGCTGCTGGGGTAAAGTCCCGCAAGAAAGATCTCATCTCATG 480
 DB 421 GACAACTCCACAGAGCTGCTGGGGTAAAGTCCCGCAAGAAAGATCTCATCTCATG 480
 QY 481 CTCAGGAGACCTGAGCTGAACAAGAGACAAAGAGAGCTGCTCATCTGCGCC 540
 DB 481 CTCAGGAGACCTGAGCTGAACAAGAGAGACAAAGAGAGCTGCTCATCTGCGCC 540
 QY 541 TCTGCCAATGGGAATTCAGAAAGTAAACCTGCTGAGAGAGATGCTCAACTTAAT 600
 DB 541 TCTGCCAATGGGAATTCAGAAAGTAAACCTGCTGAGAGAGATGCTCAACTTAAT 600
 QY 601 GTGCTTGACAAACAAAGAGAGAGAGCTGATGAAGGCGGTACAAATGCCAGAAATGA 660
 DB 601 GTGCTTGACAAACAAAGAGAGAGAGCTGATGAAGGCGGTACAAATGCCAGAAATGA 660
 QY 661 TGTGCGTAAATGTTGCTGGAACATGCGACTGATCCAAATTTCCAGATGATGTGAAT 720
 DB 661 TGTGCGTAAATGTTGCTGGAACATGCGACTGATCCAAATTTCCAGATGATGTGAAT 720
 QY 721 ACCACTGCTGACCTGCTATCTAATGAAGTAAATTAATGGCCAAAGAGCTGCTTA 780
 DB 721 ACCACTGCTGACCTGCTATCTAATGAAGTAAATTAATGGCCAAAGAGCTGCTTA 780
 QY 781 TATGCTGTGATATGCAATCAAAAACAGCATAGGCTGCTCAGCAGTGTACTTGGTGA 840
 DB 781 TATGCTGTGATATGCAATCAAAAACAGCATAGGCTGCTCAGCAGTGTACTTGGTGA 840
 QY 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAATCAAGAAAAAGCGAATTTAAATGCA 900
 DB 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAATCAAGAAAAAGCGAATTTAAATGCA 900
 QY 901 CTGGATAGATATGGAAGAGAGCTGCTCCTATCTGCTATGTTGTGGATCAGCAATTA 960
 DB 901 CTGGATAGATATGGAAGAGAGCTGCTCCTATCTGCTATGTTGTGGATCAGCAATTA 960
 QY 961 GTGAGCTTCTACTTACGCAAAATATGATGATGTTCTTCAAGATCTATCTGAGACAG 1020
 DB 961 GTGAGCTTCTACTTACGCAAAATATGATGATGTTCTTCAAGATCTATCTGAGACAG 1020
 QY 1021 GCCAGAGATGATGCTGTTCTATGATCATCATATGTAATTTGCCAGTTACTTGTGACTAC 1080
 DB 1021 GCCAGAGATGATGCTGTTCTATGATCATCATATGTAATTTGCCAGTTACTTGTGACTAC 1080
 QY 1081 AAGGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAAAGACTTAAG 1140
 DB 1081 AAGGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAAAGACTTAAG 1140
 QY 1141 CTGACATCAGAGAGAAAGTACAAAGGTTCAAGGAGTGAATATAGCCAGCAGAA 1200
 DB 1141 CTGACATCAGAGAGAAAGTACAAAGGTTCAAGGAGTGAATATAGCCAGCAGAA 1200
 QY 1201 ATGCTCTAAGAACCAAGAAATTAATTAAGATGTGATAGAGGTTGAAGAAATGAAG 1260
 DB 1201 ATGCTCTAAGAACCAAGAAATTAATTAAGATGTGATAGAGGTTGAAGAAATGAAG 1260

QY 1261 AAGCATGAAAGTAAATGTTGGATTACTGAGAAAACCTGACTAAATGCTGCTGCGC 1320
DB 1261 AAGATGAAATATATANTGTGGATTACTGACAAAACCTGACTAATGCTGCTGCGC 1320
QY 1321 AATGCTGTAATGATTAATCTTCGAAAGAGAGACAGACCTGAAATTCAGCAATTT 1380
DB 1321 AATGCTGTAATGATTAATCTTCGAAAGAGAGACAGACCTGAAATTCAGCAATTT 1380
QY 1381 CCTGACAAAGAGTGAAGAGTATCAGAGATTTGCCGATTTAGTTTCGACTACAAAGAA 1440
DB 1381 CCTGACAAAGAGTGAAGAGTATCAGAGATTTGCCGATTTAGTTTCGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAATACTCTTCTGAAAACAGCAACCCAGAACAAAGATTAAAGCTGACA 1500
DB 1441 AAACAGATGCCAAATACTCTTCTGAAAACAGCAACCCAGAACAAAGATTAAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGTCAACAAAGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551
DB 1501 TCAGAGAGAGAGTCAACAAAGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551

RESULT 17
AAS9858
ID AAS9858 standard; cDNA; 2000 BP.
AC AAS9858;
XX
DT 12-MAR-2002 (first entry)
XX
DE Breast tumour-specific DNA B11a1 splice variant B11C-8.
XX
KW Human; breast cancer; PCR primer; ss; cytosstatic; immunostimulant;
KM tumour; vaccine; immunogenic.
XX
OS Homo sapiens.
XX
PN WO200190152-A2.
XX
PD 29-NOV-2001.
XX
PF 22-MAY-2001; 2001WO-US16776.
XX
PR 24-MAY-2000; 2000US-0577505.
PR 08-JUN-2000; 2000US-0590583.
PR 26-OCT-2000; 2000US-0699295.
PR 16-MAR-2001; 2001US-0810936.
XX
PA (CORI-) CORIXA CORP.
XX
PI Fridakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
PI Wang A, Skelky YAM, Harlocker SL, Day CH;
XX
DR WPI; 2002-089919/12.
XX
DR P-PSDB; AAU74378.
XX
XX
PT New breast tumour proteins and polynucleotides encoding them, useful for
PT treating and/or preventing cancer, particularly breast cancer, and for
PT eliciting humoral and/or cellular immune response
XX
XX
PS Claim 1; Page 224; 245pp; English.
XX
XX The invention relates to novel breast tumour polynucleotides and
XX polypeptides. The polypeptides and polynucleotides are useful in
XX pharmaceutical compositions for treating and/or preventing cancer,
XX particularly breast cancer, and for eliciting an immune response,
XX particularly humoral and/or cellular immune response. The polynucleotides
XX may be used as probes or primers for nucleic acid hybridisation, in the
XX design and preparation of ribozyme molecules for inhibiting expression of
XX tumour polypeptides and proteins, and in recombinant DNA molecules to
XX direct expression of a polypeptide in host cells. AAS99570-AAS99888
XX represent novel human breast cancer protein coding sequences and
XX PCR primers of the invention.

XX
SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 other;
Query Match 76.0%; Score 1551; DB 24; Length 2000;
Best Local Similarity 100.0%; Prid. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATGGTGGTGAAGTGAATTCATGCGCGCTCCCTCTCTGTAAGAAACCATTTGGTCTC 60
DB 1 AATGGTGGTGAAGTGAATTCATGCGCGCTCCCTCTCTGTAAGAAACCATTTGGTCTC 60
QY 61 AGAGCAAGATGGGCAAGTGTGCTGCTCCCTGCTTCCCTCTGAGGAGGAGCGGCAAG 120
DB 61 AGAGCAAGATGGGCAAGTGTGCTGCTCCCTGCTTCCCTCTGAGGAGGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTCTTCGAGACACAGACACTCTGTATGAAGACACTGAGGAGCAAG 180
DB 121 AGCAACGTGGGCACTCTTCGAGACACAGACACTCTGTATGAAGACACTGAGGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACGCTG 240
DB 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACGCTG 240
QY 241 GCGGCTTCTGAGACACGACGACTCTGCTATGAAGACACTGAGACACAGATGGGCAAG 300
DB 241 GCGGCTTCTGAGACACGACGACTCTGCTATGAAGACACTGAGACACAGATGGGCAAG 300
QY 301 TGGTGCTGCCACTGCTTCCCTGCTGCGAGGGGGAGCGGCAAGCAAGTGGGCTTGG 360
DB 301 TGGTGCTGCCACTGCTTCCCTGCTGCGAGGGGGAGCGGCAAGCAAGTGGGCTTGG 360
QY 361 GGAGACTACGATGACAGAGTGCCTTCATGAGGCCAGGTCCAGTCCGTGGAGAAAGATCTG 420
DB 361 GGAGACTACGATGACAGAGTGCCTTCATGAGGCCAGGTCCAGTCCGTGGAGAAAGATCTG 420
QY 421 GACAAAGCTCACAGAGCTGCTGCTGGGTTAAAGTCCCGAGAAAGATCTCATGCTATG 480
DB 421 GACAAAGCTCACAGAGCTGCTGCTGGGTTAAAGTCCCGAGAAAGATCTCATGCTATG 480
QY 481 CTCAGGGGACACTGACGTGAACAAAGAGACAAAGAAAGAGACTGCTCATCTGCGC 540
DB 481 CTCAGGGGACACTGACGTGAACAAAGAGACAAAGAAAGAGACTGCTCATCTGCGC 540
QY 541 TCTGCCAATGGGAATTCAGAGTAGTAATAACTCTGCTGAGACAGATGTCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAGTAGTAATAACTCTGCTGAGACAGATGTCAACTTAAT 600
QY 601 GTCTTGAACAACAAAAGAGAGACGCTGTGATTAAGGCCGTACAAATGCCAGGAAGATGA 660
DB 601 GTCTTGAACAACAAAAGAGAGACGCTGTGATTAAGGCCGTACAAATGCCAGGAAGATGA 660
QY 661 TGTGCGTTAATGTTGCTGGAACTGGGACGCTGATCAAAATATTCAGATGATGGAAT 720
DB 661 TGTGCGTTAATGTTGCTGGAACTGGGACGCTGATCAAAATATTCAGATGATGGAAT 720
QY 721 ACCACTGCACTACGCTATCTATTAATGAAGATAATTAATGAGCAAGCACTGCTTTA 780
DB 721 ACCACTGCACTACGCTATCTATTAATGAAGATAATTAATGAGCAAGCACTGCTTTA 780
QY 781 TATGCTGTATATGCAATCAAAAACAAAGCATGGCCCTCACACCACTGTACTGGTGA 840
DB 781 TATGCTGTATATGCAATCAAAAACAAAGCATGGCCCTCACACCACTGTACTGGTGA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAGCAATTTAAATGA 900
DB 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAGCAATTTAAATGA 900
QY 901 CTGATATATATGGAAGAGCTGCTCTCATCTCTGTATGTTGATGTCAGCAAGTATA 960
DB 901 CTGATATATATGGAAGAGCTGCTCTCATCTCTGTATGTTGATGTCAGCAAGTATA 960
QY 961 GTCAAGCTTCTACTTGAGCAAAATATGATATCTTCTCAAGATCTATCTGACAGACG 1020
DB 961 GTCAAGCTTCTACTTGAGCAAAATATGATATCTTCTCAAGATCTATCTGACAGACG 1020

```
Db 961 GTCAGCCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
OY 1021 GCCAGAGATGATGCTGTTCTAGTCAATCATGATTAATTTGCCATTTCTTCTGACTAC 1080
Db 1021 GCCAGAGATGATGCTGTTCTAGTCAATCATGATTAATTTGCCATTTCTTCTGACTAC 1080
OY 1081 AAGAAAAACAGATGCTAAAAATCTCTTGTGAAMACAGCAATCCAAACAGACTTAAAG 1140
Db 1081 AAGAAAAACAGATGCTAAAAATCTCTTGTGAAMACAGCAATCCAAACAGACTTAAAG 1140
OY 1141 CTGACATCAGAGAGAGTCCACAAAGGTTCAAGGCAAGTGAATAATGCCAGCCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTCCACAAAGGTTCAAGGCAAGTGAATAATGCCAGCCAGAGAA 1200
OY 1201 ATGTCTCAGAACCCAAATTAATAGATGCTGATAGAGAGCTTGAAGAAAGAAAG 1260
Db 1201 ATGTCTCAGAACCCAAATTAATAGATGCTGATAGAGAGCTTGAAGAAAGAAAG 1260
OY 1261 AAGCATGAAAGTAAATTAATGCTGATTAATGCTGATTAATGCTGATTAATGCTGAT 1320
Db 1261 AAGCATGAAAGTAAATTAATGCTGATTAATGCTGATTAATGCTGATTAATGCTGAT 1320
OY 1321 AATGCTGATTAATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1321 AATGCTGATTAATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
OY 1381 CGTGAACAAGAAAGTAAAGATATCACAATTTGGGATTAATTTCTGACTTCAAGAA 1440
Db 1381 CGTGAACAAGAAAGTAAAGATATCACAATTTGGGATTAATTTCTGACTTCAAGAA 1440
OY 1441 AAGAGATGCCAAATACTCTTCTGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Db 1441 AAGAGATGCCAAATACTCTTCTGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
OY 1501 TCAGAGAGAGAGTCCACAAAGGCTTGAGGCAAGTGAATAATGCCAGCCAGAG 1551
Db 1501 TCAGAGAGAGAGTCCACAAAGGCTTGAGGCAAGTGAATAATGCCAGCCAGAG 1551

RESULT 18
AAA06599
ID AAA06599 standard; cDNA; 2000 BP.
XX
AC AAA06599;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:374.
XX
KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
XX immunogenic; cytostatic; vaccine; ss.
OS
XX Homo sapiens.
XX
PN WO200004149-A2.
XX
PD 27-JAN-2000.
XX
PF 14-JUL-1999; 99WO-US15838.
XX
PR 14-JUL-1998; 98US-0115453.
XX
PR 14-JUL-1998; 98US-0116134.
XX
PR 23-SEP-1998; 98US-0159812.
XX
PR 23-SEP-1998; 98US-0159822.
XX
PR 15-JAN-1999; 99US-0232149.
XX
PR 15-JAN-1999; 99US-0232880.
XX
PR 09-APR-1999; 99US-0288946.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Harlocker SL, Yuguu J, Xu J, Mitcham Jr.;
XX
DR WPI; 2000-171268/15.
```

```
XX
PT New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein -
XX
XX Claim 50; Page 222-223; 263pp; English.
XX
CC The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumor protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC the polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AAA06241 to AAA06591 and
CC AA82000 to AA82020 represent sequences used in the exemplification of
CC the present invention.
XX
XX Sequence 2000 BP; 698 A; 387 C; 489 G; 426 T; 0 other:
XX
XX
Query Match 73.5%; Score 1500; DB 21; Length 2000;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1550; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 ATGTGCTGATGATTAATTCATGCGGCTGCTCTTCTGTGAAGAACCATTTGCTCTC 60
Db 1 ATGTGCTGATGATTAATTCATGCGGCTGCTCTTCTGTGAAGAACCATTTGCTCTC 60
OY 61 AGGAGCAAGATGGGCAAGTGGTCCGCTGCTCCCTGCTGCAAGGAGAGAGAGAGAG 120
Db 61 AGGAGCAAGATGGGCAAGTGGTCCGCTGCTCCCTGCTGCAAGGAGAGAGAGAGAG 120
OY 121 AGCAAGCTGGGCACTTCTGTGAGACCAAGAGACTGCTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAAGCTGGGCACTTCTGTGAGACCAAGAGACTGCTATGAAGACACTCAGAGCAAG 180
OY 181 ATGGGCAAGTGGTCCGCTGCTCCCTGCTGCAAGGAGAGAGAGAGAGAGAGAGAG 240
Db 181 ATGGGCAAGTGGTCCGCTGCTCCCTGCTGCAAGGAGAGAGAGAGAGAGAGAGAG 240
OY 241 GGGCTTCTGAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Db 241 GGGCTTCTGAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
OY 301 TGGTGTGCTGCTGCTCCCTGCTGCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 301 TGGTGTGCTGCTGCTCCCTGCTGCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
OY 361 GGAGACTAGATGACAGTGGCTTCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 361 GGAGACTAGATGACAGTGGCTTCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
OY 421 GACAGCTCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 421 GACAGCTCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
OY 481 CTCAGGAGACTGAGCTGAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 481 CTCAGGAGACTGAGCTGAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
OY 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGAGAGAGAGAGAGAGAGAG 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGAGAGAGAGAGAGAGAGAG 600
OY 601 GTCTTGTGACAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 601 GTCTTGTGACAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
OY 661 TGTGCTTAATGTTGCTGGAACATGGCACTGATCAAAATATTCAGATGATGAAGAT 720
Db 661 TGTGCTTAATGTTGCTGGAACATGGCACTGATCAAAATATTCAGATGATGAAGAT 720
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```
QY 721 ACCACTCTGCACCTAGCTATCTATATAGAGATAAATTAATGGCCAAAGCACTGCTCTTA 780
    |||||||
Db 721 ACCACTCTGCACCTAGCTATCTATATAGAGATAAATTAATGGCCAAAGCACTGCTCTTA 780
QY 781 TATGCTGCTGATATCGAATCAAAAAACAGACATGGCCCTCACACCACTCTTACTGGTGA 840
    |||||||
Db 781 TATGCTGCTGATATCGAATCAAAAAACAGACATGGCCCTCACACCACTCTTACTGGTGA 840
QY 841 CATGAGCAAAAAACAGCAAGTGTGTAATTTTAAATCAAGAAAAAGCAATTTAAATCA 900
    |||||||
Db 841 CATGAGCAAAAAACAGCAAGTGTGTAATTTTAAATCAAGAAAAAGCAATTTAAATCA 900
QY 901 CTGATAGATATGGAAGAGACTGCTCTACACTTCTATGTTGGATCGACAGATATA 960
    |||||||
Db 901 CTGATAGATATGGAAGAGACTGCTCTACACTTCTATGTTGGATCGACAGATATA 960
QY 961 GTCAGCCTTCTACTTGGACCAAAATATGATATCTTCTCAAGATCTATCTGGACAGACG 1020
    |||||||
Db 961 GTCAGCCTTCTACTTGGACCAAAATATGATATCTTCTCAAGATCTATCTGGACAGACG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTATTAATTTGCCAGTTTCTTGACTAC 1080
    |||||||
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTATTAATTTGCCAGTTTCTTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAAAGACTTAAAG 1140
    |||||||
Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAAAGACTTAAAG 1140
QY 1141 CTGACATCTAGAGAGAGAGTCTCAAAAGGTTCAAAAGCACTGAAATAGCCACCCAGAGAA 1200
    |||||||
Db 1141 CTGACATCTAGAGAGAGAGTCTCAAAAGGTTCAAAAGCACTGAAATAGCCACCCAGAGAA 1200
QY 1201 ATGCTCTAAGAACAGAAATTAATAGAGATGCTATAGAGAGTTGAAGAAGAAATGAAG 1260
    |||||||
Db 1201 ATGCTCTAAGAACAGAAATTAATAGAGATGCTATAGAGAGTTGAAGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTAAATATGTTGGATTAATAGAAAAACCTGACTAATGCTGCTGCTGCG 1320
    |||||||
Db 1261 AAGCATGAAAGTAAATATGTTGGATTAATAGAAAAACCTGACTAATGCTGCTGCTGCG 1320
QY 1321 AATGCTGATATGATTAATCTCTCAAAAGAGAGACAGAACACCTGAAATACAGCAATTT 1380
    |||||||
Db 1321 AATGCTGATATGATTAATCTCTCAAAAGAGAGACAGAACACCTGAAATACAGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTGAAGAGATATCACAGATTTGCCAATTAGTTTCTGACTACAAAGAA 1440
    |||||||
Db 1381 CCTGACAAAGAAAGTGAAGAGATATCACAGATTTGCCAATTAGTTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAATACTCTTCTGAAAAACAGCAACCCAGAAAGCAAGACTTAAAGCTGACA 1500
    |||||||
Db 1441 AAACAGATGCCAAATACTCTTCTGAAAAACAGCAACCCAGAAAGCAAGACTTAAAGCTGACA 1500
QY 1501 TCACAGAGAGAGTCACAAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551
    |||||||
Db 1501 TCACAGAGAGAGTCACAAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551

RESULT 19
AAC81011
ID AAC81011 standard; cdna; 1155 bp.
XX
AC AAC81011;
XX
DE 13-FEB-2001 (first entry)
XX
DE Human B11Ag1 antigen splice isoform B11C-15 cDNA.
XX
KM Human; breast tumour-specific antigen; cytosolic; vaccine;
XX breast cancer; B18Ag1; B11Ag1; B15Ag1; ss.
XX
OS Homo sapiens.
XX
```

```
PN W0200061753-A2.
XX
XX 19-OCT-2000.
XX
PF 07-APR-2000; 2000WO-US09312.
XX
XX 09-APR-1999; 99US-0289198.
XX 28-OCT-1999; 99US-0429755.
XX 23-MAR-2000; 2000US-0534825.
XX
XX (CORI-) CORIXA CORP.
XX
XX Frudakis TM, Smith JM, Reed SG, Misher LE, Retter MW, Dillon DC;
XX WPI; 2000-628403/60.
XX P-PSDB; AAB28628.
XX
XX An isolated polypeptide comprising an immunogenic portion of a breast
XX tumor protein used for inhibiting the development of cancer, especially
XX breast cancer, and monitoring cancer progression in a patient -
XX
XX Claim 4; Page 177; 187pp; English.
XX
XX The present sequence is given in a specification relating to compositions
XX and methods for the treatment and diagnosis of breast cancer. Nucleotide
XX sequences that are preferentially expressed in breast tumour tissue, and
XX the polypeptides encoded by such nucleotide sequences, are used in
XX compositions and vaccines to inhibit the development of cancer,
XX especially breast cancer. The progression of a cancer may be monitored by
XX carrying out detection of tumour-specific antigens at subsequent time
XX points and comparing the results from the different time points.
XX CD4+ and/or CD8+ T-Cells isolated from the cancer patient may be treated
XX with tumour-specific polypeptides, polynucleotides encoding the
XX polypeptides or antigen presenting cells expressing the polypeptides. The
XX cells are then administered to the patient to inhibit development of
XX cancer.
XX
XX Sequence 1155 bp; 346 A; 253 C; 297 G; 259 T; 0 other:
XX
XX
XX Query Match 55.3%; Score 1128; DB 21; Length 1155;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTGTTGAGTGGATTTCATGCGGCTGCTCTTCTGTAAGAAACCATTTGCTCTC 60
    |||||||
Db 1 ATGCTGTTGAGTGGATTTCATGCGGCTGCTCTTCTGTAAGAAACCATTTGCTCTC 60
QY 61 AGGACCAAGATGGGCAATGCTGCTGCTGCTTCCCTCTGCTGAGGAGAGCGGCAAG 120
    |||||||
Db 61 AGGACCAAGATGGGCAATGCTGCTGCTGCTTCCCTCTGCTGAGGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGGAGACACAGACACTCTGCTATGAAGACACTGAGAGCAAG 180
    |||||||
Db 121 AGCAACGTGGGCACTTCTGGAGACACAGACACTCTGCTATGAAGACACTGAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGACAGGGGAGTGGCAAGAACCTG 240
    |||||||
Db 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGACAGGGGAGTGGCAAGAACCTG 240
QY 241 GGGCTTCTGGAGACACAGACGACTCTGCTATGAAGACACTGAGAGCAAGATGGGCAAG 300
    |||||||
Db 241 GGGCTTCTGGAGACACAGACGACTCTGCTATGAAGACACTGAGAGCAAGATGGGCAAG 300
QY 301 TGGTGTGCTGCCACTGCTTCCCTGCTGCGAGGGGGAGCGGCAAGAGCAAGTGGGCTTGG 360
    |||||||
Db 301 TGGTGTGCTGCCACTGCTTCCCTGCTGCGAGGGGGAGCGGCAAGAGCAAGTGGGCTTGG 360
QY 361 GGAGACTACGATGACAGAGTCCCTTCATGAGGCCAGGTACCAAGTCCGCGGAGGAAGATCG 420
    |||||||
Db 361 GGAGACTACGATGACAGAGTCCCTTCATGAGGCCAGGTACCAAGTCCGCGGAGGAAGATCG 420
QY 421 GACAAAGTCCACAGAGCTGCTGCTGGGGTAAAGTCCCCAGAAAGATCTATGCTCATG 480
    |||||||
Db 421 GACAAAGTCCACAGAGCTGCTGCTGGGGTAAAGTCCCCAGAAAGATCTATGCTCATG 480
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Db 421 GACAACTCCACAGAGCTCGTGGGGTAAAGTCCAGAAAAGATCATGTCATG 480
Oy 481 CTCAGGACACTGACGTGAACAAGAGCAACCAAAAGAGAGCTGCTACATCGCC 540
Db 481 CTCAGGACACTGACGTGAACAAGAGCAACCAAAAGAGAGCTGCTACATCGCC 540
Oy 541 TCTGCCAATGGGAATTCAGAAAGTAGTAAATCTCTGTCAGACAGATGCTCAATTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAGTAAATCTCTGTCAGACAGATGCTCAATTAAT 600
Oy 601 GTCTTGACAAACAAAAGAGAGAGAGCTGTGATTAAGGCCGTACATGCCAGAAATGAA 660
Db 601 GTCTTGACAAACAAAAGAGAGAGAGCTGTGATTAAGGCCGTACATGCCAGAAATGAA 660
Oy 661 TGTGGCTTATGTGTGTGGAACATGSCACTGATCCAAATATTCACATGATGATGAAAT 720
Db 661 TGTGGCTTATGTGTGTGGAACATGSCACTGATCCAAATATTCACATGATGATGAAAT 720
Oy 721 ACCACTCTGACATACGCTATCTATTAATGAAGATTAATTAATGAGCAAGACATGCTCTTA 780
Db 721 ACCACTCTGACATACGCTATCTATTAATGAAGATTAATTAATGAGCAAGACATGCTCTTA 780
Oy 781 TATGCTGCTGATATCGAATCAAAAAACAAGCATGSCCTCACACCACTGTTACTTGCTGA 840
Db 781 TATGCTGCTGATATCGAATCAAAAAACAAGCATGSCCTCACACCACTGTTACTTGCTGA 840
Oy 841 CATGACCAAAACAGCAAGCTGTAATTTTAAATCAAGAAAAGCAATTAATTAATGCA 900
Db 841 CATGACCAAAACAGCAAGCTGTAATTTTAAATCAAGAAAAGCAATTAATTAATGCA 900
Oy 901 CTGGATAGATATGGAAGAGAGCTGCTCAATCTGCTGATGTTGTTGGATCAGCAAGATTA 960
Db 901 CTGGATAGATATGGAAGAGAGAGCTGCTCAATCTGCTGATGTTGTTGGATCAGCAAGATTA 960
Oy 961 GTACAGCTTCTACTTACGACAAAATATGATGATGATCTTCTCAAGATCATCTGACAGAG 1020
Db 961 GTACAGCTTCTACTTACGACAAAATATGATGATGATCTTCTCAAGATCATCTGACAGAG 1020
Oy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGATGATTAATGGCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGATGATTAATGGCAGTTACTTCTGACTAC 1080
Oy 1081 AAAAGAAAACAGATGCTAAATAATCTCTGTCGAAAACAGCAATCCAGAA 1128
Db 1081 AAAAGAAAACAGATGCTAAATAATCTCTGTCGAAAACAGCAATCCAGAA 1128

RESULT 20
AAA06598
ID AAA06598 standard; cDNA; 1155 BP.
XX
AC AAA06598;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human immunogenic prostate tumour protein cDNA sequence SPO ID NO:373.
XX
KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
XX
KW Immunogenic; cytostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200004149-A2.
XX
PD 27-JAN-2000.
XX
PF 14-JUL-1999; 99WO-US15838.
XX
PR 14-JUL-1998; 98US-0115453.
PR 14-SEP-1998; 98US-0116134.
PR 23-SEP-1998; 98US-0159812.
PR 23-SEP-1998; 98US-0159822.
PR 15-JAN-1999; 99US-0232149.
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PR 15-JAN-1999; 99US-0232880.
PR 09-APR-1999; 99US-0288946.
XX
PA (COR-) CORIXA CORP.
PI Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;
XX
DR WPI; 2000-171268/15.
XX
PT New polypeptide useful for treating and diagnosing prostate cancer
XX
PS comprises an immunogenic portion of prostate tumor protein -
XX
XX
XX Claim 50: Page 222; 263pp; English.
XX
CC The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumor protein (TRP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-Idiotypic antibodies for passive immuno therapy. A portion of
CC the polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AAA06241 to AAA0691 and
CC AAY8200 to AAY82020 represent sequences used in the exemplification of
CC the present invention.
XX
SQ Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;

Query Match 55.3%; Score 1128; DB 21; Length 1155;
Best Local Similarity 100.0%; Pred. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGCGTGTGAGGTGATTCATCCAGCCGGCTCTTCTGTGAAGAACCATTTGGTCTC 60
Db 1 ATGCGTGTGAGGTGATTCATCCAGCCGGCTCTTCTGTGAAGAACCATTTGGTCTC 60
Oy 61 AGAGCAAGATGGGCAAGTGTGCTGCGCTGCTCCCTGTCGAGGGGAGTGGCAAGCGCAAG 120
Db 61 AGAGCAAGATGGGCAAGTGTGCTGCGCTGCTCCCTGTCGAGGGGAGTGGCAAGCGCAAG 120
Oy 121 AGCAAGTGGGCACTTCTGAGACCAAGAGACTGTGATGAAGACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACCAAGAGACTGTGATGAAGACTCAGAGCAAG 180
Oy 181 ATGGGCAAGTGTGCGCCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGTGCGCCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
Oy 241 GGGGCTTCTGGAGACCAAGCAAGCTGTGATGAAGACTCAGAGCAAGATGGGCAAG 300
Db 241 GGGGCTTCTGGAGACCAAGCAAGCTGTGATGAAGACTCAGAGCAAGATGGGCAAG 300
Oy 301 TGGTGTGCGCACTGCTTCCCTGCTGAGGGGAGGCGCAAGCAAGTGGGCGCTTGG 360
Db 301 TGGTGTGCGCACTGCTTCCCTGCTGAGGGGAGGCGCAAGCAAGTGGGCGCTTGG 360
Oy 361 GGAAGCTACAGATGACAGTGTGCTTCAATGAGCCAGGTACCAAGTCCGTGAGAAATCTG 420
Db 361 GGAAGCTACAGATGACAGTGTGCTTCAATGAGCCAGGTACCAAGTCCGTGAGAAATCTG 420
Oy 421 GACAAGCTCCACAGAGCTGCTGGGGTAAAGTCCCAAGAAAGATTCATGTCATG 480
Db 421 GACAAGCTCCACAGAGCTGCTGGGGTAAAGTCCCAAGAAAGATTCATGTCATG 480
Oy 481 CTCAGGACACTGACGTGAACAAGAGCAACCAAAAGAGAGCTGCTACATCGCC 540
Db 481 CTCAGGACACTGACGTGAACAAGAGCAACCAAAAGAGAGCTGCTACATCGCC 540
Oy 541 TCTGCCAATGGGAATTCAGAAAGTAGTAAATCTCTGTCAGACAGATGCTCAATTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAGTAAATCTCTGTCAGACAGATGCTCAATTAAT 600
```

QY 601 GTCCCTGCAACAAAAGAGAGCAGCTGTGATAAAGCCGTACATGCCAGGAAGATGA 660
DB 601 GTCCCTGCAACAAAAGAGAGCAGCTGTGATAAAGCCGTACATGCCAGGAAGATGA 660
QY 661 TGTCCGTTATGTTGCTGGAACATGCGACATGCCAATATTCCAGATGATGGAAT 720
DB 661 TGTCCGTTATGTTGCTGGAACATGCGACATGCCAATATTCCAGATGATGGAAT 720
QY 721 ACCACTGCACTACGCTATCTATATGAATGAATTAATGAGCAAGCCTGCTCTTA 780
DB 721 ACCACTGCACTACGCTATCTATATGAATGAATTAATGAGCAAGCCTGCTCTTA 780
QY 781 TATGTCGTGATATGCAATCAAAAACAAAGCATGGCCCTCACACCATGTTACTTGCTGA 840
DB 781 TATGTCGTGATATGCAATCAAAAACAAAGCATGGCCCTCACACCATGTTACTTGCTGA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGTAATTTTATCAAGAAAAAGCAATTTAATGCA 900
DB 841 CATGAGCAAAAACAGCAAGTGTGTAATTTTATCAAGAAAAAGCAATTTAATGCA 900
QY 901 CTGATGATATGAGAGAGACTGCTCTCACTTGTGATGTTGATGATGCAAGTATA 960
DB 901 CTGATGATATGAGAGAGACTGCTCTCACTTGTGATGTTGATGATGCAAGTATA 960
QY 961 GTGAGCCTTCTACTTGAGCAAAATATTGATGATCTTCTCAAGATCTATCGACAGACG 1020
DB 961 GTGAGCCTTCTACTTGAGCAAAATATTGATGATCTTCTCAAGATCTATCGACAGACG 1020
QY 1021 GCCAGAGAGTATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTGACTAC 1080
DB 1021 GCCAGAGAGTATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGAAAAACAGCAATCCAGAA 1128
DB 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGAAAAACAGCAATCCAGAA 1128

RESULT 21
AAI67211
ID AAI67211 standard; cDNA; 1155 BP.
XX
AC AAI67211;
XX
DT 11-FEB-2002 (first entry)
XX
DE B305D isoform C splice variant 1 encoding cDNA.
XX
KW Genetic subfraction: DNA microarray analysis; polymerase chain reaction;
KW cancer: B305D; ss.
XX
OS Homo sapiens.
XX
FH Key location/Qualifiers
FT CDS 1..1155
FT /*tag- a
FT /product- "B305D isoform C splice variant"
PN WO200175171-A2.
XX
PD 11-OCT-2001.
XX
PF 02-APR-2001; 2001WO-US10631.
XX
PR 03-APR-2000; 2000US-194241P.
PR 20-JUL-2000; 2000US-219862P.
PR 27-JUL-2000; 2000US-221300P.
PR 18-DEC-2000; 2000US-256592P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Houghton RL, Dillon DC, Molesh DA, Xu J, Zehentner B, Persing DH;

DR WPI: 2001-626449/72.
DR P-PSDB: AAG65976.
XX
PT Identifying tissue (tumour)-specific polynucleotides overexpressed in
PT tissue of interest as compared to control tissue, for detecting cancer
PT cells in patient, comprises DNA microarray analysis or quantitative
PT polymerase chain reaction -
XX
PS Claim 4; Page 93-94; 127pp; English.
XX
CC The invention relates to identifying tissue-specific polynucleotides (P)
CC that involves performing a genetic subtraction to identify pool of (P)
CC from tissue of interest (TI), performing DNA microarray analysis to
CC identify first subset of polynucleotides (SP1) at least 2-fold over
CC expressed in TI, and performing quantitative polymerase chain reaction
CC (PCR) analysis on SP1 to identify second subset of (P). The method is
CC useful for determining the presence or absence of a cancer cell in a
CC patient, monitoring the progression of cancer in a patient using a
CC biological sample such as blood, serum, lymph nodes, bone marrow, sputum,
CC urine or a tumour biopsy sample. The methods are useful for determining
CC the presence or absence of or monitoring progression of prostate, breast,
CC colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver,
CC gastric, kidney, bladder, pancreatic or endometrial cancer. The present
CC sequence represents a cDNA encoding a B305D isoform C splice variant.
XX
SQ Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;

Query Match 55.3%; Score 1128; DB 22; Length 1155;

Best Local Similarity 100.0%; Pred. No. 0; Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTTGATGAGTTGATTCATGCGGCTCCCTTCTGTGAAGAACCAATTGGTCTC 60
DB 1 ATGTGTTGATGAGTTGATTCATGCGGCTCCCTTCTGTGAAGAACCAATTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAATGCTGCTGCCGTTGCTTCCCTCTGCAAGGAGAGGGCCAG 120
DB 61 AGGAGCAAGATGGGCAATGCTGCTGCCGTTGCTTCCCTCTGCAAGGAGAGGGCCAG 120
QY 121 AGCAACGTGGGCACTTCTGGAGACACAGACAGCTCTGTATGAAGACACTCAGGAGCA 180
DB 121 AGCAACGTGGGCACTTCTGGAGACACAGACAGCTCTGTATGAAGACACTCAGGAGCA 180
QY 181 ATGGGCAAGTGGTGGCCGCACTGCTCCCTGCTGACAGGGGAGTGGCAAGCAACGTG 240
DB 181 ATGGGCAAGTGGTGGCCGCACTGCTCCCTGCTGACAGGGGAGTGGCAAGCAACGTG 240
QY 241 ATGGGCAAGTGGTGGCCGCACTGCTCCCTGCTGACAGGGGAGTGGCAAGCAACGTG 240
DB 241 ATGGGCAAGTGGTGGCCGCACTGCTCCCTGCTGACAGGGGAGTGGCAAGCAACGTG 240
QY 181 ATGGGCAAGTGGTGGCCGCACTGCTCCCTGCTGACAGGGGAGTGGCAAGCAACGTG 240
DB 181 ATGGGCAAGTGGTGGCCGCACTGCTCCCTGCTGACAGGGGAGTGGCAAGCAACGTG 240
QY 241 GCGGCTTCTGGAGACACAGACAGCTCTGTATGAAGACACTCAGGAGCAACGTG 300
DB 241 GCGGCTTCTGGAGACACAGACAGCTCTGTATGAAGACACTCAGGAGCAACGTG 300
QY 301 TGTGTCCTCCACTGCTTCCCTGCTGACAGGGGAGTGGCAAGCAACGTG 360
DB 301 TGTGTCCTCCACTGCTTCCCTGCTGACAGGGGAGTGGCAAGCAACGTG 360
QY 361 GAGAGCTACGATGACAGTGCCTTCATGAGGCCACAGTACCACTGCTGAGAAAGATG 420
DB 361 GAGAGCTACGATGACAGTGCCTTCATGAGGCCACAGTACCACTGCTGAGAAAGATG 420
QY 421 GACAACTCCACAGAGCTGCTGTTGAGGTTAAAGTCCCAAAAGAGATCTATGCTATG 480
DB 421 GACAACTCCACAGAGCTGCTGTTGAGGTTAAAGTCCCAAAAGAGATCTATGCTATG 480
QY 481 GACAACTCCACAGAGCTGCTGTTGAGGTTAAAGTCCCAAAAGAGATCTATGCTATG 480
DB 481 GACAACTCCACAGAGCTGCTGTTGAGGTTAAAGTCCCAAAAGAGATCTATGCTATG 480
QY 481 CTGAGGCACTGACGTGTAACAGAGAGCAAGCAAAAGAGAGCTCTCATCTGAGCC 540
DB 481 CTGAGGCACTGACGTGTAACAGAGAGCAAGCAAAAGAGAGCTCTCATCTGAGCC 540
QY 541 TCTGCAATGGGAATTGAGAGTAGTAAACTCTGCTGACAGACGATGTCACCTTAAT 600
DB 541 TCTGCAATGGGAATTGAGAGTAGTAAACTCTGCTGACAGACGATGTCACCTTAAT 600
QY 601 GTCCCTGCAACAAAAGAGAGCAGCTGTGATAAAGCCGTACATGCCAGGAAGATGA 660
DB 601 GTCCCTGCAACAAAAGAGAGCAGCTGTGATAAAGCCGTACATGCCAGGAAGATGA 660

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Db 601 GTCTTGACAAACAAAAGAGACAGCTCTGATAAAGCCGTACAAATGCCAGGAATGAA 660
Qy 661 TGTGGCTTAATGTTGCTGGACATGGCACTGATCCAAATATTCAGATGATGAAAT 720
Db 661 TGTGGCTTAATGTTGCTGGACATGGCACTGATCCAAATATTCAGATGATGAAAT 720
Qy 721 AACACTGCACTAGCTATCTATATGAAGATTAATTAATGAGCAAGCACTGCTTTA 780
Db 721 AACACTGCACTAGCTATCTATATGAAGATTAATTAATGAGCAAGCACTGCTTTA 780
Qy 781 TATGCTGTGATATGCAATCAAAAAACAAGCATGGCCCTCACACCACTGTTACTGGTGA 840
Db 781 TATGCTGTGATATGCAATCAAAAAACAAGCATGGCCCTCACACCACTGTTACTGGTGA 840
Qy 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCCGAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCCGAATTTAAATGCA 900
Qy 901 CTGATATGATATGAAAGAGACTGCTCATACTTGTGATGTTGTGATCAGCAAGTATA 960
Db 901 CTGATATGATATGAAAGAGACTGCTCATACTTGTGATGTTGTGATCAGCAAGTATA 960
Qy 961 GTGACCTCTTACTTGTGACCAAAATATGATGATCTTCAAGATCTATCTGAGACAGC 1020
Db 961 GTGACCTCTTACTTGTGACCAAAATATGATGATCTTCAAGATCTATCTGAGACAGC 1020
Qy 1021 GCCAAGAGATATGCTGTTTCTAGTATCATCATGTAATTTGGCAGTACTTCTGACTAC 1080
Db 1021 GCCAAGAGATATGCTGTTTCTAGTATCATCATGTAATTTGGCAGTACTTCTGACTAC 1080
Qy 1081 AAAGAAAACAGATGCTAAAAATCTCTTGAAAAACAGCAATCCAGAA 1128
Db 1081 AAAGAAAACAGATGCTAAAAATCTCTTGAAAAACAGCAATCCAGAA 1128

RESULT 22
AAS63807
ID AAS63807 standard; cDNA; 1155 BP.
XX
AC AAS63807;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human prostate cDNA clone B305D splice variant #8.
XX
KW Human; prostate cancer; ss; cytosolic; immunostimulant; tumour.
XX
OS Homo sapiens.
XX
PN WC200173032-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US09919.
XX
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 26-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0651279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stoik JA, Day CH, Vedgick TS, Carter D;
PI Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;
XX
DR WPI; 2001-639232/73.

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DR P-PSDB; AAU69777.
XX
PT New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
PS Claim 1; Page 349; 579pp; English.
XX
CC The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides
CC and the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.
XX
SQ Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;

Query Match          55.3%; Score 1128; DB 22; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGCTTGAAGTATGATTCATGCGCGCTCTTCTGTGAAGAAGCAATTTGGTCTC 60
Db 1 ATGCTGCTTGAAGTATGATTCATGCGCGCTCTTCTGTGAAGAAGCAATTTGGTCTC 60
Qy 61 AGAGCAAGATGGCAAGTGTGCTGCTTCTGCTTCTGCTGCGAGGAGAGCGGCAAG 120
Db 61 AGAGCAAGATGGCAAGTGTGCTGCTTCTGCTTCTGCTGCGAGGAGAGCGGCAAG 120
Qy 121 AGCAAGTGGGCACTTCTGAGACCAAGCAAGCACTGCTATGAAGCACTGAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACCAAGCAAGCACTGCTATGAAGCACTGAGAGCAAG 180
Qy 181 ATGGGCAAGTGTGCGGCACTGCTTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
Db 181 ATGGGCAAGTGTGCGGCACTGCTTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
Qy 241 GCGGCTTCTGAGACCAAGCAAGCACTGCTATGAAGCACTGAGAGCAAGTGGCAAG 300
Db 241 GCGGCTTCTGAGACCAAGCAAGCACTGCTATGAAGCACTGAGAGCAAGTGGCAAG 300
Qy 301 TGTGCTGCTGAGTGTGCTTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Db 301 TGTGCTGCTGAGTGTGCTTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Qy 361 GGAGACTAGATGACAGTGTGCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Db 361 GGAGACTAGATGACAGTGTGCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Qy 421 GACAACTTCAAGAGCTGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
Db 421 GACAACTTCAAGAGCTGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
Qy 481 CTCAGGACACTGAGCTGAGTGAAGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
Db 481 CTCAGGACACTGAGCTGAGTGAAGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
Qy 541 TCTGCCAATGGGAATTCAGAAATGTAATCTCTGCTGAGAGAGAGATGCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATGTAATCTCTGCTGAGAGAGATGCAACTTAAT 600
Qy 601 GTCTTGGACAAACAAAAGAGAGAGCTGTGATTAAGGCGCTACATGCCAGAAATGAA 660
Db 601 GTCTTGGACAAACAAAAGAGAGAGCTGTGATTAAGGCGCTACATGCCAGAAATGAA 660
Qy 661 TGTGGCTTAATGTTGCTGGACATGGCACTGATCCAAATATTCAGATGATGAAAT 720

```

Db 661 TGTGCGTTAATGTTGCTGGACATGGCAGTCGATCCAAATATTCAGATGAGTATGAAAT 720
Qy 721 ACCACTGTGCATACGCTATCTATATGAATGAATTAATGGCCAAAGCACTGCTCTTA 780
Db 721 ACCACTGTGCATACGCTATCTATATGAATGAATTAATGGCCAAAGCACTGCTCTTA 780
Qy 781 TATGTCCTGATATCGAATCAAAAACACAGATGGCTCACACCACCTGTTACTTGGTGTGA 840
Db 781 TATGTCCTGATATCGAATCAAAAACACAGATGGCTCACACCACCTGTTACTTGGTGTGA 840
Qy 841 CATGAGCAAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGGCAATTTAAATGCA 900
Qy 901 CTGATATGATATGGAAGAGCTGCTCTCATCTGCTGATGTTGGATGACGAATGATA 960
Db 901 CTGATATGATATGGAAGAGCTGCTCTCATCTGCTGATGTTGGATGACGAATGATA 960
Qy 961 GTGAGCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGACG 1020
Db 961 GTGAGCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGACG 1020
Qy 1021 GCCAGAGATGATGCTGTTCTAGTCATCATCATGTAATTTGCCAGTACTTTCGACTAC 1080
Db 1021 GCCAGAGATGATGCTGTTCTAGTCATCATCATGTAATTTGCCAGTACTTTCGACTAC 1080
Qy 1081 AAAGAAAAACAGATGCTTAAATCTCTTCTGAAAAACAGCAATCCAGAA 1128
Db 1081 AAAGAAAAACAGATGCTTAAATCTCTTCTGAAAAACAGCAATCCAGAA 1128

RESULT 23

AAH93714 ID AAH93714 standard; cDNA; 1155 BP.

XX AAH93714;

XX 04-OCT-2001 (first entry)

XX Human prostate-specific cDNA sequence B305D splice variant #8.

XX Human prostate cancer; prostate-specific; diagnosis; vaccine;

XX Human prostate cancer; prostate-specific; diagnosis; vaccine;

XX Homo sapiens.

XX MO200151633-A2.

XX 19-JUL-2001.

XX 16-JAN-2001; 2001MO-US01574.

XX 14-JAN-2000; 2000US-0483672.

XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kujos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAM;
PI Wang A, Meagher MJ;

XX WPI; 2001-425873/45.

XX New polynucleotide encoding a prostate-specific protein, for
PT diagnosis, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -

XX Claim 1; Page 347; 543pp; English.

XX The present invention describes polynucleotide sequences (I) which encode

XX prostate-specific proteins (II). (I) and (II) have cytostatic activity,

XX and can be used in vaccine production and gene therapy. (I), (II),

XX antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used treat cancer in a patient.

CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH0115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.

XX Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;

Query Match 55.3%; Score 1128; DB 22; Length 1155;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGTGATGAGTGTGATTCATCCGCGGCTCTCTGTAAGAACCATTTGGTCTC 60
Db 1 ATGCTGTGATGAGTGTGATTCATCCGCGGCTCTCTGTAAGAACCATTTGGTCTC 60
Qy 61 AGAGCAAGATGGGCAAGTGGTGCCTGCTCCCTGCTGCAAGGAGCGCAAG 120
Db 61 AGAGCAAGATGGGCAAGTGGTGCCTGCTCCCTGCTGCAAGGAGCGCAAG 120
Qy 121 AGCAAGCTGGGCACTTCTGAGACACAGACACTGCTATGAAGACATCAGAGCAAG 180
Db 121 AGCAAGCTGGGCACTTCTGAGACACAGACACTGCTATGAAGACATCAGAGCAAG 180
Qy 181 ATGGGCAAGTGGGCGGCACTGCTCCCTGCTGCAAGGAGGAGTGGCAAGACAGT 240
Db 181 ATGGGCAAGTGGGCGGCACTGCTCCCTGCTGCAAGGAGGAGTGGCAAGACAGT 240
Qy 241 GGGCTTCTGAGACACAGACACTGCTATGAAGACACTCAGAAACAGATGGCAAG 300
Db 241 GGGCTTCTGAGACACAGACACTGCTATGAAGACACTCAGAAACAGATGGCAAG 300
Qy 301 TGTGCTGCTGCACTGCTTCCCTGCTGCAAGGAGGAGCGCAAGAGTGGCGCTTGG 360
Db 301 TGTGCTGCTGCACTGCTTCCCTGCTGCAAGGAGGAGCGCAAGAGTGGCGCTTGG 360
Qy 361 GGAGACTAGCATGACATGCTTCATGAGCCAGGACGACGCTGCTGAGAAAGATCTG 420
Db 361 GGAGACTAGCATGACATGCTTCATGAGCCAGGACGACGCTGCTGAGAAAGATCTG 420
Qy 421 GACAAAGCTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421 GACAAAGCTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Qy 481 CTCAGGACACTGACGCTGAACAGAGACAGCAAGAAAGAGACTGCTTACATCTGGCC 540
Db 481 CTCAGGACACTGACGCTGAACAGAGACAGCAAGAAAGAGACTGCTTACATCTGGCC 540
Qy 541 TGTGCAATGGGAATGAGAGTGAAGTAAATCTGCTGCAAGAGAGTCAACTTAAT 600
Db 541 TGTGCAATGGGAATGAGAGTGAAGTAAATCTGCTGCAAGAGAGTCAACTTAAT 600
Qy 601 GTCTTGACAAACAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 601 GTCTTGACAAACAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Qy 661 TGTGCGTTAATGTTGCTGGAACATGGCATGATCCAAATATTCAGATGAGTGAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGGCATGATCCAAATATTCAGATGAGTGAAT 720
Qy 721 ACCACTGTGCATACGCTATCTATATGAAGATTAATTAATGGCCAAAGCACTGCTTGA 780
Db 721 ACCACTGTGCATACGCTATCTATATGAAGATTAATTAATGGCCAAAGCACTGCTTGA 780
Qy 781 TATGTCCTGATATCGAATCAAAAACACAGATGGCTCACACCACCTGTTACTTGGTGTGA 840
Db 781 TATGTCCTGATATCGAATCAAAAACACAGATGGCTCACACCACCTGTTACTTGGTGTGA 840
Qy 841 CATGAGCAAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGGCAATTTAAATGCA 900

|||||
Db 841 CATGAGCAAAACAGCAAGCTGTGAATTTTAAATCAGAAAAAGCGAATTTAAATGCA 900
Qy 901 CTGATATATATGGAAGACACGCTCTCATACTGCTATATGTTGGATCAGCAAGTATA 960
Db 901 CTGATATATATGGAAGACACGCTCTCATACTGCTATATGTTGGATCAGCAAGTATA 960
Qy 961 CTCAGCCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGACAGC 1020
Db 961 CTCAGCCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGACAGC 1020
Qy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
Qy 1081 AAGAAAAACAGATCTTAAAAATCTCTTCTGAAAAACAGCAATCCAGAA 1128
Db 1081 AAGAAAAACAGATCTTAAAAATCTCTTCTGAAAAACAGCAATCCAGAA 1128

RESULT 24

AAH85028 standard; cDNA; 1155 BP.

AAH85028;

25-SEP-2001 (first entry)

Human prostate-specific cDNA sequence B305D splice variant #8.

Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
chromosome 22q11.2; prostate-specific protein; chromosome 1;
prostate specific antigen; PSA; ss.

Homo sapiens.

W0200134802-A2.

17-MAY-2001.

09-NOV-2000; 2000WO-US30904.

12-NOV-1999; 99US-0439313.

18-NOV-1999; 99US-0443686.

(CORI-) CORIXA CORP.

Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;

Kalos MD, Retter MW, Stolk JA, Day CH, Skelky YAW, Wang A;

WPI: 2001-308785/32.

Isolated polypeptide comprising at least an immunogenic portion of a

prostate cancer -

Claim 31; Page 246-247; 325pp; English.

The present invention describes an isolated polypeptide (P1) comprising
at least an immunogenic portion of a prostate-specific protein, or its
variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
(N1) have cytostatic activity and can be used in vaccine production.

The polypeptides, nucleic acids and antibodies from the present
invention are useful in the diagnosis and therapy of prostate cancer.

Prostate specific genes P704P, P712P, P774P, P775P and B305D are located
in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
region. Prostate specific antigen (PSA) P501S was located on

chromosome 1. AAH84671 to AAH85143 and AAG9000 to AAG9077 represent
polynucleotide and polypeptide sequences used in the exemplification
of the present invention.

Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;

Query Match 55.3%; Score 1128; DB 22; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGTGTTGAGGTTGATTCATGCCGGCTGCTCTTCTGTGAAGAGCCATTGGTCTC 60
Db 1 ATGTGTTGAGGTTGATTCATGCCGGCTGCTCTTCTGTGAAGAGCCATTGGTCTC 60
Qy 61 AGGAGCAAGATGGGCAAGGTTGCTGCTTCCCTGCTCCGTCGAGGGAGGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGGTTGCTGCTTCCCTGCTCCGTCGAGGGAGGAGCGGCAAG 120
Qy 121 AGCAAGTGGGCACTTCTGAGACCAAGCAAGCACTGCTATGAAGCACTAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACCAAGCAAGCACTGCTATGAAGCACTAGAGCAAG 180
Qy 181 ATGGGCAAGTGGTGGCCGCTGCTTCCCTGCTGAGGGAGGCAAGCAAGTGGGCGCTTG 240
Db 181 ATGGGCAAGTGGTGGCCGCTGCTTCCCTGCTGAGGGAGGCAAGCAAGTGGGCGCTTG 240
Qy 241 GCGGCTTCTGAGACCAAGCAAGCACTGCTATGAAGCACTAGAGCAAGTGGGCGCTTG 300
Db 241 GCGGCTTCTGAGACCAAGCAAGCACTGCTATGAAGCACTAGAGCAAGTGGGCGCTTG 300
Qy 301 TGTGCTGCTGCTGCTTCCCTGCTGAGGGAGGCAAGCAAGTGGGCGCTTG 360
Db 301 TGTGCTGCTGCTGCTTCCCTGCTGAGGGAGGCAAGCAAGTGGGCGCTTG 360
Qy 361 GGAGACTACGATGAGAGTCCCTTCATGAGCCAGGTACACGCTCCGTGGAGAGATCTG 420
Db 361 GGAGACTACGATGAGAGTCCCTTCATGAGCCAGGTACACGCTCCGTGGAGAGATCTG 420
Qy 421 GACAAGCTCACAGAGCTCTGTTGGGTTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
Db 421 GACAAGCTCACAGAGCTCTGTTGGGTTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
Qy 481 CTCAGGACACTGAGCTGTAAGCAAGAAAGCAAGAAAGCAAGCTCTATCATCTGGCC 540
Db 481 CTCAGGACACTGAGCTGTAAGCAAGAAAGCAAGAAAGCAAGCTCTATCATCTGGCC 540
Qy 541 TCTGCCAATGGGAATTCAGAACTAGTAAATCTCTGCTGGAGAGAGATGTCAACTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAACTAGTAAATCTCTGCTGGAGAGAGATGTCAACTAAT 600
Qy 601 GTCTTGGACAAACAAAAGAGACAGCTCTGATTAAGGCGCTACATGCGCAGAAATGAA 660
Db 601 GTCTTGGACAAACAAAAGAGACAGCTCTGATTAAGGCGCTACATGCGCAGAAATGAA 660
Qy 661 TGTGCGTTATATGTTGCTGTAAGATGGCACTGATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGCGTTATATGTTGCTGTAAGATGGCACTGATCCAAATATTCAGATGATGGAAT 720
Qy 721 ACCACTCTGCTAGCTATCTATATGAAGATTAATTAATGGCCAAAGCACTGCTCTTA 780
Db 721 ACCACTCTGCTAGCTATCTATATGAAGATTAATTAATGGCCAAAGCACTGCTCTTA 780
Qy 781 TATGTTGCTGATATGATCAACAAAAGCAAGCACTGCTATGTTGGATCAGCAATATA 840
Db 781 TATGTTGCTGATATGATCAACAAAAGCAAGCACTGCTATGTTGGATCAGCAATATA 840
Qy 841 CATGAGCAAAACAGCAAGTCTGAAATTTTAAATCAAGAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAACAGCAAGTCTGAAATTTTAAATCAAGAAAGCAATTTAAATGCA 900
Qy 901 CTGATATGATATGGAAGACACGCTCTCATACTGCTATATGTTGGATCAGCAATATA 960
Db 901 CTGATATGATATGGAAGACACGCTCTCATACTGCTATATGTTGGATCAGCAATATA 960
Qy 961 CTCAGCCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGACAGC 1020
Db 961 CTCAGCCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGACAGC 1020
Qy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080

|||||
Db 1021 GCCAGAGATGCTGTTTCTAGCATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
QY 1081 AAGAGAAAAAGATGCTAAATAATCTTTCTGAAACAGCAATCCAGAA 1128
Db 1081 AAGAGAAAAAGATGCTAAATAATCTTTCTGAAACAGCAATCCAGAA 1128
RESULT 25
AAH02779
ID AAH02779 standard; cDNA; 1155 BP.
XX AAH02779;
AC AAH02779;
XX
DT 14-JUN-2001 (first entry)
XX
DE Prostate tumour antigen determined cDNA splice variant of B305D #8.
XX
KW Human: prostate tumour antigen; prostate tumour; therapy; diagnosis;
KW Prostate cancer; immunogenic; cytostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN W020012572-2.
XX
PD 12-APR-2001.
XX
PF 04-OCT-2000; 2000MO-US27464.
XX
PR 04-OCT-1999; 99US-0157455.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Skeiky YAM, Reed SG, Cheever MA;
XX
DR WPI: 2001-245062/25.
DR P-PSDB: AAB74815.
XX
PT Prostate specific protein and its encoding polynucleotide, useful for
PT the treatment and diagnosis of prostate cancer -
XX
PS Claim 50: Page 231-232: 276pp; English.
XX
CC The present invention describes an isolated polypeptide (I) comprising
CC at least an immunogenic portion of a prostate tumour antigen protein or
CC its variant. (I) have cytostatic activity and can be used in vaccine
CC production. (I), prostate tumour antigen polynucleotides, an antigen
CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
CC pharmaceutical composition containing (I) are useful for inhibiting the
CC development of cancer in a patient. Antibodies specific for prostate
CC polynucleotide that encodes or absence of a cancer or monitoring the
CC progression the progression of a cancer, especially prostate cancer.
CC AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences
CC used in the exemplification of the present invention.
XX
SQ Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;
Query Match 55.3%; Score 1128; DB 22; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 121 AGCAAGCTGGGCACTTCTGGAGACCACAGACACTCTCTATGAAGACATCCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTCCGCCCACTGCTCCCTGCTGACAGGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGGTCCGCCCACTGCTCCCTGCTGACAGGGGAGTGGCAAGCAAGCTG 240
QY 241 GGGCTTCTGGAGACACAGACGACTGTGTATGAAGACACTCAGAACAAAGATGGCAAG 300
Db 241 GGGCTTCTGGAGACACAGACGACTGTGTATGAAGACACTCAGAACAAAGATGGCAAG 300
QY 301 TGGTGTGGCCACCTGCTTCCCTGCTGACAGGGGAGCGGCAAGACAGATGGGGCTTGG 360
Db 301 TGGTGTGGCCACCTGCTTCCCTGCTGACAGGGGAGCGGCAAGACAGATGGGGCTTGG 360
QY 361 GGAGACTACGATGACAGTGCCTTCATGAGGCCACAGTACCAGCTCCGTGGAGAAATCTG 420
Db 361 GGAGACTACGATGACAGTGCCTTCATGAGGCCACAGTACCAGCTCCGTGGAGAAATCTG 420
QY 421 GACAAAGCTCCACAGAGCTGCTGGGGGTAAAGTCCCAAGAAAGATCTCANTGTCATG 480
Db 421 GACAAAGCTCCACAGAGCTGCTGGGGGTAAAGTCCCAAGAAAGATCTCANTGTCATG 480
QY 481 CTCAGGGACACTGACGTGAACAAAGAGACAAAGAGAGTGTCTTACATCTGGCC 540
Db 481 CTCAGGGACACTGACGTGAACAAAGAGAGACAAAGAGAGTGTCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCTGCTGGACAGACGATGCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCTGCTGGACAGACGATGCAACTTAAT 600
QY 601 GTCCCTGACAAACAAAAGAGAGCAGCTGTGATAAAGCCGTACAAATCCAGAAAGATGA 660
Db 601 GTCCCTGACAAACAAAAGAGAGCAGCTGTGATAAAGCCGTACAAATCCAGAAAGATGA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGSCATGATCCAAATATTCAGATGATGTAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGSCATGATCCAAATATTCAGATGATGTAAT 720
QY 721 ACCACTCTGACACTGCTATCTATATGAATGAATGAATGAATGACCAAGCACTGCTTGA 780
Db 721 ACCACTCTGACACTGCTATCTATATGAATGAATGAATGAATGACCAAGCACTGCTTGA 780
QY 781 TATGTCCTGATATGCAATCAAAAAACAGCATGCGCTCACACCACTGTAAGTGA 840
Db 781 TATGTCCTGATATGCAATCAAAAAACAGCATGCGCTCACACCACTGTAAGTGA 840
QY 841 CATGAGCAAAAAACGCAAGTCGTGAATTTTATATCAAAAAAGGAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACGCAAGTCGTGAATTTTATATCAAAAAAGGAATTTAAATGCA 900
QY 901 CTGATATGATATGGAAGAGACTGCTCATACTTCTGATGTTGTGATGACGAAGTATA 960
Db 901 CTGATATGATATGGAAGAGACTGCTCATACTTCTGATGTTGTGATGACGAAGTATA 960
QY 961 GTCAAGCTTCTACTTGAAGCAAAATATGATATCTTCTCAAGATCTATCTGACAGAGC 1020
Db 961 GTCAAGCTTCTACTTGAAGCAAAATATGATATCTTCTCAAGATCTATCTGACAGAGC 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGCATCATCATATATTTGCCAGTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGCATCATCATATATTTGCCAGTACTTCTGACTAC 1080
QY 1081 AAGAGAAAAAGATGCTAAATAATCTTTCTGAAACAGCAATCCAGAA 1128
Db 1081 AAGAGAAAAAGATGCTAAATAATCTTTCTGAAACAGCAATCCAGAA 1128
RESULT 26
ABL95178
ID ABL95178 standard; cDNA; 1155 BP.
XX ABL95178;
AC
XX

DT 19-JUL-2002 (first entry)
XX Human B305D splice variant cDNA sequence SEQ ID NO 373.
DE Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
XX gene therapy; gene; ss.
XX Homo sapiens.
OS
XX US2002022248-A1.
PN
XX
PD 21-FEB-2002.
PF
XX 12-JAN-2001; 2001US-0759143.
XX
PR 25-FEB-1997; 97US-0806099.
PR 01-AUG-1997; 97US-0904804.
PR 09-FEB-1998; 98US-0020956.
PR 25-FEB-1998; 98US-0030607.
PR 14-JUL-1998; 98US-0115453.
PR 23-SEP-1998; 98US-0159812.
PR 15-JAN-1999; 99US-0232149.
PR 09-APR-1999; 99US-0288946.
PR 13-JUL-1999; 99US-0352616.
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
PR 14-JAN-2000; 2000US-0483672.
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0651236.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
XX (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler W, Heppler WT, Henderson RA;
XX WPI: 2002-255649/30.
XX
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer
XX
XX Claim 1: SEQ ID NO 373; 87bp; English.
XX
XX The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX

Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;
SQ
Query Match 55.3%; Score 1128; DB 24; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTGTGAGTGGATTCATCCATGCCGGCTGCTCTTGTGAAGAAAGCATTTGGTCTC 60
DB 1 ATGGTGTGTTGAGGTGATTCATCCATGCCGGCTGCTCTTGTGAAGAAAGCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGCTTCCTCCCTGTCAGGAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCGCTTCCTCCCTGTCAGGAGAGCGGCAAG 120
QY 121 ACCAAGGTGGGCACTTCTGGAACCCAGCGACTCTGCTATGAAGCACTCAGAGCAAG 180
DB 121 ACCAAGGTGGGCACTTCTGGAACCCAGCGACTCTGCTATGAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAAGTGG 240
DB 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAAGTGG 240
QY 241 GCGGCTTCTGAGACCAAGCAAGTCTGCTATGAAGCACTCAGAAAGATGGGCAAG 300
DB 241 GCGGCTTCTGAGACCAAGCAAGTCTGCTATGAAGCACTCAGAAAGATGGGCAAG 300
QY 301 TGGTGTGCTGCTGCTTCCCTGCTGCAAGGGGAGGGGCAAGCAAGTGGGCGCTTGG 360
DB 301 TGGTGTGCTGCTGCTTCCCTGCTGCAAGGGGAGGGGCAAGCAAGTGGGCGCTTGG 360
QY 361 GGAGACTACGATGAGACAGTCTTCATGAGCCAGGTACAGCTCCGTGGAGAAATCTG 420
DB 361 GGAGACTACGATGAGACAGTCTTCATGAGCCAGGTACAGCTCCGTGGAGAAATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGTTGGGGTAAAGTCCCGAAGAAAGATCTCATCTGATG 480
DB 421 GACAAGCTCCACAGAGCTGCTGTTGGGGTAAAGTCCCGAAGAAAGATCTCATCTGATG 480
QY 481 CTCAGGGACACTGAGCTGTAACAAAGGCAAGCAAGCAAGCAAGTCTTACATCTGGCC 540
DB 481 CTCAGGGACACTGAGCTGTAACAAAGGCAAGCAAGCAAGCAAGTCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAATGTAAGAACTCTGCTGAGAGAGATGTCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAATGTAAGAACTCTGCTGAGAGAGATGTCAACTTAAT 600
QY 601 GTCTTGTGACCAAAAAAGAGAGAGCTGTGATTAAGGCGGTACAAATGCCAGAAATGAA 660
DB 601 GTCTTGTGACCAAAAAAGAGAGAGCTGTGATTAAGGCGGTACAAATGCCAGAAATGAA 660
QY 661 TGTGCGTTAATGTTGTGTAACATGGCACTGATCCAAATATTCAGATAGTATGGAAT 720
DB 661 TGTGCGTTAATGTTGTGTAACATGGCACTGATCCAAATATTCAGATAGTATGGAAT 720
QY 721 ACCACTCTGCTACAGCTTCTATATGAAGTAATTAATGAGCCAAAGCACTGCTTA 780
DB 721 ACCACTCTGCTACAGCTTCTATATGAAGTAATTAATGAGCCAAAGCACTGCTTA 780
QY 781 TATGTTGCTGATATGCAATCAAAAAAAGCAAGTGGCTCACACACTGTACTTGGTGA 840
DB 781 TATGTTGCTGATATGCAATCAAAAAAAGCAAGTGGCTCACACACTGTACTTGGTGA 840
QY 841 CATGAGCAAAAAAGCAAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
DB 841 CATGAGCAAAAAAGCAAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
QY 901 CTGGATAGATATGGAAGGAGCTCTCATATCTGCTATGTTGGATCAGCAAGTATA 960
DB 901 CTGGATAGATATGGAAGGAGCTCTCATATCTGCTATGTTGGATCAGCAAGTATA 960
QY 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAGAG 1020
DB 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAGAG 1020

QY	1021	GCACAGGTATGCGTCTTCTATGCATATCATCTGTAAATTTGGCACTTCTTCTACATAC	1080
Db	1021	GCCACAGAGTATGCTGTTTCTAGTATCATCATGTAAATTTGCCACTTCTCTTCTGACATAC	1080
QY	1081	AAGAGAAAAACAGATGCTAAATAATCTCTCTGTAACACAGCAATCCAGAA	1128
Db	1081	AAAGAAAAAACAGATGCTAAATAATCTCTCTGTAACAAACAGCAATCCAGAA	1128
RESULT 27			
ID	AAS99857	standard; cDNA: 1155 BP.	
XX	AAS99857;		
AC			
XX			
DT	12-MAR-2002	(first entry)	
XX			
DE	Breast tumour-specific DNA B11Aq1 splice variant B11C-15.		
XX			
KW	Human; breast cancer; PCR primer; ss; cytostatic; immunostimulant;		
XX	tumour; vaccine; immunogenic.		
OS	Homo sapiens.		
XX			
PN	MO200190152-A2.		
BD			
XX	29-NOV-2001.		
PF	22-MAY-2001; 2001WO-US16776.		
XX			
PR	24-MAY-2000; 2000US-0577505.		
XX			
PR	08-JUN-2000; 2000US-0590583.		
XX			
PR	26-OCT-2000; 2000US-0698295.		
XX			
PR	16-MAR-2001; 2001US-0810936.		
XX			
PA	(CORI-) CORIXA CORP.		
XX			
PI	Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;		
XX			
PI	Wang A, Skelky YAM, Harlocker SL, Day CH;		
XX			
DR	WPI: 2002-089919/12.		
XX			
DR	P-PSDB; AAU74377.		
XX			
PT	New breast tumour proteins and polynucleotides encoding them, useful for		
XX	treating and/or preventing cancer, particularly breast cancer, and for		
XX	eliciting humoral and/or cellular immune response		
XX			
PS	Claim 1; Page 223; 245pp; English.		
XX			
XX	The invention relates to novel breast tumour polynucleotides and		
CC	polypeptides. The polypeptides and polynucleotides are useful in		
CC	pharmaceutical compositions for treating and/or preventing cancer,		
CC	particularly breast cancer, and for eliciting an immune response,		
CC	particularly humoral and/or cellular immune response. The polynucleotides		
CC	may be used as probes or primers for nucleic acid hybridisation, in the		
CC	design and preparation of ribozyme molecules for inhibiting expression of		
CC	tumour polypeptides and proteins, and in recombinant DNA molecules to		
CC	direct expression of a polypeptide in host cells. AAS99570-AAS99888		
CC	represent novel human breast cancer protein coding sequences and		
CC	PCR primers of the invention.		
XX			
SO	Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;		
Query Match 55.3%; Score 1128; DB 24; Length 1155;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	ATGCTGTTGAGAGTTGATTCATGCGCGCTGCTTCTGTGAAGAAGCCATTGTGCTC	60
Db	1	ATGCGTGTGAGAGTTGATTCATGCGCGCTGCTTCTGTGAAGAAGCCATTGTGCTC	60
QY	61	AGGACCAAGATGGCAAGTGCTGCTCCGCTTCCCTCCCTGCTGAGGAGAGCGGCAAG	120

Db	61	AGGACGAGATGGGCAAGTGGTGTGCGCTTCCCTGCTGCGAGGGAGCGGGCAAG	120
Qy	121	ACGCAACGTGGGCACTTGTGGAGACCAAGCACTGTCTATGAAGACACTCAGAGCAAG	180
Db	121	ACCAAGTGGGCACTTGTGGAGACCAAGCAAGCACTGTCTATGAAGACACTCAGAGCAAG	180
Qy	181	ATGGGCAAGTGGTGGCCGCACTGTCTTCCCTGCTGAGGGGGAGTGGCAAGCAAGTGG	240
Db	181	ATGGGCAAGTGGTGGCCGCACTGTCTTCCCTGCTGAGGGGGAGTGGCAAGCAAGTGG	240
Qy	241	GGCGGTTCGGAGACAGCAAGCACTGTCTATGAAGACACTCAGCAAGATGGGCAAG	300
Db	241	GGCGGTTCGGAGACAGCAAGCACTGTCTATGAAGACACTCAGCAAGATGGGCAAG	300
Qy	301	TGGTGTGCGCACTGGTTCCTCCCTGTGTCAGAGGGGAGCGGCAAGGATGGGCGCTTGG	360
Db	301	TGGTGTGCGCACTGGTTCCTCCCTGTGTCAGAGGGGAGCGGCAAGGATGGGCGCTTGG	360
Qy	361	GGAGACATCAGATGACAGTGGCTTCATGGAGCCAGGTACCACTCGTGGAGAAATCTG	420
Db	361	GGAGACATCAGATGACAGTGGCTTCATGGAGCCAGGTACCACTCGTGGAGAAATCTG	420
Qy	421	GACAAGCTCCAGAGAGCTGCGGTGGGGTAAAGTCCCGCAAGAGATGTCAATCGCATG	480
Db	421	GACAAGCTCCAGAGAGCTGCGGTGGGGTAAAGTCCCGCAAGAGATGTCAATCGCATG	480
Qy	481	CTCAGGGCACTGACGTGAAACAAGAGCAAGCAAAAGAGACTGCTTACATCTGGCC	540
Db	481	CTCAGGGCACTGACGTGAAACAAGAGCAAGCAAAAGAGACTGCTTACATCTGGCC	540
Qy	541	TCTGCCAATGGGAATTCAGAAATAGTAAACCTCTGTGTGACAGACAGATGTCACTTAAT	600
Db	541	TCTGCCAATGGGAATTCAGAAATAGTAAACCTCTGTGTGACAGACAGATGTCACTTAAT	600
Qy	601	GTGCTTGACAAACAAAAGGAGCACTGTGATAAAGCCGTCATAGCCAGGAAGATGA	660
Db	601	GTGCTTGACAAACAAAAGGAGCACTGTGATAAAGCCGTCATAGCCAGGAAGATGA	660
Qy	661	TGTGGCTTAATGTGTGTGGAACATGGCACTGATCCAAATATTCACAGATGATGGAAT	720
Db	661	TGTGGCTTAATGTGTGTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT	720
Qy	721	ACCACTGTGCACTACGCTATCTATTAATGAAGATAATTAATGGCCAAAGCACTGCTTTA	780
Db	721	ACCACTGTGCACTACGCTATCTATTAATGAAGATAATTAATGGCCAAAGCACTGCTTTA	780
Qy	781	TATGGTGCATATGGAATCAAAAACAAGCAAGTGGCTCAGCCACTGTACTTGGTGTGA	840
Db	781	TATGGTGCATATGGAATCAAAAACAAGCAAGTGGCTCAGCCACTGTACTTGGTGTGA	840
Qy	841	CATGAGCAAAAAACAGCAAGTCCGTGAATTTTATCAAGAAAAAAGCGAATTTAATGCA	900
Db	841	CATGAGCAAAAAACAGCAAGTCCGTGAATTTTATCAAGAAAAAAGCGAATTTAATGCA	900
Qy	901	CTGATATGATATGAAGGAGCTGCTCATACTTCTGTATGTGTGGATCAGCAAGTATA	960
Db	901	CTGATATGATATGAAGGAGCTGCTCATACTTCTGTATGTGTGGATCAGCAAGTATA	960
Qy	961	GTCACGCTTCTACTGTGAGCAAAATATGATGATCTTCAGAGATCTATCGGACAGAG	1020
Db	961	GTCACGCTTCTACTGTGAGCAAAATATGATGATCTTCAGAGATCTATCGGACAGAG	1020
Qy	1021	GGCAGAGATATGCTGTTTCTAGTATCATCATCTGTAATTTGCCAGTACTTCTGTACTAC	1080
Db	1021	GGCAGAGATATGCTGTTTCTAGTATCATCATCTGTAATTTGCCAGTACTTCTGTACTAC	1080
Qy	1081	AAAGAAAAACAGATGCTAAAAATCTCTTGTGAAAAACAGCAATCCAGAA 1128	
Db	1081	AAAGAAAAACAGATGCTAAAAATCTCTTGTGAAAAACAGCAATCCAGAA 1128	

AAS9869
ID AAS9869 standard; DNA; 1590 BP.
XX
AC AAS9869;
XX
DT 12-MAR-2002 (first entry)
XX
DE Breast tumour-specific gene B305D fusion construct.
XX
KW Human; breast cancer; PCR primer; ss; cytostatic; immunostimulant;
KW tumour; vaccine; immunogenic.
XX
OS Homo sapiens.
XX
PN W020190152-A2.
XX
PD 29-NOV-2001.
XX
PF 22-MAY-2001; 2001WO-0516776.
XX
PR 24-MAY-2000; 2000US-0577505.
PR 08-JUN-2000; 2000US-0590583.
PR 26-OCT-2000; 2000US-0699295.
PR 16-MAR-2001; 2001US-0810936.
XX
PA (CORI-) CORIXA CORP.
XX
PI Fridakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
PI Wang A, Skelky YAW, Harlocker SL, Day CH;
XX
DR WPI; 2002-089919/12.
XX
PT New breast tumour proteins and polynucleotides encoding them, useful for
PT treating and/or preventing cancer, particularly breast cancer, and for
PT eliciting humoral and/or cellular immune response
XX
PS Example 8; Page 235; 245pp; English.
XX
CC The invention relates to novel breast tumour polynucleotides and
CC polypeptides. The polypeptides and polynucleotides are useful in
CC pharmaceutical compositions for treating and/or preventing cancer,
CC particularly breast cancer, and for eliciting an immune response,
CC particularly humoral and/or cellular immune response. The polynucleotides
CC may be used as probes or primers for nucleic acid hybridisation, in the
CC design and preparation of ribozyme molecules for inhibiting expression of
CC tumour polypeptides and proteins, and in recombinant DNA molecules to
CC direct expression of a polypeptide in host cells. AAS9570-AAS9988
CC represent novel human breast cancer protein coding sequences and
CC PCR primers of the invention.
XX
SQ Sequence 1590 BP; 424 A; 403 C; 433 G; 329 T; 1 other:
Query Match 51.2%; Score 1044; DB 24; Length 1590;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1094; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 34 TCTTCTGTAAGAGCAATTTGCTCAGAGCAAGATGGGCAAGTGGTCTCCGTTGC 93
DB 469 TCTTCTGTAAGAGCAATTTGCTCAGAGCAAGATGGGCAAGTGGTCTCCGTTGC 528
XX
QY 94 TTCCCTGCTGCGAGAGCGGCAAGACAGCAAGTGGGCACTCTTGAGACGACAGAC 153
DB 529 TTCCCTGCTGCGAGAGCGGCAAGACAGCAAGTGGGCACTCTTGAGACGACAGAC 588
XX
QY 154 TCTGCTATGAAGACTCAGAGCAAGATGGGCAAGTGGTGGCCGCACTGCTTCCCTGC 213
DB 589 TCTGCTATGAAGACTCAGAGCAAGATGGGCAAGTGGTGGCCGCACTGCTTCCCTGC 648
XX
QY 214 TCGAGGGGAGTGGCAAGCAAGCTGGGCGCTTCTGGAGACCAAGCACTCTGTATG 273
DB 649 TCGAGGGGAGTGGCAAGCAAGCTGGGCGCTTCTGGAGACCAAGCACTCTGTATG 708
XX
QY 274 AAGACACTCAGAAAGATGGGCAAGTGGTCTGCACTGCTTCCCTCTCTCAAGGGG 333

DB 709 AAGACACTCAGAAAGATGGGCAAGTGGTCTGCACTGCTTCCCTCTCTCAAGGGG 768
QY 334 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTACGATGACAGTCCCTTCATGAGCCC 933
DB 769 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTACGATGACAGTCCCTTCATGAGCCC 828
QY 394 AGGTACACAGTCCGCTGAGAAAGATCTGAGCAAGCTCCACAGAGCTGCTGGGTAA 453
DB 829 AGGTACACAGTCCGCTGAGAAAGATCTGAGCAAGCTCCACAGAGCTGCTGGGTAA 888
QY 454 GTCCCCAGAAAGATCTCATCTGATGCTCAGGAGCACTGACGTGAAGAAAGACAA 513
DB 889 GTCCCCAGAAAGATCTCATCTGATGCTCAGGAGCACTGACGTGAAGAAAGACAA 948
QY 514 CAAAAGAGACTGCTTACATCTGGGCTGCGCCAAATGGGAATTCAGAAAGTAAATC 573
DB 949 CAAAAGAGACTGCTTACATCTGGGCTGCGCCAAATGGGAATTCAGAAAGTAAATC 1008
QY 574 CTGCTGAGACAGATGTCACCTTAATGTCCTGACAAACAAAAGAGACGCTGATA 633
DB 1009 CTGCTGAGACAGATGTCACCTTAATGTCCTGACAAACAAAAGAGACGCTGATA 1068
QY 634 AAGCGGTACAAATGCCAGAAAGATGAATGCGTTAATGTTGCTGGAACATGGCACTGAT 693
DB 1069 AAGCGGTACAAATGCCAGAAAGATGAATGCGTTAATGTTGCTGGAACATGGCACTGAT 1128
QY 694 CCAATATTTCCAGATGATGGAATACCAGTCTGCACTACCTATCTAATGAAGAT 753
DB 1129 CCAATATTTCCAGATGATGGAATACCAGTCTGCACTACCTATCTAATGAAGAT 1188
QY 754 AATTAATGGCCAAAGACAGCTCTAATATGATGATGATGATGATGATGATGATGAT 813
DB 1189 AATTAATGGCCAAAGACAGCTCTAATATGATGATGATGATGATGATGATGATGAT 1248
QY 814 GGCTCAGACACACTGTTACTTGGTGTACATGAGCAAAAACAGCAAGTGTGAATTTTA 873
DB 1249 GGCTCAGACACACTGTTACTTGGTGTACATGAGCAAAAACAGCAAGTGTGAATTTTA 1308
QY 874 ATCAAGAAAAACCAATTTAATGCAGTGGATGATGATGATGATGATGATGATGAT 933
DB 1309 ATCAAGAAAAACCAATTTAATGCAGTGGATGATGATGATGATGATGATGATGAT 1368
QY 934 GCTGATGTTGTGATGAGCAAGATGATGATGATGATGATGATGATGATGATGATGAT 993
DB 1369 GCTGATGTTGTGATGAGCAAGATGATGATGATGATGATGATGATGATGATGATGAT 1428
QY 994 TCTTCTCAAGATCTATCTGAGACAGCGGCCAGAGATGCTGTTTCTACTCATCAT 1053
DB 1429 TCTTCTCAAGATCTATCTGAGACAGCGGCCAGAGATGCTGTTTCTACTCATCAT 1488
QY 1054 GTAATTTGCCAGTACTTCTGACTACAAAGAAAACAGATGCTTAATCTCTTGAA 1113
DB 1489 GTAATTTGCCAGTACTTCTGACTACAAAGAAAACAGATGCTTAATCTCTTGAA 1548
XX
QY 1114 AAGCAATTCAGAA 1128
DB 1549 AAGCAATTCAGAA 1563
XX
RESULT 29
AAS9872
ID AAS9872 standard; DNA; 1155 BP.
XX
AC AAS9872;
XX
DT 12-MAR-2002 (first entry)
XX
DE Breast tumour-specific gene B305D homologue #2.
XX
KW Human; breast cancer; PCR primer; ss; cytostatic; immunostimulant;
KW tumour; vaccine; immunogenic.
XX

PA (CORI-) CORIXA CORP.
 XX Fridakis TN, Reed SG, Smith JM;
 XX WPI: 1998-557473/47.
 DR
 XX New DNA sequences isolated from endogenous human retroviral element
 PT - and related vectors, transformed cells, proteins and antibodies,
 PT useful for diagnosis, treatment and prevention of breast cancer
 XX
 PS Claim 1: Page 137-138; 173pp; English.
 XX
 XX AAV68800 to AAV68998 represent nucleotide sequences which encode human
 CC breast tumour specific polypeptides. Detection or measurement of
 CC human breast tumour specific polypeptides and nucleotide sequences,
 CC or the corresponding RNA in a sample, is used for diagnosis and
 CC monitoring of breast cancer. Human breast tumour specific polypeptides
 CC and nucleotide sequences, and the vectors containing the DNAs, are also
 CC useful in vaccines for inhibiting development (for prevention or
 CC therapy) of breast cancer. The polypeptides may also be used to
 CC raise monoclonal antibodies, used as immunoassay reagents.
 XX
 SQ Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other:
 Query Match 24.1%; Score 491; DB 19; Length 1512;
 Best Local Similarity 99.4%; Pred. No. 6.4e-180;
 Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 OY 34 TCTTGTGTAAGAGCCATTGGTCTCAGAGCAAGAGTGGCAAGTGTGCTGCCGTTCG 93
 DB 256 TCTTGTGTAAGAGCCATTGGTCTCAGAGCAAGAGTGGCAAGTGTGCTGCCGTTCG 315
 OY 94 TTCCCTGTGAGGAGAGCGGCGCAAGAGCAAGTGGCAAGTGGCAAGCAAGCAAGC 153
 DB 316 TTCCCTGTGAGGAGAGCGGCGCAAGAGCAAGTGGCAAGTGGCAAGCAAGCAAGC 375
 OY 154 TCTGCTATGAAAGACACTGAGAGCAAGATGGCAAGTGGCGCCACTGTTCCCTTC 213
 DB 376 TCTGCTATGAAAGACACTGAGAGCAAGATGGCAAGTGGCGCCACTGTTCCCTTC 435
 OY 214 TGCAGGGGAGTGGCAAGAGCAAGTGGCGCTTCTGAGAGCAAGCAAGCAAGCTGCTATG 273
 DB 436 TGCAGGGGAGTGGCAAGAGCAAGTGGCGCTTCTGAGAGCAAGCAAGCAAGCTGCTATG 495
 OY 274 AAGAACTCAGAAAGAAATGGGCAAGTGGCTGCTCCACTGTTCCCTGCGCAAGGGG 333
 DB 496 AAGAACTCAGAAAGAAATGGGCAAGTGGCTGCTCCACTGTTCCCTGCGCAAGGGG 555
 OY 334 AGCGGCAAGAGCAAGTGGCGCTTGGGAGACTGAGATGAGAGTGGCTTCATGGAGCCC 393
 DB 556 AGCGGCAAGAGCAAGTGGCGCTTGGGAGACTGAGATGAGAGTGGCTTCATGGAGCCC 615
 OY 394 AGGTACACAGTCCGTGGAGAAAGATGGAAGCTCCACAGAGCTGCCGTGGGGGTAAA 453
 DB 616 AGGTACACAGTCCGTGGAGAAAGATGGAAGCTCCACAGAGCTGCCGTGGGGGTAAA 675
 OY 454 GTCCCAAGAAAGAGATCTGCTCATGCTCAGAGGACACTGAGATGAACAAGAGCAAG 513
 DB 676 GTCCCAAGAAAGAGATCTGCTCATGCTCAGAGGACACTGAGATGAACAAGAGCAAG 735
 OY 514 CAAAGAGAGAGTCTCTACATGCTGCTGCAATGGGAATTGAGAAATAGTAAATC 573
 DB 736 CAAAGAGAGAGTCTCTACATGCTGCTGCAATGGGAATTGAGAAATAGTAAATC 795
 OY 574 CTGCTGAGACAGATGTCACCTTAATGCTTGAACAAAGAGAGAGACAGCTTGATA 633
 DB 796 STGCTGAGACAGATGTCACCTTAATGCTTGAACAAAGAGAGAGACAGCTTGATA 855
 OY 634 AAGGCGGTACATGGCAGGAAGATGAATGGCTTAATTTCTCTGGAATGGCACTGAT 693
 DB 856 AAGGCGGTACATGGCAGGAAGATGAATGGCTTAATTTCTCTGGAATGGCACTGAT 915
 OY 694 CCAATATTTCCAGATGATGGAATAACACTCT 728

DB 916 CCAATATTTCCAGATGATGGAATAACACTCT 950
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 RESULT 31
 AAC81006
 ID AAC81006 standard; cDNA; 1512 BP.
 XX
 AC AAC81006;
 DT
 XX 13-FEB-2001 (first entry)
 DE Human B11a1 antigen protein coding exon cDNA SEQ ID NO: 294.
 XX
 XX Human; breast tumour-specific antigen; cytostatic; vaccine;
 KM breast cancer; B18a1; B11a1; B15a1; ss.
 XX
 OS Homo sapiens.
 XX
 PN W020061753-A2.
 PD 19-OCT-2000.
 PF 07-APR-2000; 2000WO-US09312.
 PR 09-APR-1999; 99US-0289198.
 PR 28-OCT-1999; 99US-0429755.
 PR 23-MAR-2000; 2000US-0534825.
 XX
 XX (CORI-) CORIXA CORP.
 PI Fridakis TN, Smith JM, Reed SG, Misher LE, Retter MW, Dillon DC;
 DR WPI: 2000-628403/60.
 XX
 PT An isolated polypeptide comprising an immunogenic portion of a breast
 PT tumor protein used for inhibiting the development of cancer, especially
 PT breast cancer, and monitoring cancer progression in a patient -
 PS
 PS Claim 4; Page 172; 187pp; English.
 XX
 CC The present sequence is given in a specification relating to compositions
 CC and methods for the treatment and diagnosis of breast cancer. Nucleotide
 CC sequences that are preferentially expressed in breast tumour tissue, and
 CC the polypeptides encoded by such nucleotide sequences, are used in
 CC compositions and vaccines to inhibit the development of cancer,
 CC especially breast cancer. The progression of a cancer may be monitored by
 CC carrying out detection of tumour-specific antigens at subsequent time
 CC points and comparing the results from the different time points.
 CC CD4+ and/or CD8+ T-cells isolated from the cancer patient may be treated
 CC with tumour-specific polypeptides, polynucleotides encoding the
 CC polypeptides or antigen presenting cells expressing the polypeptides. The
 CC cells are then administered to the patient to inhibit development of
 CC cancer.
 XX
 SQ Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other:
 Query Match 24.1%; Score 491; DB 21; Length 1512;
 Best Local Similarity 99.4%; Pred. No. 6.4e-180;
 Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 OY 34 TCTTGTGTAAGAGCCATTGGTCTCAGAGCAAGAGTGGCAAGTGTGCTGCCGTTCG 93
 DB 256 TCTTGTGTAAGAGCCATTGGTCTCAGAGCAAGAGTGGCAAGTGTGCTGCCGTTCG 315
 OY 94 TTCCCTGTGAGGAGAGCGGCGCAAGAGCAAGTGGCAAGTGGCAAGCAAGCAAGC 153
 DB 316 TTCCCTGTGAGGAGAGCGGCGCAAGAGCAAGTGGCAAGTGGCAAGCAAGCAAGC 375
 OY 154 TCTGCTATGAAAGACACTGAGAGCAAGATGGCAAGTGGCGCCACTGTTCCCTTC 213
 DB 376 TCTGCTATGAAAGACACTGAGAGCAAGATGGCAAGTGGCGCCACTGTTCCCTTC 435

QY 214 TGCAGGGGAGTGGCAAGCAACGATGGCGCTTCTGGAGACGACGACTGTGCTATG 273
| | | | |
Db 436 TGCAGGGGAGTGGCAAGCAACGATGGCGCTTCTGGAGACGACGACTGTGCTATG 495
QY 274 AAGCACTTCAGGAACAGATGGGCAAGTGGTGCCTGCACGTGCTTCCCTCTGTCAGGGG 333
| | | | |
Db 496 AAGCACTTCAGGAACAGATGGGCAAGTGGTGCCTGCACGTGCTTCCCTCTGTCAGGGG 555
QY 334 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTAGCATGACAGTGCCTTCATGGAGCC 393
| | | | |
Db 556 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTAGCATGACAGTGCCTTCATGGAGCC 615
QY 394 AGGTACCAAGTCCGTGGAGAAATCTGGACAGCTCCACAGAGCTGCTGGTGGGTTAA 453
| | | | |
Db 616 AGGTACCAAGTCCGTGGAGAAATCTGGACAGCTCCACAGAGCTGCTGGTGGGTTAA 675
QY 454 GTCCCGAAGAAAGATCTCATGCTGCTGACGGGACACTGACGTGAACAAAGAGACAG 513
| | | | |
Db 676 GTCCCGAAGAAAGATCTCATGCTGCTGACGGGACACTGACGTGAACAAAGAGACAG 735
QY 514 CAAAAGAGACTGCTTACATCTTGCCCTTGCCAAATGGAAATTCAGAGTAGTAAACTC 573
| | | | |
Db 736 CAAAAGAGACTGCTTACATCTTGCCCTTGCCAAATGGAAATTCAGAGTAGTAAACTC 795
QY 574 CTGCTGACAGACGATGTCAACTTAATGTCTTGACAAACAAAAGAGACAGCTGTGATA 633
| | | | |
Db 796 STGCTGACAGACGATGTCAACTTAATGTCTTGACAAACAAAAGAGACAGCTGTGATA 855
QY 634 AAGGCGCTTACAAATGCCAGAAAGATGTGCGTTAATGTGCGAAACATGGACATGAT 693
| | | | |
Db 856 AAGGCGCTTACAAATGCCAGAAAGATGTGCGTTAATGTGCGAAACATGGACATGAT 915
QY 694 CCAATATTCAGATGAGTATGGAATACCACTCT 728
| | | | |
Db 916 CCAATATTCAGATGAGTATGGAATACCACTCT 950
RESULT 32
AAA06593
ID AAA06593 standard; cDNA; 1512 BP.
XX
AC AAA06593;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:368.
XX
KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW immunogenic; cytosolic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN W0200004149-A2.
XX
PD 27-JAN-2000.
XX
PF 14-JUL-1999; 99MO-US15838.
XX
PR 14-JUL-1998; 98US-0115453.
PR 14-JUL-1998; 98US-0116134.
PR 23-SEP-1998; 98US-0159612.
PR 23-SEP-1998; 98US-0159612.
PR 15-JAN-1999; 99US-0232149.
PR 15-JAN-1999; 99US-0232880.
PR 09-APR-1999; 99US-0288946.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;
XX WPI; 2000-171268/15.
XX
PT New polypeptide useful for treating and diagnosing prostate cancer

PT comprises an immunogenic portion of prostate tumor protein -
XX
XX Claim 50; Page 219; 263pp; English.

CC The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumour protein (PRP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC the polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AAA06241 to AAA06691 and
CC AY82000 to AY82020 represent sequences used in the exemplification of
CC the present invention.

XX Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;

Query Match 24.1%; Score 491; DB 21; Length 1512;

Best Local Similarity 99.4%; Pred. No. 6, 4e-180;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAACCATTTTGTCTCAGAGCAAGATGGGCAAGTGGTCCGTTGC 93
| | | | |
Db 256 TCTTCTGTGAAGAACCATTTTGTCTCAGAGCAAGATGGGCAAGTGGTCCGTTGC 315
QY 94 TTCCCTGCTGACAGGAGACGGCAAGCAACCTGGGCACTTGTGAGACACAGACAG 153
| | | | |
Db 316 TTCCCTGCTGACAGGAGACGGCAAGCAACCTGGGCACTTGTGAGACACAGACAG 375
QY 154 TCTGCTATGAAGACATCAGAGACCAAGATGGGCAAGTGGTCCGCACTGCTCCCTGC 213
| | | | |
Db 376 TCTGCTATGAAGACATCAGAGACCAAGATGGGCAAGTGGTCCGCACTGCTCCCTGC 435
QY 214 TGCAGGGGAGTGGCAAGACAGTGGGCGCTTCTGAGAACACAGACAGCTGTGATG 273
| | | | |
Db 436 TGCAGGGGAGTGGCAAGACAGTGGGCGCTTCTGAGAACACAGACAGCTGTGATG 495
QY 274 AAGCACTTCAGGAACAGATGGGCAAGTGGTGCCTGCACGTGCTTCCCTCTGTCAGGGG 333
| | | | |
Db 496 AAGCACTTCAGGAACAGATGGGCAAGTGGTGCCTGCACGTGCTTCCCTCTGTCAGGGG 555
QY 334 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTAGCATGACAGTGCCTTCATGGAGCC 393
| | | | |
Db 556 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTAGCATGACAGTGCCTTCATGGAGCC 615
QY 394 AGGTACCAAGTCCGTGGAGAAATCTGGACAGCTCCACAGAGCTGCTGGTGGGTTAA 453
| | | | |
Db 616 AGGTACCAAGTCCGTGGAGAAATCTGGACAGCTCCACAGAGCTGCTGGTGGGTTAA 675
QY 454 GTCCCGAAGAAAGATCTCATGCTGCTGACGGGACACTGACGTGAACAAAGAGACAG 513
| | | | |
Db 676 GTCCCGAAGAAAGATCTCATGCTGCTGACGGGACACTGACGTGAACAAAGAGACAG 735
QY 514 CAAAAGAGACTGCTTACATCTTGCCCTTGCCAAATGGAAATTCAGAGTAGTAAACTC 573
| | | | |
Db 736 CAAAAGAGACTGCTTACATCTTGCCCTTGCCAAATGGAAATTCAGAGTAGTAAACTC 795
QY 574 CTGCTGACAGACGATGTCAACTTAATGTCTTGACAAACAAAAGAGACAGCTGTGATA 633
| | | | |
Db 796 STGCTGACAGACGATGTCAACTTAATGTCTTGACAAACAAAAGAGACAGCTGTGATA 855
QY 634 AAGGCGCTTACAAATGCCAGAAAGATGTGCGTTAATGTGCGAAACATGGACATGAT 693
| | | | |
Db 856 AAGGCGCTTACAAATGCCAGAAAGATGTGCGTTAATGTGCGAAACATGGACATGAT 915
QY 694 CCAATATTCAGATGAGTATGGAATACCACTCT 728
| | | | |
Db 916 CCAATATTCAGATGAGTATGGAATACCACTCT 950

RESULT	33
AAS63802	
ID	AAS63802 standard; cDNA: 1512 BP.
XX	
AC	AAS63802;
XX	
DE	29-JAN-2002 (first entry)
XX	
XX	Human prostate cDNA B305D splice variant #3.
KM	Human; prostate cancer; ss; cytosstatic; immunostimulant; tumour.
OS	Homo sapiens.
XX	
PN	MO200173032-A2.
XX	
PD	04-OCT-2001.
PF	27-MAR-2001; 2001WO-US09919.
XX	
PR	27-MAR-2000; 2000US-0536857.
PR	09-MAY-2000; 2000US-0568100.
PR	12-MAY-2000; 2000US-0570737.
PR	13-JUN-2000; 2000US-0593793.
PR	27-JUN-2000; 2000US-0605783.
PR	10-AUG-2000; 2000US-0636215.
PR	29-AUG-2000; 2000US-0651236.
PR	06-SEP-2000; 2000US-0657279.
PR	02-OCT-2000; 2000US-0679426.
PR	10-OCT-2000; 2000US-0685166.
XX	
PA	(CORI-) CORIXA CORP.
PI	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI	Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI	Ll SX, Wang A, Skeiky YAM, Hepler WT, Henderson RA;
XX	
DR	WPI: 2001-639232/73.
XX	
PT	New human prostate-specific polypeptides and polynucleotides useful for
PT	the diagnosis and treatment of cancer, especially prostate cancer -
PS	Claim 1; Page 345-346; 579pp; English.
XX	
CC	The invention relates to isolated prostate-specific
CC	polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC	antibodies raised against the polypeptides (or antigenic epitopes
CC	derived from them) and antigen-presenting cells expressing the
CC	polypeptides. The antibodies are useful for detecting the presence of
CC	cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC	T cells specific for a tumour protein, and for inhibiting the development
CC	of cancer especially prostate cancer. Compositions comprising the
CC	polynucleotide and/or polypeptide are useful for stimulating an immune
CC	response, and for treating cancer. The oligonucleotide is useful for
CC	detecting cancer. The present sequence is a prostate specific
XX	polynucleotide of the invention.
SQ	Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;
Query Match	24.1%; Score 491; DB 22; Length 1512;
Best Local Similarity	99.4%; Pred. No. 6.4e-180;
Matches 691; Conservative	0; Mismatches 4; Indels 0; Gaps 0;
OY	34 TCTTGTGGAAGAACCCATTGGCTCTCAGGAGCAAGATGGCGAACTGGTGCTGCCGTTGC 93
Db	256 TCTTGTGGAAGAACCCATTGGCTCTCAGGAGCAAGATGGCGAACTGGTGCTGCCGTTGC 315
OY	94 TTCCCTCTCTCAGGAGGAGCGCAAGAGCAACTGGGCACTTTCGAGACACGACGAC 153
Db	316 TTCCCTCTCTCAGGAGGAGCGCGCAAGACGTCGGCACATCTTCGAGACACGACGAC 375
OY	154 TCTGCTATGGAACACTCTCAGGAGCAAGATGGGCAAGTGGTGCTGCCGCACTGCTCCCTGC 213

Db	376	TTCTGCTATTGAAGACACTCTGAGAGCAAGTGGCAAGTGTGTCGCCCACTCTTCCCTTGC	435
Oy	214	TGCAGGGGAGTGGCAAGACACAGTGGGCGCTTCTGAGACACAGACACTGTGCTATG	273
Db	436	TGCAGGGGAGTGGCAAGACACAGTGGGCGCTTCTGAGACACAGACAGATTCGCTATG	495
Oy	274	AAGACACTCAGAGAACAGATGGGCAAGTGTGTCACACTGCTTCCCTCTGCAAGGGG	333
Db	496	AAGACACTCAGAGAACAGATGGGCAAGTGTGTCACACTGCTTCCCTCTGCAAGGGG	555
Oy	334	AGCGCAGAGACCAAGTGGGCGCTTGGGGAGACTACGATACAGTGGCTTCATGAGGCC	393
Db	556	AGCGCAGAGACCAAGTGGGCGCTTGGGGAGACTACGATACAGTGGCTTCATGAGGCC	615
Oy	394	AGGTATCCAGTCGCGTGAGAGATCTGGACAAAGCTCCACAGAGTGCCTGGTGGGTTAA	453
Db	616	AGGTATCCAGTCGCGTGAGAGATCTGGACAAAGCTCCACAGAGTGCCTGGTGGGTTAA	675
Oy	454	GTCCCCAGAAAGATCTTCATCCTCATGCTCAGGGACACTGACGTGAACAAAGAGACAG	513
Db	676	GTCCCCAGAAAGATCTTCATCCTCATGCTCAGGGACACTGACGTGAACAAAGAGACAG	735
Oy	514	CAAAAGAGAGTGCCTCTCATCTGTGGCCTCTGCCAATGGGAATTCAGAAAGTAAATCTC	573
Db	736	CAAAAGAGAGTGCCTCTCATCTGTGGCCTCTGCCAATGGGAATTCAGAAAGTAAATCTC	795
Oy	574	CTGCTGGACAGACAGTGTCACTTAATGTCCCTTGACAAACAAAAGAGACAGCTGTGAT	633
Db	796	STGCTGGACAGACAGTGTCACTTAATGTCCCTTGACAAACAAAAGAGACAGCTGTGAT	855
Oy	634	AAGGCCGTACAGATGCGCAGGAAGATGAATGTGCGTTAATGTTGCTGGAACATGGCAGTAT	693
Db	856	AAGGCCGTACAGATGCGCAGGAAGATGAATGTGCGTTAATGTTGCTGGAACATGGCAGTAT	915
Oy	694	CCAAATATTTCCAGATGAGTATGGAAATACCACTCT	728
Db	916	CCAAATATTTCCAGATGAGTATGGAAATACCACTCT	950
RESULT 34			
AAH93709			
ID	AAH93709	standard; cDNA: 1512 BP.	
AC	AAH93709;		
XX	04-OCT-2001	(first entry)	
DE	Human prostate-specific cDNA sequence B305D splice variant #3.		
KW	Human; prostate cancer; prostate-specific; diagnosis; vaccine;		
KW	cytostatic; gene therapy; metastasis; ss.		
OS	Homo sapiens.		
PN	WO200151633-A2.		
PD	19-JUL-2001.		
PF	16-JAN-2001; 2001WO-US01574.		
PR	14-JAN-2000; 2000US-0483672.		
PA	(CORI-) CORIXA CORP.		
PI	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;		
PI	Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skelky YAW,		
PI	Wang A, Meagher MJ;		
DR	WPI: 2001-425873/45.		
PT	New polynucleotide encoding a prostate-specific protein, for		
PT	diagnosing, monitoring and treating prostate cancer in a patient and		

PT for use in vaccines -

XX PS Claim 1; Page 343-344; 543pp; English.

XX CC The present invention describes polynucleotide sequences (I) which encode
XX CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
XX CC and can be used in vaccine production and gene therapy. (I), (II),
XX CC antibodies to (II), fusion proteins comprising (II), and isolated
XX CC T cells prepared using (I) or (II) are used treat cancer in a patient.
XX CC (I) and the antibodies are also used in the detection of cancer in a
XX CC patient. The cancer that is diagnosed or treated is particularly
XX CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
XX CC (I) can be used for monitoring the progression of cancer in a patient.
XX CC (I) and (II) can also be used to improve diagnostic and therapeutic
XX CC methods for prostate cancer. They can indicate the level of metastasis
XX CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
XX CC AAH01318 represent polynucleotide and amino acid sequences used in the
XX CC exemplification of the present invention.

SQ Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;

Query Match 24.1%; Score 491; DB 22; Length 1512;

Best Local Similarity 99.4%; Pred. No. 6,4e-180; Mismatches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

XX 34 TCTTCTGTGAAGAACCATTTGTTCTCAGAGCAAGATGGGCAAGTGGTCTGCTCCCTTGC 93
XX 256 TCTTCTGTGAAGAACCATTTGTTCTCAGAGCAAGATGGGCAAGTGGTCTGCTCCCTTGC 315
XX 94 TTCCCTGTCTCAGAGGAGGCGCAAGCAAGTGGGCAAGTGGTCTGCTCCCTTGCAGCAGC 153
XX 316 TTCCCTGTCTCAGAGGAGGCGCAAGCAAGTGGGCAAGTGGTCTGCTGAGCAGCAGCAGC 375
XX 154 TCTCTATGAAGACACTCAGAGCAAGTGGGCAAGTGGTCTGCTCCCTTGCCTCCCTGC 213
XX 376 TCTCTATGAAGACACTCAGAGCAAGTGGGCAAGTGGTCTGCTCCCTTGCCTCCCTGC 435
XX 214 TGCAGGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGACCAAGCAAGTCTGCTATG 273
XX 436 TGCAGGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGACCAAGCAAGTCTGCTATG 495
XX 274 AAGCACTCAGAGCAAGTGGGCAAGTGGTCTGCTCCCTTGCCTGTCAGAGGGG 333
XX 496 AAGCACTCAGAGCAAGTGGGCAAGTGGTCTGCTCCCTTGCCTGTCAGAGGGG 555
XX 334 AGCGCAAGAGCAAGTGGGCGCTTGGGAGACTATCAGTACAGTGGCTTCATGAGAGCC 393
XX 556 AGCGCAAGAGCAAGTGGGCGCTTGGGAGACTATCAGTACAGTGGCTTCATGAGAGCC 615
XX 394 AGTACCAAGTGGTGGAGAAATCTGAGCAAGTCTCAGAGAGTGGCTGGTGGTAAA 453
XX 616 AGTACCAAGTGGTGGAGAAATCTGAGCAAGTCTCAGAGAGTGGCTGGTGGTAAA 675
XX 454 GTCCCGAAGAAAGTATCATCTGATCTCAGAGCAAGTGGGCAAGTGGGCAAGAGCAAG 513
XX 676 GTCCCGAAGAAAGTATCATCTGATCTCAGAGCAAGTGGGCAAGTGGGCAAGAGCAAG 735
XX 514 CAAAAGAGAGTGTCTACATCTGCTGCTCCCAATGGGAATAGAGAATAGTAAACTC 573
XX 736 CAAAAGAGAGTGTCTACATCTGCTGCTCCCAATGGGAATAGAGAATAGTAAACTC 795
XX 574 CTGCTGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAGAGAGAGCTCTGATA 633
XX 796 STGCTGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAGAGAGAGCTCTGATA 855
XX 634 AAGGCGCTTACAAATGCCAGGAAGATGATGTCCTTAATGTTGCTGGAACATGGCAGTAT 693
XX 856 AAGGCGCTTACAAATGCCAGGAAGATGATGTCCTTAATGTTGCTGGAACATGGCAGTAT 915
XX 694 CCAATATTCAGATGATGATGAAATACCACTCT 728
XX 916 CCAATATTCAGATGATGATGAAATACCACTCT 950

RESULT 35

AAH85023 ID AAH85023 standard; cDNA; 1512 BP.

XX AAH85023;

XX 25-SEP-2001 (first entry)

XX Human prostate-specific cDNA sequence B305D splice variant #3.

XX Human: prostate cancer; therapy; diagnosis; cat eye syndrome;

XX chromosome 22q11.2; prostate-specific protein; chromosome 1;

XX prostate specific antigen; PSA; ss.

OS Homo sapiens.

XX W0200134802-A2.

XX 17-MAY-2001.

XX 09-NOV-2000; 2000MO-US30904.

XX 12-NOV-1999; 9905-0439313.

XX 18-NOV-1999; 9905-0443686.

XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;

XX Kalos MD, Rietter MW, Stolk JA, Day CH, Skeiky YAM, Wang A;

XX WPI; 2001-308785/32.

XX Isolated polypeptide comprising at least an immunogenic portion of a

XX prostate-specific protein, useful in the diagnosis and therapy of a

XX prostate cancer -

XX Claim 31; Page 243-244; 325pp; English.

XX The present invention describes an isolated polypeptide (P1) comprising

XX at least an immunogenic portion of a prostate-specific protein, or its

XX variant. Also described are polynucleotides (N1) encoding (P1). (P1) and

XX (N1) have cytostatic activity and can be used in vaccine production.

XX The polypeptides, nucleic acids and antibodies from the present

XX invention are useful in the diagnosis and therapy of prostate cancer.

XX Prostate specific genes P704P, P712P, P774P, P775P and B305D are located

XX in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome

XX region. Prostate specific antigen (PSA) P501S was located on

XX chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent

XX polynucleotide and polypeptide sequences used in the exemplification

XX of the present invention.

SQ Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;

Query Match 24.1%; Score 491; DB 22; Length 1512;

Best Local Similarity 99.4%; Pred. No. 6,4e-180; Mismatches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 274 AAGACTCAGAGAACAGTGGGCAAGTGGTCTGCTCCACTGCTCCCTGCTGACAGGGG 333
 DB 496 AAGACTCAGAGAACAGTGGGCAAGTGGTCTGCTCCACTGCTCCCTGCTGACAGGGG 555
 QY 334 AAGCCGCAAGAGCAGTGGGCGCTTGGGGAGACTAGCATGACAGTGGCTTTCATGAGCCC 393
 DB 556 AAGCCGCAAGAGCAGTGGGCGCTTGGGGAGACTAGCATGACAGTGGCTTTCATGAGCCC 615
 QY 394 AAGTACCAAGTCCGCGGAGAGATCTGGACAGCTCCACAGAGCTGCCCTGGTGGGGTAAA 453
 DB 616 AAGTACCAAGTCCGCGGAGAGATCTGGACAGCTCCACAGAGCTGCCCTGGTGGGGTAAA 675
 QY 454 GTCCCCAGAAAGAGTCTATCTGTCATGCTCAGAGCACTGAGCTGAACAAGAGAGCAAG 513
 DB 676 GTCCCCAGAAAGAGTCTATCTGTCATGCTCAGAGCACTGAGCTGAACAAGAGAGCAAG 735
 QY 514 CAAAAGAGAGTCTCTCTACATCTGCGCTCTGCGCAATGGGAATTCAGAACTAGTAAACTC 573
 DB 736 CAAAAGAGAGTCTCTCTACATCTGCGCTCTGCGCAATGGGAATTCAGAACTAGTAAACTC 795
 QY 574 CTGCTGACAGAGATGTCATCTAATGCTTGTGACAAACAAAGAGACAGCTCTGATA 633
 DB 796 STGCTGACAGAGATGTCATCTAATGCTTGTGACAAACAAAGAGACAGCTCTGATA 855
 QY 634 AAGGCCGTACATGCGCAGAGAGATGATGCGTTAATGTTGCTGGAACATGACACTGAT 693
 DB 856 AAGGCCGTACATGCGCAGAGAGATGATGCGTTAATGTTGCTGGAACATGACACTGAT 915
 QY 694 CCAATATTCCAGATGATGGAATACCACTCT 728
 DB 916 CCAATATTCCAGATGATGGAATACCACTCT 950

RESULT 36

AAH02774 ID AAH02774 standard; cDNA: 1512 BP.

AC AAH02774;

DT 14-JUN-2001 (first entry)

DE Prostate tumour antigen determined cDNA splice variant of B305D #3.

XX Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;

KW prostate cancer; immunogenic; cytostatic; vaccine; ss.

OS Homo sapiens.

PN WO200125272-A2.

PD 12-APR-2001.

PF 04-OCT-2000; 2000WO-US27464.

PR 04-OCT-1999; 99US-0157455.

PA (CORI-) CORIXA CORP.

PI Xu J, Skeiky YAM, Reed SG, Cheever MA;

DR WPI: 2001-245062/25.

PT Prostate specific protein and its encoding polynucleotide, useful for

XX the treatment and diagnosis of prostate cancer -

XX Claim 50; Page 229; 276pp; English.

CC The present invention describes an isolated polypeptide (I) comprising
 CC at least an immunogenic portion of a prostate tumour antigen protein or
 CC its variant. (I) have cytostatic activity and can be used in vaccine
 CC production. (I), prostate tumour antigen polynucleotides, an antigen
 CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a

CC pharmaceutical composition containing (I) are useful for inhibiting the
 CC development of cancer in a patient. Antibodies specific for prostate
 CC specific proteins and oligonucleotides that hybridize to a
 CC polynucleotide that encodes a prostate specific protein are useful
 CC for detecting the presence or absence of a cancer or monitoring the
 CC progression the progression of a cancer, especially prostate cancer.
 CC AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences
 CC used in the exemplification of the present invention.
 XX

SQ Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;

Query Match 24.1%; Score 491; DB 22; Length 1512;

Best Local Similarity 99.4%; Pred. No. 6.4e-180; Mismatches 4; Indels 0; Gaps 0;

Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAAGCATTTTGTCTCAGAGACAGATGGGCAAGTGGCTGCGCTTGC 93
 DB 256 TCTTCTGTGAAGAAGCATTTTGTCTCAGAGACAGATGGGCAAGTGGCTGCGCTTGC 315
 QY 94 TTCCCTGCTGAGGAGAGAGCGGCAAGACAGCACTGGGCACTTGTGAGACAGCAGCAG 153
 DB 316 TTCCCTGCTGAGGAGAGAGCGGCAAGACAGCACTGGGCACTTGTGAGACAGCAGCAG 375
 QY 154 TCTGCTATGAAAGACACTCAGAGCAAGATGGGCAAGTGGTGGCGGCACTTCCCTTGC 213
 DB 376 TCTGCTATGAAAGACACTCAGAGCAAGATGGGCAAGTGGTGGCGGCACTTCCCTTGC 435
 QY 214 TGCAGGGGGAGTGGCAAGACAGCACTGGGCGCTTCTGAGACAGCAGCAGCTCTGATG 273
 DB 436 TGCAGGGGGAGTGGCAAGACAGCACTGGGCGCTTCTGAGACAGCAGCAGCTCTGATG 495
 QY 274 AAGACTCAGAGAACAGTGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 333
 DB 496 AAGACTCAGAGAACAGTGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 555
 QY 334 AAGCCGCAAGAGCAGTGGGCGCTTGGGGAGACTAGCATGACAGTGGCTTTCATGAGCCC 393
 DB 556 AAGCCGCAAGAGCAGTGGGCGCTTGGGGAGACTAGCATGACAGTGGCTTTCATGAGCCC 615
 QY 394 AAGTACCAAGTCCGCGGAGAGATCTGGACAGCTCCACAGAGCTGCCCTGGTGGGGTAAA 453
 DB 616 AAGTACCAAGTCCGCGGAGAGATCTGGACAGCTCCACAGAGCTGCCCTGGTGGGGTAAA 675
 QY 454 GTCCCCAGAAAGAGTCTATCTGTCATGCTCAGAGCACTGAGCTGAACAAGAGAGCAAG 513
 DB 676 GTCCCCAGAAAGAGTCTATCTGTCATGCTCAGAGCACTGAGCTGAACAAGAGAGCAAG 735
 QY 514 CAAAAGAGAGTCTCTCTACATCTGCGCTCTGCGCAATGGGAATTCAGAACTAGTAAACTC 573
 DB 736 CAAAAGAGAGTCTCTCTACATCTGCGCTCTGCGCAATGGGAATTCAGAACTAGTAAACTC 795
 QY 574 CTGCTGACAGAGATGTCATCTAATGCTTGTGACAAACAAAGAGACAGCTCTGATA 633
 DB 796 STGCTGACAGAGATGTCATCTAATGCTTGTGACAAACAAAGAGACAGCTCTGATA 855
 QY 634 AAGGCCGTACATGCGCAGAGAGATGATGCGTTAATGTTGCTGGAACATGACACTGAT 693
 DB 856 AAGGCCGTACATGCGCAGAGAGATGATGCGTTAATGTTGCTGGAACATGACACTGAT 915
 QY 694 CCAATATTCCAGATGATGGAATACCACTCT 728
 DB 916 CCAATATTCCAGATGATGGAATACCACTCT 950

RESULT 37

ABL95173 ID ABL95173 standard; cDNA: 1512 BP.

XX ABL95173;

DT 19-JUL-2002 (first entry)

DE Human B305D splice variant cDNA sequence SEQ ID NO 368.

XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX Homo sapiens.
XX US200202248-A1.
XX 21-FEB-2002.
XX 12-JAN-2001; 2001US-0759143.
XX 25-FEB-1997; 97US-0806099.
XX 01-AUG-1997; 97US-0904804.
XX 09-FEB-1998; 98US-0020956.
XX 25-FEB-1998; 98US-0030607.
XX 14-JUL-1998; 98US-0115453.
XX 23-SEP-1998; 98US-0159812.
XX 15-JAN-1999; 99US-0232149.
XX 09-APR-1999; 99US-0288946.
XX 13-JUL-1999; 99US-0352616.
XX 12-NOV-1999; 99US-0439313.
XX 18-NOV-1999; 99US-0443686.
XX 14-JAN-2000; 2000US-0483672.
XX 27-MAR-2000; 2000US-0536857.
XX 09-MAY-2000; 2000US-0568100.
XX 12-MAY-2000; 2000US-0570737.
XX 13-JUN-2000; 2000US-0593793.
XX 27-JUN-2000; 2000US-0605783.
XX 10-AUG-2000; 2000US-0636215.
XX 29-AUG-2000; 2000US-0651236.
XX 06-SEP-2000; 2000US-0657279.
XX 02-OCT-2000; 2000US-0679426.
XX 10-OCT-2000; 2000US-0685166.
XX (XUJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PI XU J, DILLON DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX WPI; 2002-255649/30.
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer
XX
XX Claim 1: SEQ ID NO 368; 87pp; English.
XX
XX The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention.
XX
XX Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;
SO Query Match 24.1%; Score 491; DB 24; Length 1512;

Best Local Similarity 99.4%; Pred. No. 6.4e-180;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 34 TCTTCTGTGAAGAAAGCCATTGGCTCAGAGCAAGATGGGCAAGTGTGCTCCGTTGC 93
DB 256 TCTTCTGTGAAGAAAGCCATTGGCTCAGAGCAAGATGGGCAAGTGTGCTCCGTTGC 315
QY 94 TTCCTCTGTGAGAGGAGAGCGGCAAGAGCAACGTGGGCACTTCTGTGAGCAACAGAGAC 153
DB 316 TTCCTCTGTGAGAGGAGAGCGGCAAGAGCAACGTGGGCACTTCTGTGAGCAACAGAGAC 375
QY 154 TCTGCTATGAAGACACCTCAGAGCAAGATGGGCAAGTGTGCTCCGTTGCCTCCCTGC 213
DB 376 TCTGCTATGAAGACACCTCAGAGCAAGATGGGCAAGTGTGCTCCGTTGCCTCCCTGC 435
QY 214 TGCAGGGGGAGTGCAAGAGCAACGTGGGCACTTCTGTGAGCAACAGAGCACTGTATG 273
DB 436 TGCAGGGGGAGTGCAAGAGCAACGTGGGCACTTCTGTGAGCAACAGAGCACTGTATG 495
QY 274 AAGCACTCAGGAACAAGATGGGCAAGTGTGCTGCTCCACTCTCCCTGCTCAGGGGG 333
DB 496 AAGCACTCAGGAACAAGATGGGCAAGTGTGCTGCTCCACTCTCCCTGCTCAGGGGG 555
QY 334 AGCGGCAAGAGCAAGTGGGCGCTTGGGGAGACTAGCATGACTGCTTCACTGAGGCC 393
DB 556 AGCGGCAAGAGCAAGTGGGCGCTTGGGGAGACTAGCATGACTGCTTCACTGAGGCC 615
QY 394 AGGTACCAAGTCGCTGAGAGAGATCTTGAGACAGTCCACAGAGCTGCTGGGGGATA 453
DB 616 AGGTACCAAGTCGCTGAGAGAGATCTTGAGACAGTCCACAGAGCTGCTGGGGGATA 675
QY 454 GTCCCCAGAAAGATCTCATCTGATGCTCAGGAGCACTAGCTGAAACAAGAGCAAG 513
DB 676 GTCCCCAGAAAGATCTCATCTGATGCTCAGGAGCACTAGCTGAAACAAGAGCAAG 735
QY 514 CAAAAGAGAGCTGCTCATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 573
DB 736 CAAAAGAGAGCTGCTCATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 795
QY 574 CTGCTGAGAGAGATGCTCAACTTAATGCTTGCCTGACAAACAAAAGAGAGAGCTGCTGATA 633
DB 796 STGCTGAGAGAGATGCTCAACTTAATGCTTGCCTGACAAACAAAAGAGAGAGCTGCTGATA 855
QY 634 AAGGCCGTACAAATGCCAGAAATGAATGCGTTAATGTTGCTGGAACATGGCACTGAT 693
DB 856 AAGGCCGTACAAATGCCAGAAATGAATGCGTTAATGTTGCTGGAACATGGCACTGAT 915
QY 694 CCAATATTTCCAGATGAGTATGGAATACCACTCT 728
DB 916 CCAATATTTCCAGATGAGTATGGAATACCACTCT 950
RESULT 38
ABK46896
ID ABK46896 standard; DNA: 1512 BP.
AC ABK46896;
XX
XX 05-JUN-2002 (first entry)
XX
XX Human breast tumour-specific DNA B1a91, protein coding exon #3.
XX
XX Human; breast tumour-specific protein; vaccine; breast cancer;
KW gene; ds.
XX
XX Homo sapiens.
XX
XX US6344550-B1.
XX
XX 05-FEB-2002.
PD
XX 17-APR-1998; 98US-0062451.
XX

PR 01-JAN-1996; 96US-0585392.
PR 20-AUG-1996; 96US-0700014.
PR 10-JAN-1997; 97WO-US00485.
PR 09-APR-1997; 97US-0838762.
PR 11-DEC-1997; 97US-0991789.
XX
XX (CORI-) CORIXA CORP.
XX
XX Frudakis TN, Smith JM, Reed SG;
XX
XX WPI: 2002-215084/27.
XX
XX Polynucleotide encoding breast-specific tumour polypeptides useful as
XX vaccine for preventing and treating breast cancer in a subject -
XX
PS Claim 1; Column 211-213; 128pp; English.
XX
XX The invention relates to an isolated DNA molecule (I) encoding breast-
XX tumour-specific polypeptides. (I) is useful as a vaccine for preventing
XX and treating breast cancer in a subject. The polypeptide encoded by (I)
XX is used for production of compounds such as antibodies useful in
XX diagnosing and monitoring the progression of breast cancer. ABK6614-
XX CC ABK46899 represent human breast tumour-specific coding sequences and
XX related PCR primers of the invention.
XX
SQ Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;

Query Match 24.1%; Score 491; DB 24; Length 1512;

Best Local Similarity 99.4%; Pred. No. 6.4e-180;

Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 34 TCTTCTGTGAAGAACCCATTGTTGCTCAGAGCAGATGGGCAAGTGGTGCCTGCGTTC
DB 256 TCTTCTGTGAAGAACCCATTGTTGCTCAGAGCAGATGGGCAAGTGGTGCCTGCGTTC
OY 94 TTCCCTCTGCGAGGAGAGCGGCAAGAGCAACGTGGGCACTTCTGAGACCAACGACGAC
DB 316 TTCCCTCTGCGAGGAGAGCGGCAAGAGCAACGTGGGCACTTCTGAGACCAACGACGAC
OY 154 TCTGCTATGAAGACACTCAGAGAGCAAGATGGGCAAGTGGTGCCTGCGTTCCTCCCTGC
DB 376 TCTGCTATGAAGACACTCAGAGAGCAAGATGGGCAAGTGGTGCCTGCGTTCCTCCCTGC
OY 214 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGACCAACGACACTCTGTATG
DB 436 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGACCAACGACACTCTGTATG
OY 274 AAGACACTCAGAGAACAGATGGGCAAGTGGTGCCTGCGTTCCTCCCTGCTGACAGGGG
DB 496 AAGACACTCAGAGAACAGATGGGCAAGTGGTGCCTGCGTTCCTCCCTGCTGACAGGGG
OY 334 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTACGATGACAGTGCCTTCAATGAGACCC
DB 556 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTACGATGACAGTGCCTTCAATGAGACCC
OY 394 AGGTACCAAGTCCGTGGAGAAATCTGGCAAGTCCACAGAGTGCCTGGGGGTAA
DB 616 AGGTACCAAGTCCGTGGAGAAATCTGGCAAGTCCACAGAGTGCCTGGGGGTAA
OY 454 GTCCCCAGAAAGATCTCATCTGTCATGCTCAGAGCACTGACGTGAACAAGAGCAAG
DB 676 GTCCCCAGAAAGATCTCATCTGTCATGCTCAGAGCACTGACGTGAACAAGAGCAAG
OY 514 CAAAAGAGAGCTCTCTACATCTGGCCTCTGCAATGGGAATTCAGAACTAGTAAACTC
DB 796 CAAAAGAGAGCTCTCTACATCTGGCCTCTGCAATGGGAATTCAGAACTAGTAAACTC
OY 574 CTGCTGACAGAGATGTCACCTTATGCTTGAACAACAAAGAGGACACTCTGATA
DB 855 CTGCTGACAGAGATGTCACCTTATGCTTGAACAACAAGAGGACACTCTGATA
OY 634 AAGGCGTACAAATGCGCAGAGAAATGATGCTTAAATGCTGGAACATGGCACTGAT
|||||

DB 856 AAGGCGTACAAATGCGCAGAGAAATGATGCTTAAATGCTGGAACATGGCACTGAT 915
OY 694 CCAATATTCCAGATGAGTGAATAATACACTCT 728
DB 916 CCAATATTCCAGATGAGTGAATAATACACTCT 950

RESULT 39
AAS99852
ID AAS99852 standard; cDNA, 1512 BP.
XX
XX AAS99852;
XX
XX 12-MAR-2002 (first entry)
XX
XX Breast tumour-specific DNA #225.
XX
XX Human; breast cancer; PCR primer; ss; cytosolic; immunostimulant;
XX tumour; vaccine; immunogenic.
XX
XX Homo sapiens.
XX
XX WO200190152-A2.
XX
XX 29-NOV-2001.
XX
XX 22-MAY-2001; 2001WO-US16776.
XX
XX 24-MAY-2000; 2000US-0577505.
XX
XX 08-JUN-2000; 2000US-0590583.
XX
XX 26-OCT-2000; 2000US-069295.
XX
XX 16-MAR-2001; 2001US-0810936.
XX
XX (CORI-) CORIXA CORP.
XX
XX Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
XX Wang A, Skelky YAM, Harlocker SL, Day CH;
XX
XX WPI: 2002-089919/12.
XX
XX New breast tumour proteins and polynucleotides encoding them, useful for
XX treating and/or preventing cancer, particularly breast cancer, and for
XX eliciting humoral and/or cellular immune response -
XX
PS Claim 1; Page 219; 245pp; English.

XX The invention relates to novel breast tumour polynucleotides and
XX polypeptides. The polypeptides and polynucleotides are useful in
XX pharmaceutical compositions for treating and/or preventing cancer,
XX particularly breast cancer, and for eliciting an immune response.
XX CC particularly humoral and/or cellular immune response. The polynucleotides
XX CC may be used as probes or primers for nucleic acid hybridisation. In the
XX CC design and preparation of ribozyme molecules for inhibiting expression of
XX CC tumour polypeptides and proteins, and in recombinant DNA molecules to
XX CC direct expression of a polypeptide in host cells. AAS9570-AAS9888
XX CC represent novel human breast cancer protein coding sequences and
XX CC PCR primers of the invention.

SQ Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;

Query Match 24.1%; Score 491; DB 24; Length 1512;

Best Local Similarity 99.4%; Pred. No. 6.4e-180;

Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 34 TCTTCTGTGAAGAACCCATTGTTGCTCAGAGCAGATGGGCAAGTGGTGCCTGCGTTC
DB 256 TCTTCTGTGAAGAACCCATTGTTGCTCAGAGCAGATGGGCAAGTGGTGCCTGCGTTC
OY 94 TTCCCTCTGCGAGGAGAGCGGCAAGAGCAACGTGGGCACTTCTGAGACCAACGACGAC
DB 316 TTCCCTCTGCGAGGAGAGCGGCAAGAGCAACGTGGGCACTTCTGAGACCAACGACGAC
OY 154 TCTGCTATGAAGACACTCAGAGAGCAAGATGGGCAAGTGGTGCCTGCGTTCCTCCCTGC
|||||

```

Db 376 TCTGCTATGAGACACACAGAGAGCAGATGGGCAAGTGGGCCCCCACTGCTCCCTGC 435
QY 214 TGCAGGGGAGTGGCAAGACAGCTGGGGCTTCTGAGACACGACGACTGCTATG 273
Db 436 TGCAGGGGAGTGGCAAGACAGCTGGGGCTTCTGAGACACGACGACTGCTATG 495
QY 274 AAGACACTCAGGAACAAGATGGGCAAGTGGTGTCTGACACTGCTTCCCTCGCAGGGG 333
Db 496 AAGACACTCAGGAACAAGATGGGCAAGTGGTGTCTGACACTGCTTCCCTCGCAGGGG 555
QY 334 AGCGGCAAGACAGATGGGGCGCTTGGGGAGCTACAGTACAGTGGCTTCTATGAGACC 393
Db 556 AGCGCAAGACAGATGGGGCGCTTGGGGAGCTACAGTACAGTGGCTTCTATGAGACC 615
QY 394 AGTACACAGCTCCGTGAGAGATCTGAGACAGCTCCACAGAGCTGCTGGGGGTAA 453
Db 616 AGTACACAGCTCCGTGAGAGATCTGAGACAGCTCCACAGAGCTGCTGGGGGTAA 675
QY 454 GTCCCCGAAAGATCTCATCTCATGCTCAGGACACTGACGTGAACAAGAGACAG 513
Db 676 GTCCCCGAAAGATCTCATCTCATGCTCAGGACACTGACGTGAACAAGAGACAG 735
QY 514 CAAAAGAGACTGCTCTACATCTGGCTCTGCCAATGGGAATTGAGAAGTAAACTC 573
Db 736 CAAAAGAGACTGCTCTACATCTGGCTCTGCCAATGGGAATTGAGAAGTAAACTC 795
QY 574 CTCTGACAGACAGATGTCAACTTAATGTCTTGACAAACAAAAGAGACAGCTGATA 633
Db 796 STCTGACAGACAGATGTCAACTTAATGTCTTGACAAACAAAAGAGACAGCTGATA 855
QY 634 AAGCCGTACAAATGCCAGAAATGAATGTCGTTAATGTTCTGTAACATGGCAGTGA 693
Db 856 AAGCCGTACAAATGCCAGAAATGAATGTCGTTAATGTTCTGTAACATGGCAGTGA 915
QY 694 CCAAAATATCCAGATGATGTAATGAAATACCACTCT 728
Db 916 CCAAAATATCCAGATGATGTAATGAAATACCACTCT 950

RESULT 40
AAV68996
ID AAV68996 standard; DNA; 1853 BP.
XX
AC AAV68996;
XX
DT 22-JAN-1999 (first entry)
XX
DE DNA molecule encoding a breast tumour specific polypeptide #188.
XX
KW Human; breast cancer; breast tumour tissue; diagnosis; treatment;
XX vaccine; epitope; endogenous; retroviral element; ss.
XX
OS Homo sapiens.
XX
PN WO9845328-A2.
XX
PD 15-OCT-1998.
XX
PF 09-APR-1998; 98MO-US06939.
XX
PR 11-DEC-1997; 97US-0991789.
XX
PR 09-APR-1997; 97US-0838762.
XX
PA (CORI-) CORIXA CORP.
XX
PI Frudakis TN, Reed SG, Smith JM;
XX
DR WPI: 1998-557473/47.
XX
PT New DNA sequences isolated from endogenous human retroviral element
PT - and related vectors, transformed cells, proteins and antibodies,
PT useful for diagnosis, treatment and prevention of breast cancer
```

```

XX
PS Claim 1; Page 138-139; 173pp; English.
XX
CC AAV68800 to AAV68998 represent nucleotide sequences which encode human
CC breast tumour specific polypeptides. Detection or measurement of
CC human breast tumour specific polypeptides and nucleotide sequences,
CC or the corresponding RNA in a sample, is used for diagnosis and
CC monitoring of breast cancer. Human breast tumour specific polypeptides
CC and nucleotide sequences, and the vectors containing the DNAs, are also
CC useful in vaccines for inhibiting development (for prevention or
CC therapy) of breast cancer. The polypeptides may also be used to
CC raise monoclonal antibodies, used as immunoassay reagents.
XX
SQ Sequence 1853 BP; 521 A; 381 C; 492 G; 431 T; 28 other;
XX
Query Match 12.4%; Score 252; DB 19; Length 1853;
Best Local Similarity 99.7%; Pred. No. 8.9e-88;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 34 TCTTCTGTGAAGAGCCATTGCTCTCAGAGCAAGATGGGCAAGTGGTCCCGTTGC 93
Db 256 TCTTCTGTGAAGAGCCATTGCTCTCAGAGCAAGATGGGCAAGTGGTCCCGTTGC 315
QY 94 TTCCCTCTGCTGCAGGAGAGCGGCAAGCAAGCTGGGCACTTCTGAGACACAGAGAC 153
Db 316 TTCCCTCTGCTGCAGGAGAGCGGCAAGCAAGCTGGGCACTTCTGAGACACAGAGAC 375
QY 154 TCTGCTATGAAGACACTCAGAGACAGATGGGCAAGTGGTGGCCGCACTTCCCTGC 213
Db 376 TCTGCTATGAAGACACTCAGAGACAGATGGGCAAGTGGTGGCCGCACTTCCCTGC 435
QY 214 TGCAGGGGAGTGGCAAGACCAACGTGGCGCTTCTGAGACACAGACGACTGCTATG 273
Db 436 TGCAGGGGAGTGGCAAGACCAACGTGGCGCTTCTGAGACACAGACGACTGCTATG 495
QY 274 AAGACACTCAGGAACAAGATGGGCAAGTGGTGTCTGACACTGCTTCCCTCGCAGGGG 333
Db 496 AAGACACTCAGGAACAAGATGGGCAAGTGGTGTCTGACACTGCTTCCCTCGCAGGGG 555
QY 334 AGC 336
Db 556 AGC 558

RESULT 41
AAC81007
ID AAC81007 standard; cDNA; 1853 BP.
XX
AC AAC81007;
XX
DT 13-FEB-2001 (first entry)
XX
DE Human B1Agl antigen protein coding exon cDNA seq ID NO: 295.
XX
KW Human; breast tumour-specific antigen; cytostatic; vaccine;
XX breast cancer; B1Agl1; B1Agl1; B15Agl1; ss.
XX
OS Homo sapiens.
XX
PN WO200061753-A2.
XX
PD 19-OCT-2000.
XX
PF 07-APR-2000; 2000MO-US09312.
XX
PR 09-APR-1999; 99US-0289198.
XX
PR 28-OCT-1999; 99US-0429755.
XX
PR 23-MAR-2000; 2000US-0534825.
XX
PA (CORI-) CORIXA CORP.
XX
PI Frudakis TN, Smith JM, Reed SG, Misher LE, Retter MM, Dillon DC;
XX
```

DR WPI: 2000-628403/60.

XX An isolated polypeptide comprising an immunogenic portion of a breast
PT tumor protein used for inhibiting the development of cancer, especially
PT breast cancer, and monitoring cancer progression in a patient -
XX
XX
PS Claim 4; Page 172-173; 187pp; English.

CC The present sequence is given in a specification relating to compositions
CC and methods for the treatment and diagnosis of breast cancer. Nucleotide
CC sequences that are preferentially expressed in breast tumour tissue, and
CC the polypeptides encoded by such nucleotide sequences, are used in
CC compositions and vaccines to inhibit the development of cancer,
CC especially breast cancer. The progression of a cancer may be monitored by
CC carrying out detection of tumour-specific antigens at subsequent time
CC points and comparing the results from the different time points.
CC CD4+ and/or CD8+ T-cells isolated from the cancer patient may be treated
CC with tumour-specific polypeptides, polynucleotides encoding the
CC polypeptides or antigen presenting cells expressing the polypeptides. The
CC cells are then administered to the patient to inhibit development of
CC cancer.

XX
SQ Sequence 1853 BP; 521 A; 381 C; 492 G; 431 T; 28 other;

Query Match 12.4%; Score 252; DB 21; Length 1853;
Best Local Similarity 99.7%; Pred. No. 8.9e-88;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAGCCATTGTTGCTCAGAGAGCAAGTGGGCAAGTGTGCGCCGTTGC 93
DB TCTTCTGTGAAGAGCCATTGTTGCTCAGAGAGCAAGTGGGCAAGTGTGCGCCGTTGC 315

QY 94 TTCCCTGCTGCAGGAGAGCGCGCAAGAGCAAGTGGGCAAGTGTGCGCCGTTGC 153
DB TTCCCTGCTGCAGGAGAGCGCGCAAGAGCAAGTGGGCAAGTGTGCGCCGTTGC 375

QY 154 TCTGATATGAAGCACTCTGAGAGCAAGTGGGCAAGTGGGCAAGTGTGCGCCGTTGC 213
DB TCTGATATGAAGCACTCTGAGAGCAAGTGGGCAAGTGGGCAAGTGTGCGCCGTTGC 435

QY 214 TGCAGGGGGAGTGGCAAGAGCAAGTGGGCAAGTGGGCAAGTGTGCGCCGTTGC 273
DB TGCAGGGGGAGTGGCAAGAGCAAGTGGGCAAGTGGGCAAGTGTGCGCCGTTGC 495

QY 274 AAGACACTAGAGAAAGATGGGCAAGTGGGCAAGTGGGCAAGTGTGCGCCGTTGC 333
DB AAGACACTAGAGAAAGATGGGCAAGTGGGCAAGTGGGCAAGTGTGCGCCGTTGC 555

QY 334 AGC 336
DB 556 AGC 558

RESULT 42
AAA06594
ID AAA06594 standard; cDNA; 1853 BP.

XX
XX
AC AAA06594;
XX
XX
DT 13-JUN-2000 (first entry)
XX
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:369.
XX
XX Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW immunogenic; cytostatic; vaccine; ss.
XX
XX Homo sapiens.
OS
XX
PN WO200004149-A2.
XX
XX 27-JAN-2000.
PD
XX
PF 14-JUL-1999; 99WO-US15838.

XX
PR 14-JUL-1998; 98US-0115453.
PR 14-JUL-1998; 98US-0116134.
PR 23-SEP-1998; 98US-0159812.
PR 23-SEP-1998; 98US-0159822.
PR 15-JAN-1999; 98US-0232149.
PR 15-JAN-1999; 98US-0232880.
PR 09-APR-1999; 99US-0288946.
XX
XX (CORI-) CORIXA CORP.
XX
XX Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;
WPI: 2000-171268/15.

DR
PT New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein -
XX
XX
PS Claim 50; Page 219-220; 263pp; English.

CC The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumour protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC the polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AA06241 to AA06691 and
CC AA06200 to AA06200 represent sequences used in the exemplification of
CC the present invention.

XX
SQ Sequence 1853 BP; 521 A; 381 C; 492 G; 431 T; 28 other;

Query Match 12.4%; Score 252; DB 21; Length 1853;
Best Local Similarity 99.7%; Pred. No. 8.9e-88;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAGCCATTGTTGCTCAGAGAGCAAGTGGGCAAGTGTGCGCCGTTGC 93
DB TCTTCTGTGAAGAGCCATTGTTGCTCAGAGAGCAAGTGGGCAAGTGTGCGCCGTTGC 315

QY 94 TTCCCTGCTGCAGGAGAGCGCGCAAGAGCAAGTGGGCAAGTGTGCGCCGTTGC 153
DB TTCCCTGCTGCAGGAGAGCGCGCAAGAGCAAGTGGGCAAGTGTGCGCCGTTGC 375

QY 154 TCTGATATGAAGCACTCTGAGAGCAAGTGGGCAAGTGGGCAAGTGTGCGCCGTTGC 213
DB TCTGATATGAAGCACTCTGAGAGCAAGTGGGCAAGTGGGCAAGTGTGCGCCGTTGC 435

QY 214 TGCAGGGGGAGTGGCAAGAGCAAGTGGGCAAGTGGGCAAGTGTGCGCCGTTGC 273
DB TGCAGGGGGAGTGGCAAGAGCAAGTGGGCAAGTGGGCAAGTGTGCGCCGTTGC 495

QY 274 AAGACACTAGAGAAAGATGGGCAAGTGGGCAAGTGGGCAAGTGTGCGCCGTTGC 333
DB AAGACACTAGAGAAAGATGGGCAAGTGGGCAAGTGGGCAAGTGTGCGCCGTTGC 555

QY 334 AGC 336
DB 556 AGC 558

RESULT 43
AAS63803
ID AAS63803 standard; cDNA; 1853 BP.

XX
XX
AC AAS63803;
XX
XX
DT 29-JAN-2002 (first entry)
XX

DE Human prostate cDNA clone B305D splice variant #4.
 XX Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
 KW Homo sapiens.
 OS
 XX MO200173032-A2.
 PN
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001MO-US09919.
 XX
 PR 27-MAR-2000; 2000US-0536857.
 PR 09-MAY-2000; 2000US-0568100.
 PR 12-MAY-2000; 2000US-0570737.
 PR 13-JUN-2000; 2000US-0593793.
 PR 27-JUN-2000; 2000US-0605783.
 PR 10-AUG-2000; 2000US-0636215.
 PR 29-AUG-2000; 2000US-0651236.
 PR 06-SEP-2000; 2000US-0657279.
 PR 10-OCT-2000; 2000US-0679426.
 PR 10-OCT-2000; 2000US-0685166.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;
 XX
 DR MPI; 2001-639232/73.
 XX
 PT New human prostate-specific polypeptides and polynucleotides useful for
 PT the diagnosis and treatment of cancer, especially prostate cancer -
 XX
 PS Claim 1; Page 346-347; 579pp; English.
 XX
 CC The invention relates to isolated prostate-specific
 CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
 CC antibodies raised against the polypeptides (or antigenic epitopes
 CC derived from them) and antigen-presenting cells expressing the
 CC polypeptides. The antibodies are useful for detecting the presence of
 CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
 CC the antigen-presenting cells are useful for stimulating and/or expanding
 CC T cells specific for a tumour protein, and for inhibiting the development
 CC of cancer especially prostate cancer. Compositions comprising the
 CC polynucleotide and/or polypeptide are useful for stimulating an immune
 CC response, and for treating cancer. The oligonucleotide is useful for
 CC detecting cancer. The present sequence is a prostate specific
 CC polynucleotide of the invention.
 CC
 XX Sequence 1853 BP; 521 A; 381 C; 492 G; 431 T; 28 other;
 SQ
 Query Match 12.4%; Score 252; DB 22; Length 1853;
 Best Local Similarity 99.7%; Pred. No. 8.9e-88;
 Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 34 TCTTCTGTGAAGAAGCCATTGGTCTCAGAGCAAGATGGGCAAGTGGTCCGCTTGC 93
 DB 256 TCTTCTGTGAAGAAGCCATTGGTCTCAGAGCAAGATGGGCAAGTGGTCCGCTTGC 315
 QY 94 TTCCTCTGTGCAAGGAGAGCGGCAAGAGCAACGTGGGCACTTCTGAGACCAAGAGAC 153
 DB 316 TTCCTCTGTGCAAGGAGAGCGGCAAGAGCAACGTGGGCACTTCTGAGACCAAGAGAC 375
 QY 154 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGTCCGCTTCCCTGC 213
 DB 376 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGTCCGCTTCCCTGC 435
 QY 214 TGGAGGGGAGTGGCAAGCAACGTGGGCGTCTGAGACCAAGCAAGCACTGCTATG 273
 DB 436 TGGAGGGGAGTGGCAAGCAACGTGGGCGTCTGAGACCAAGCAAGCACTGCTATG 495
 QY 274 AAGACACTGAGAAAGATGGGCAAGTGGTCTGAGCACTTCCCTCTCAGAGGGG 333

DB 496 AAGACACTGAGAAAGATGGGCAAGTGGGCAAGTGGTCCGCTTCCCTGAGAGGGG 555
 QY 334 AGC 336
 DB 556 AGC 558
 RESULT 44
 AAH93710
 ID AAH93710 standard; cDNA; 1853 BP.
 XX
 AC AAH93710;
 XX
 DT 04-OCT-2001 (first entry)
 XX
 DE Human prostate-specific cDNA sequence B305D splice variant #4.
 XX
 KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
 KW cytostatic; gene therapy; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO200151633-A2.
 XX
 PD 19-JUL-2001.
 XX
 PF 16-JAN-2001; 2001MO-US01574.
 XX
 PR 14-JAN-2000; 2000US-0483672.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
 PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skelky YAW;
 PI Wang A, Meagher MJ;
 XX
 DR MPI; 2001-425873/45.
 XX
 PT New polynucleotide encoding a prostate-specific protein, for
 PT diagnosing, monitoring and treating prostate cancer in a patient and
 PT for use in vaccines -
 XX
 PS Claim 1; Page 344-345; 543pp; English.
 XX
 CC The present invention describes polynucleotide sequences (I) which encode
 CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
 CC and can be used in vaccine production and gene therapy. (I), (II),
 CC antibodies to (II), fusion proteins comprising (II), and isolated
 CC T cells prepared using (I) or (II) are used treat cancer in a patient.
 CC (I) and the antibodies are also used in the detection of cancer in a
 CC patient. The cancer that is diagnosed or treated is particularly
 CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
 CC (I) can be used for monitoring the progression of cancer in a patient.
 CC (I) and (II) can also be used to improve diagnostic and therapeutic
 CC methods for prostate cancer. They can indicate the level of metastasis
 CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
 CC AAH01318 represent polynucleotide and amino acid sequences used in the
 CC exemplification of the present invention.
 CC
 XX Sequence 1853 BP; 521 A; 381 C; 492 G; 431 T; 28 other;
 SQ
 Query Match 12.4%; Score 252; DB 22; Length 1853;
 Best Local Similarity 99.7%; Pred. No. 8.9e-88;
 Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 34 TCTTCTGTGAAGAAGCCATTGGTCTCAGAGCAAGATGGGCAAGTGGTCCGCTTGC 93
 DB 256 TCTTCTGTGAAGAAGCCATTGGTCTCAGAGCAAGATGGGCAAGTGGTCCGCTTGC 315
 QY 94 TTCCTCTGTGCAAGGAGAGCGGCAAGAGCAACGTGGGCACTTCTGAGACCAAGAGAC 153
 DB 316 TTCCTCTGTGCAAGGAGAGCGGCAAGAGCAACGTGGGCACTTCTGAGACCAAGAGAC 375

QY 154 TCTGCTATGAGACACTCAGAGCAAGATGGGCAAGTGGTGGCCGCTTCCCTGC 213
DB 376 TCTGCTATGAGACACTCAGAGCAAGATGGGCAAGTGGTGGCCGCTTCCCTGC 435
QY 214 TGCAGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACACGACGACTCTGTATG 273
DB 436 TGCAGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACACGACGACTCTGTATG 495
QY 274 AAGACACTCAGAGCAAGATGGGCAAGTGGTGGCCGCTTCCCTGCAGAGGGG 333
DB 496 AAGACACTCAGAGCAAGATGGGCAAGTGGTGGCCGCTTCCCTGCAGAGGGG 555
QY 334 AGC 336
DB 556 AGC 558

RESULT 45
AAH85024
ID AAH85024 standard; CDNA; 1853 BP.
AC AAH85024;
XX 25-SEP-2001 (first entry)
XX
DE Human prostate-specific cDNA sequence B305D splice variant #4.
XX
XX Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
KM chromosome 22q11.2; prostate-specific protein; chromosome 1;
KW prostate specific antigen; PSA; ss.
XX
OS Homo sapiens.
XX
XX WO200134802-A2.
XX
XX 17-MAY-2001.
XX
XX 09-NOV-2000; 2000WO-US30904.
XX
XX 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Reltter MW, Stolk JA, Day CH, Skelky YAW, Wang A;
XX
XX WPI; 2001-308785/32.
XX
XX
XX Isolated polypeptide comprising at least an immunogenic portion of a
PT prostate-specific protein, useful in the diagnosis and therapy of
PT prostate cancer -
XX
PS Claim 31; Page 244; 325pp; English.
XX
XX The present invention describes an isolated polypeptide (P1) comprising
CC at least an immunogenic portion of a prostate-specific protein, or its
CC variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
CC (N1) have cytostatic activity and can be used in vaccine production.
CC The polypeptides, nucleic acids and antibodies from the present
CC invention are useful in the diagnosis and therapy of prostate cancer.
CC Prostate specific genes p704P, p712P, p774P, p775P and B305D are located
CC in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
CC region. Prostate specific antigen (PSA) P501S was located on
CC chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent
CC polynucleotide and polypeptide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 1853 BP; 521 A; 381 C; 492 G; 431 T; 28 other;

Query Match 12.4%; Score 252; DB 22; Length 1853;
Best Local Similarity 99.7%; Pred. NO. 8.9e-88;

Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 34 TCTTCTGTAAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGGTGGCCGCTGC 93
DB 256 TCTTCTGTAAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGGTGGCCGCTGC 315
QY 94 TTCCCTGCTGAGGAGAGAGCGGCAAGCAAGTGGGCACTTCTGAGACGACGAGC 153
DB 316 TTCCCTGCTGAGGAGAGAGCGGCAAGCAAGTGGGCACTTCTGAGACGACGAGC 375
QY 154 TCTGCTATGAGACACTCAGAGCAAGATGGGCAAGTGGTGGCCGCTTCCCTGC 213
DB 376 TCTGCTATGAGACACTCAGAGCAAGATGGGCAAGTGGTGGCCGCTTCCCTGC 435
QY 214 TGCAGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACACGACGACTCTGTATG 273
DB 436 TGCAGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACACGACGACTCTGTATG 495
QY 274 AAGACACTCAGAGCAAGATGGGCAAGTGGTGGCCGCTTCCCTGCAGAGGGG 333
DB 496 AAGACACTCAGAGCAAGATGGGCAAGTGGTGGCCGCTTCCCTGCAGAGGGG 555
QY 334 AGC 336
DB 556 AGC 558

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OM nucleic - nucleic search, using sw model

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Word size : 15

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Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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23: /SIDS2/gcgdata/geneSeq/geneSeqn-emb1/NA2001B.DAT.*
24: /SIDS2/gcgdata/geneSeq/geneSeqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2000	100.0	2000	21 AAC81012	Human B1Agl1 antiig
2	2000	100.0	2000	22 AA167212	B305D isoform C sp
3	2000	100.0	2000	22 AAS63808	Human prostate CDN
4	2000	100.0	2000	22 AAH93715	Human prostate-spe
5	2000	100.0	2000	22 AAH85029	Human prostate-spe
6	2000	100.0	2000	22 ABL95179	Human prostate-spe
7	2000	100.0	2000	24 AAS99859	Human B305D splice
8	2000	100.0	2000	24 AAS99858	Breast tumour-spec
9	1949	97.5	2000	21 AAA06599	Human immunogenic

10	1551	77.5	2040	21 AAC81013	Human B1Agl1 antiig
11	1551	77.5	2040	22 AA167213	B305D isoform C sp
12	1551	77.5	2040	22 AAS63809	Human prostate CDN
13	1551	77.5	2040	22 AAH93716	Human prostate-spe
14	1551	77.5	2040	22 AAH85030	Human prostate-spe
15	1551	77.5	2040	22 AAH02781	Prostate tumour an
16	1551	77.5	2040	24 ABL95180	Human B305D splice
17	1551	77.5	2040	24 AAS99859	Breast tumour-spec
18	1500	75.0	2040	21 AAA06600	Human immunogenic
19	1128	56.4	1155	21 AAC81011	Human B1Agl1 antiig
20	1128	56.4	1155	21 AAA06598	Human immunogenic
21	1128	56.4	1155	22 AA167211	B305D isoform C sp
22	1128	56.4	1155	22 AAS63807	Human prostate CDN
23	1128	56.4	1155	22 AAH93714	Human prostate-spe
24	1128	56.4	1155	22 AAH85028	Human prostate-spe
25	1128	56.4	1155	22 AAH02779	Prostate tumour an
26	1128	56.4	1155	24 ABL95178	Human B305D splice
27	1128	56.4	1155	24 AAS99857	Breast tumour-spec
28	1044	52.2	1590	24 AAS99869	Breast tumour-spec
29	975	48.8	1155	24 AAS99872	Breast tumour-spec
30	491	24.6	1512	19 AAV68995	DNA molecule endod
31	491	24.6	1512	21 AAC81006	Human B1Agl1 antiig
32	491	24.6	1512	21 AAA06593	Human immunogenic
33	491	24.6	1512	22 AAS63802	Human prostate CDN
34	491	24.6	1512	22 AAH93709	Human prostate-spe
35	491	24.6	1512	22 AAS985023	Human prostate-spe
36	491	24.6	1512	22 AAH02774	Prostate tumour an
37	491	24.6	1512	24 ABL95173	Human B305D splice
38	491	24.6	1512	24 ABL95173	Human breast tumou
39	491	24.6	1512	24 AAS99852	Breast tumour-spec
40	252	12.6	1853	19 AAV68996	DNA molecule endod
41	252	12.6	1853	21 AAC81007	Human B1Agl1 antiig
42	252	12.6	1853	21 AAA06594	Human immunogenic
43	252	12.6	1853	22 AAS63803	Human prostate CDN
44	252	12.6	1853	22 AAH93710	Human prostate-spe
45	252	12.6	1853	22 AAH85024	Human prostate-spe

ALIGNMENTS

RESULT 1	
AAC81012	
ID	AAC81012 strand; cDNA; 2000 BP.
AC	AAC81012;
DT	13-FEB-2001 (first entry)
DE	Human B1Agl1 antigen splice isoform B1C-8 cDNA.
XX	Human; breast tumour-specific antigen; cytosolic; vaccine;
KW	breast cancer; B1Agl1; B1Agl1; B1Agl1; ss.
KW	
OS	Homo sapiens.
XX	
PN	WO200061753-A2.
XX	
PD	19-OCT-2000.
XX	
PF	07-APR-2000; 2000WO-US09312.
XX	
PR	09-APR-1999; 990US-0288198.
XX	
PR	28-OCT-1999; 990US-0429755.
XX	
PR	23-MAR-2000; 2000US-0534825.
XX	
PA	(CORI-) CORIXA CORP.
PI	Frudakis TN, Smith JM, Reed SG, Misher LE, Retter MM, Dillon DC;
XX	
DR	WPI; 2000-628403/60.
XX	
DR	P-PSDB; AAB28629.
XX	

QY 1801 ATTCGATCATGAGAAAAAGCAGATAGAGTGTGAAATTAATGATTCGAGCTTCT 1860
|||||
DB 1801 ATTCGATCATGAGAAAAAGCAGATAGAGTGTGAAATTAATGATTCGAGCTTCT 1860
QY 1861 CTTACTGTGTAAGAAAAAGACATCTTCGATGAAATAGTACGTGGCGGAGAAAT 1920
|||||
DB 1861 CTTACTGTGTAAGAAAAAGACATCTTCGATGAAATAGTACGTGGCGGAGAAAT 1920
QY 1921 GCCATGCTAAGAGCTGAGCTAGACACATGAACATCAGAGCGAGCTAAATTAATTA 1980
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DB 1921 GCCATGCTAAGAGCTGAGCTAGACACATGAACATCAGAGCGAGCTAAATTAATTA 1980
QY 1981 AAAAAAAAAAAAAAAAAA 2000
|||||
DB 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 2
AA167212
ID AA167212 standard; cDNA; 2000 BP.
XX
AC AA167212;
XX
DI 11-FEB-2002 (first entry)
XX
DE B305D isoform C splice variant 2 encoding cDNA.
XX
KM Genetic subtraction; DNA microarray analysis; polymerase chain reaction;
KM cancer; B305D; ss.
OS Homo sapiens.
FH Key 1.1971
FT CDS /tag= a
FT /product= "B305D isoform C splice variant"
PN WO200175171-A2.
XX 11-OCT-2001.
XX 02-APR-2001; 2001WO-US10631.
XX 03-APR-2000; 2000US-194241P.
PR 20-JUL-2000; 2000US-219862P.
PR 27-JUL-2000; 2000US-221300P.
PR 18-DEC-2000; 2000US-256592P.
XX (CORI-) CORIXA CORP.
PA
PI Houghton RL, Dillon DC, Molesch DA, Xu J, Zehentner B, Persing DH;
XX WPI: 2001-626449/72.
DR P-PSDB; AAG63977.
XX
PT Identifying tissue (tumour)-specific polynucleotides overexpressed in
PT tissue of interest as compared to control tissue, for detecting cancer
PT cells in patient, comprises DNA microarray analysis or quantitative
PT polymerase chain reaction -
XX
PS Claim 4: Page 94; 127pp; English.
XX
CC The invention relates to identifying tissue-specific polynucleotides (P)
CC that involves performing a genetic subtraction to identify pool of (P)
CC from tissue of interest (TI), performing DNA microarray analysis to
CC identify first subset of polynucleotides (SP1) at least 2-fold over
CC expressed in TI, and performing quantitative polymerase chain reaction
CC (PCR) analysis on SP1 to identify second subset of (P). The method is
CC useful for determining the presence or absence of a cancer cell in a
CC patient, monitoring the progression of cancer in a patient using a
CC biological sample such as blood, serum, lymph nodes, bone marrow, sputum,
CC urine or a tumour biopsy sample. The methods are useful for determining
CC the presence or absence of or monitoring progression of prostate, breast,

CC colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver,
CC gastric, kidney, bladder, pancreatic or endometrial cancer. The present
CC sequence represents a cDNA encoding a B305D isoform C splice variant.
XX
SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 other:
Query Match 100.0%; Score 2000; DB 22; Length 2000;
Best local similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGCTTGAGTGGTATTCATGCGCGCTCTTCTGTGAAGAACCATTTGGTCTC 60
|||||
DB 1 ATGTGCTTGAGTGGTATTCATGCGCGCTCTTCTGTGAAGAACCATTTGGTCTC 60
QY 61 AGAGCAAGATGGGCAAGTGGTCCGCTGCTCCCTGCGAGGGAGAGCGGCAAG 120
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DB 61 AGAGCAAGATGGGCAAGTGGTCCGCTGCTCCCTGCGAGGGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGGAGACACAGACGACTGCTATGAAAGCACTCAGAGCAAG 180
|||||
DB 121 AGCAACGTGGGCACTTCTGGAGACACAGAGACTGCTATGAAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTCCGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACGTG 240
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DB 181 ATGGGCAAGTGGTCCGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACGTG 240
QY 241 GCGGCTTCTGGAGACCCAGACGACCTGCTATGAAACACTCAGAAACAGATGGGCAAG 300
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DB 241 GCGGCTTCTGGAGACCCAGACGACCTGCTATGAAACACTCAGAAACAGATGGGCAAG 300
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|||||
DB 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGGAGGGCAAGCAAGGAGGCGCTTGG 360
QY 361 GGAGACTACGATGACAGTCCCTTCATGAGCCAGGTACACGCTCGGTGGAGAGATCTG 420
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DB 361 GGAGACTACGATGACAGTCCCTTCATGAGCCAGGTACACGCTCGGTGGAGAGATCTG 420
QY 421 GACAACTCCACAGAGCTCCGTGGGTAAAGTCCCAAGAAAGATCTCATCTGCATG 480
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DB 421 GACAACTCCACAGAGCTCCGTGGGTAAAGTCCCAAGAAAGATCTCATCTGCATG 480
QY 481 CTCAGGACACTGACGTGTAACAAGAGCAAGCAAGAGCACTCTACATCTGGCC 540
|||||
DB 481 CTCAGGACACTGACGTGTAACAAGAGCAAGCAAGAGCACTCTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAACTCTCTGCTGGACAGACGATGTCACTTAAT 600
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DB 541 TCTGCCAATGGGAATTCAGAACTCTCTGCTGGACAGACGATGTCACTTAAT 600
QY 601 GTCCCTTGACAAACAAAAGAGACGCTCGATTAAGGCGGTACAAATGCCAGAAATGAA 660
|||||
DB 601 GTCCCTTGACAAACAAAAGAGACGCTCGATTAAGGCGGTACAAATGCCAGAAATGAA 660
QY 661 TGTGCGTAAATGCTGTGGAACATGGCACTGATCCAAATATTCAGATGATGAAT 720
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DB 661 TGTGCGTAAATGCTGTGGAACATGGCACTGATCCAAATATTCAGATGATGAAT 720
QY 721 ACCACTCTGACCTAGCGTATCTATAATGAAGATTAATGAGCCAAAGCACTGCTTA 780
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DB 721 ACCACTCTGACCTAGCGTATCTATAATGAAGATTAATGAGCCAAAGCACTGCTTA 780
QY 781 TATGTCGCTGATATGCAATCAAAAAACAGCATGGCTCACACACTGTACTTGGTGA 840
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DB 781 TATGTCGCTGATATGCAATCAAAAAACAGCATGGCTCACACACTGTACTTGGTGA 840
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|||||
DB 901 CTGATATGATATGAAGAGCTGCTCATATCTGTATGTTGTGATCAGCAAGTATA 960

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QY 1261 AAGCATAAAGTATATATGTTGGGATTTACTAGAAAACTGACTAATGGTGTCTGCTGCC 1320
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QY 1381 CCTGACACAGCAAGAGTATCAGAGATTTGGCAATTTAGTTCTGACTACAAAGAA 1440
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Db 1381 CCTGACACAGCAAGAGTATCAGAGATTTGGCAATTTAGTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAATCTCTCTGAAACAGCAACCCAGAACAGCTTAAACCTGACA 1500
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QY 1561 TTTATGCTCTTCCAGAAATGAGAGACACGGAATCTCTGTCGATTCCTCCAGAAAC 1620
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QY 1621 CTGACTAATGTTGCTGCTGCTGCAATGCTGATGATTAATTCCTCCAGAGAAAGC 1680
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QY 1681 AGAAGACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAAGTATCAAGTACGAGAA 1740
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Db 1681 AGAAGACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAAGTATCAAGTACGAGAA 1740
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Db 1741 CAAAATGATCTCAGAGCAATTTTGTGAAGAACAGAACTGGAATATTACACGATGAG 1800
QY 1801 ATTTCTGATGATGAAAGAGCAGATGAAAGTGTGTAATAAATGATTTCTGACCTTTCT 1860
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Db 1801 ATTTCTGATGATGAAAGAGCAGATGAAAGTGTGTAATAAATGATTTCTGACCTTTCT 1860
QY 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGCAATGAAATAGTACGTTGCGGGAAGAAATT 1920
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QY 1921 GCCATGCTAAGACTGAGAGCTAGACACAATGAATCAAGACAGCCAGCTAAAAAAGAAAA 1980
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Db 1921 GCCATGCTAAGACTGAGAGCTAGACACAATGAATCAAGACAGCCAGCTAAAAAAGAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAA 2000
    |||||||
Db 1981 AAAAAAAAAAAAAAAAAAAAA 2000

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RESULT 3
AAS63808
ID AAS63808 standard; cDNA; 2000 BP.
XX
AC AAS63808;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human prostate cDNA clone B305D splice variant #9.
XX
KM Human; prostate cancer; ss; cytosolic; immunostimulant; tumour.
XX
OS Homo sapiens.
XX
PN W0200173032-A2.
XX
PD 04-OCT-2001.
XX
PE 27-MAR-2001; 2001WC-US09919.
XX
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657219.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Ketter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAM, Hepler WT, Henderson RA;
XX
DR WPI: 2001-639232/73.
XX
DR P-PSDB; AA069778.
XX
XX New human prostate-specific polypeptides and polynucleotides useful for
XX the diagnosis and treatment of cancer, especially prostate cancer -
XX
PS Claim 1; Page 349-350; 579pp; English.
XX
CC The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
CC the antigen-presenting cells are useful for stimulating and/or expanding
CC T cells specific for a tumour protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.
XX
SQ Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 other;
XX
Query Match 100.0%; Score 2000; DB 22; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGTTGAGTGTGATTCATCCGCGCTCTCTCTGTGAAGAACCAATTGGTCTC 60
    |||||||
Db 1 ATGTGTTGAGTGTGATTCATCCGCGCTCTCTCTGTGAAGAACCAATTGGTCTC 60
QY 61 AGAGCAAGATGGCAAGTGGTGGCTGCTTCCCTGCTGACGAGAGCGGCAAG 120
    |||||||
Db 61 AGAGCAAGATGGCAAGTGGTGGCTGCTTCCCTGCTGACGAGAGCGGCAAG 120

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QY	121	AGCAAGCTGGGCACTTCTGGAAGCCACGACGACTGCTGTATGAAACACTAGAGCAAG	180
Db	121	AGCAAGCTGGGCACTTCTGGAAGCCACGACGACTGCTGTATGAAACACTAGAGCAAG	180
QY	181	ATGGGCAAGAGGAGCGGCCCACTGCTTCCCTGCTGAGGGGGAGTGGCAAGCAAGCTG	240
Db	181	ATGGGCAAGAGTGTGCGGCCCACTGCTTCCCTGCTGAGGGGGAGTGGCAAGCAAGCTG	240
QY	241	GGCGCTTCTGAGAACCCACGACGACTGCTGTATGAAGACACTCAGGAACAAATGGGCAAG	300
Db	241	GGCGCTTCTGAGAACCCACGACGACTGCTGTATGAAGACACTCAGGAACAAATGGGCAAG	300
QY	301	TGGTGCTGGCACTGCTTCCCTGCTGCTCAGGGGGAGGGGCAAGAGTGGCGCTTGG	360
Db	301	TGGTGCTGGCACTGCTTCCCTGCTGCTCAGGGGGAGGGGCAAGAGTGGCGCTTGG	360
QY	361	GGAGACTACGATACAGAGTGGCTTCATGAGAGCCAGGTACCAAGTCCGTGAGAAATGTG	420
Db	361	GGAGACTACGATACAGAGTGGCTTCATGAGAGCCAGGTACCAAGTCCGTGAGAAATGTG	420
QY	421	GACAACTCCACAGAGTGGCTGTGGGGTAAAGTCCCGAAGAGATCTATGCTCATG	480
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QY	481	CTCAGGACACTACAGCGTGAACAGAGGAGCAAGCAAAAGAGACTGCTATCATGTGCC	540
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QY	541	TCCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGGACAGACGATGTCACATTAT	600
Db	541	TCCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGGACAGACGATGTCACATTAT	600
QY	601	GTCCTTGACAAACAAAAGAGAGAGTCTGATPAAAGCCGTACATGCGCAGAAATATA	660
Db	601	GTCCTTGACAAACAAAAGAGAGAGTCTGATPAAAGCCGTACATGCGCAGAAATATA	660
QY	661	TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGAGATGGAAT	720
Db	661	TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGAGATGGAAT	720
QY	721	ACCACTGTGACACAGCTATCTATATGAAGATTAATTAATGCGCCAAAGCACTGCTTA	780
Db	721	ACCACTGTGACACAGCTATCTATATGAAGATTAATTAATGCGCCAAAGCACTGCTTA	780
QY	781	TATGTCGTATATTCGATCAATAAAACAAAGCATGGCGCTCACACCACTGTTATGGTGA	840
Db	781	TATGTCGTATATTCGATCAATAAAACAAAGCATGGCGCTCACACCACTGTTATGGTGA	840
QY	841	CATGAGCAAAACAGCAAGTGTGAATTTTATCATAGAAAAAAGCGAATTTAAATGCA	900
Db	841	CATGAGCAAAACAGCAAGTGTGAATTTTATCATAGAAAAAAGCGAATTTAAATGCA	900
QY	901	CTGATATGATATGGAAGGATGCTGCTCATAACTGCTGTATGTTGGATCAGCAAGTATA	960
Db	901	CTGATATGATATGGAAGGATGCTGCTCATAACTGCTGTATGTTGGATCAGCAAGTATA	960
QY	961	GTCAGCTTACTTGAGCAAAATATTTGATATCTTCCAAAGATCTATCTGGACAGAG	1020
Db	961	GTCAGCTTACTTGAGCAAAATATTTGATATCTTCCAAAGATCTATCTGGACAGAG	1020
QY	1021	GGCAGAGATGCTGTTTATCTATCATCATGTAATTTGGCAGTACTTCTGACTATC	1080
Db	1021	GGCAGAGATGCTGTTTATCTATCATCATGTAATTTGGCAGTACTTCTGACTATC	1080
QY	1081	AAAGAAAAACAGATGCTAAAAAATCTTTGTGAAGACGCAATCCAGAAACAGACTTAAAG	1140
Db	1081	AAAGAAAAACAGATGCTAAAAAATCTTTGTGAAGACGCAATCCAGAAACAGACTTAAAG	1140
QY	1141	CTGACATCAGAGAGAGTACAAAGCTTCAAAGGCTCAAAGGAGTAAATAGCCAGCAGAGAA	1200
Db	1141	CTGACATCAGAGAGAGTACAAAGGCTCAAAGGCTCAAAGGAGTAAATAGCCAGCAGAGAA	1200

QY	1201	ATGTCCTAAAGACCCAGAAATTAATTAAGAGTGGTGATAGAGAGTTGAAGAAATGAAG	1260
Db	1201	ATGTCCTAAAGACCCAGAAATTAATTAAGAGTGGTGATAGAGAGTTGAAGAAATGAAG	1260
QY	1261	AAGCATGAAAGTAAATATATGGGATACGTAGAAAACCTACATAATGGTGCTACTGCTGGC	1320
Db	1261	AAGCATGAAAGTAAATATATGGGATACGTAGAAAACCTACATAATGGTGCTACTGCTGGC	1320
QY	1321	AATGGTATATGGAATTAATTCCTCAAAGAGAGCAGAAACCTCGAAATTCAGCAATTT	1380
Db	1321	AATGGTATATGGAATTAATTCCTCAAAGAGAGCAGAAACCTCGAAATTCAGCAATTT	1380
QY	1381	CTTGACACAAGAAAGTGAGAGTATCACAGATTTGCGAATTATGTTCTTGACTACAAAGA	1440
Db	1381	CTTGACACAAGAAAGTGAGAGTATCACAGATTTGCGAATTATGTTCTTGACTACAAAGA	1440
QY	1441	AAACAGATGCCAAATATACCTTCTTGAAAACACGACCCGAAACAGACTTAAGCTGACA	1500
Db	1441	AAACAGATGCCAAATATACCTTCTTGAAAACACGACCCGAAACAGACTTAAGCTGACA	1500
QY	1501	TCACAGAAAGAGTCACAAAGCTTTGAGGCGAGTGAATAATGGCCAGCCAGACTAGAAAT	1560
Db	1501	TCACAGAAAGAGTCACAAAGCTTTGAGGCGAGTGAATAATGGCCAGCCAGAGCTAGAAAT	1560
QY	1561	TTTATGCGCTATCGAGAAATGAGAAAGACACGGAAATCATCTGCGATTTCCACAGAAAC	1620
Db	1561	TTTATGCGCTATCGAGAAATGAGAAAGACACGGAAATCATCTGCGATTTCCACAGAAAC	1620
QY	1621	CTGACTAATGGTGCCACTGCTGGCCATTTGGTATGATGATTAATTCTCCAAAGAAAGC	1680
Db	1621	CTGACTAATGGTGCCACTGCTGGCCATTTGGTATGATGATTAATTCTCCAAAGAAAGC	1680
QY	1681	AGAACACCTGAAAGCCAGCAATTTCCCTGCACACTGAGAAATGAGAGTATCACAGTACGAA	1740
Db	1681	AGAACACCTGAAAGCCAGCAATTTCCCTGCACACTGAGAAATGAGAGTATCACAGTACGAA	1740
QY	1741	CAAAATGATACCTCGAAGCAATTTTGTGAAGAACAGAACACTGGAATATTACAGATGAG	1800
Db	1741	CAAAATGATACCTCGAAGCAATTTTGTGAAGAACAGAACACTGGAATATTACAGATGAG	1800
QY	1801	ATTCCTGATTCATGAGAAAGACGATRAGAAAGTGTTGAATAATGATTCGACGTTTCT	1860
Db	1801	ATTCCTGATTCATGAGAAAGACGATRAGAAAGTGTTGAATAATGATTCGACGTTTCT	1860
QY	1861	CTTAGTGTGAAGAAAGAAAGACATCTTGCAATGAATAATGATACGTTGCGGGAGAAAT	1920
Db	1861	CTTAGTGTGAAGAAAGAAAGACATCTTGCAATGAATAATGATACGTTGCGGGAGAAAT	1920
QY	1921	GCCATGCTAAGACTGAGCTAGACACATGAAACATCAGAGCCAGCTAAAAA	1980
Db	1921	GCCATGCTAAGACTGAGCTAGACACATGAAACATCAGAGCCAGCTAAAAA	1980
QY	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
RESULT 4			
AAH93715			
ID	AAH93715	standard; cDNA; 2000 BP.	
XX	AAH93715;		
XX	04-Oct-2001	(first entry)	
DE	Human prostate-specific cDNA sequence B305D splice variant #9.		
KW	Human: prostate cancer; prostate-specific; diagnosis; vaccine;		
KW	cytostatic; gene therapy; metastasis; ss.		
XX	Homo sapiens.		
XX	OS		
XX	MO200151633-A2.		
XX	FN		

QY	1561	TTTTGGCTATCGAAGAAATGAAAGACGCGAGTACTCATGTGCGATTCCCGAAGAAC	1620
Dp	1561	TTTTTGGCTATCGAAGAAATGAAAGACGCGAGTACTCATGTGCGATTCCCGAAGAAC	1620
QY	1621	CTGACTAATGGTCCCACTGCTGGCAATGGTGATGATGATTAAATTCCTCCAAAGAGAGC	1680
Dp	1621	CTGACTAATGGTCCCACTGCTGGCAATGGTGATGATGATTAAATTCCTCCAAAGAGAGC	1680
QY	1681	AGAACACCTAAGGCCAGCAATTTCTGACACTGAGAAATGAAGATATCACAGTGCAGAA	1740
Dp	1681	AGAACACCTAAGGCCAGCAATTTCTGACACTGAGAAATGAAGATATCACAGTGCAGAA	1740
QY	1741	CAAAATGATCTCAGAGCAATTTTGTGAAGAAACAGAACACTGGAATTTACAGATGAG	1800
Dp	1741	CAAAATGATCTCAGAGCAATTTTGTGAAGAAACAGAACACTGGAATTTACAGATGAG	1800
QY	1801	ATTCTGATTCATGACAGAAAGCAGATAGAGTGTTGAAAAAATGAATTCCTGAGCTTCT	1860
Dp	1801	ATTCTGATTCATGACAGAAAGCAGATAGAGTGTTGAAAAAATGAATTCCTGAGCTTCT	1860
QY	1861	CTTAGTGTGTAAGAAAGAAAGACATCTGCATGAAATATGATAGCTGCGGGAGAAATT	1920
Dp	1861	CTTAGTGTGTAAGAAAGAAAGACATCTGCATGAAATATGATAGCTGCGGGAGAAATT	1920
QY	1921	GCCATGCTAAGACTGAGCTAGACACATGAAGAACATCAGAGCCACCTAAAAAAGAAAAA	1980
Dp	1921	GCCATGCTAAGACTGAGCTAGACACATGAAGAACATCAGAGCCACCTAAAAAAGAAAAA	1980
QY	1981	AAAAAAAAAAAAAAAAAAAA 2000	
Dp	1981	AAAAAAAAAAAAAAAAAAAA 2000	

XX	AAH85029	
ID	AAH85029 standard; CDNA; 2000 BP.	
XX		
AC	AAH85029;	
XX		
DT	25-SEP-2001 (first entry)	
DE		
XX	Human prostate-specific cDNA sequence B305D splice variant #9.	
KM	Human: prostate cancer; therapy; diagnosis; cat eye syndrome;	
KW	chromosome 22q11.2; prostate-specific protein; chromosome 1;	
XX	prostate specific antigen; PSA; ss.	
OS	Homo sapiens.	
PN	WO200134802-A2.	
XX		
PD	17-MAY-2001.	
XX		
PF	09-NOV-2000; 2000WO-US30904.	
XX		
PR	12-NOV-1999; 99US-0439313.	
XX	18-NOV-1999; 99US-0443686.	
PA	(CORI-) CORIXA CORP.	
PI	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;	
PI	Kalos MD, Retter MW, Stolk JA, Day CH, Skeiky YAW, Wang A;	
DR	WPI; 2001-308785/32.	
PT	Isolated polypeptide comprising at least an immunogenic portion of a	
PT	prostate-specific protein, useful in the diagnosis and therapy of	
PS	prostate cancer .	
XX		
XX	claim 31; Page 247-248; 325pp; English.	
XX	The present invention describes an isolated polypeptide (p1) comprising	
XX	at least an immunogenic portion of a prostate-specific protein, or its	

CC variant. Also described are polynucleotides (N1) encoding (P1) and
CC (N1) have cytostatic activity and can be used in vaccine production.
CC The polypeptides, nucleic acids and antibodies from the present
CC invention are useful in the diagnosis and therapy of prostate cancer.
CC Prostate specific genes P704P, P712P, P712P, P774P, P775P and B305d are located
CC in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
CC region. Prostate specific antigen (PSA) P501s was located on
CC chromosome 1. AAH84671 to AAH85143 and AAC99000 to AAC99977 represent
CC polynucleotide and polypeptide sequences used in the exemplification
CC of the present invention.

50 sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 other;

Query Match	100.0%	Score 2000;	DB 22;	Length 2000;
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Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

29 1 ATGGTGGTGAGGTTGATTCATGCCGGCTGCCCTCTTCTGTGAAGAAGCCATTGGTCTC 60

Db 1 ATGGTGGTTGAGGTTGATTCATGCCGGCTGCCCTCTTCTGTGAGAGCAGCCATTGGTCTC 60

61 AGAGCAAGATGGGCAAGTGGTCTGCTTCCCTGCTGCAGGGAGAGCGGCAAG 120

Db 61 AGGAGCAAGATGGGCAAGTGGTCTGCCGTTGCTTCCCTGCTGCAGGAGAGCGGCAAG 120

QY 121 AGCAACGTGGGCACTTCTGGAGACCACGACGACTCTGCTATGAAGACACTCAGGAGCAAG 180

Db 121 AGCAACGTGGGCACTTCTGGAGACCACGACGACTCTGCTATGAAGACACTCAGGAGCAAG 180

181 ATGGCAGTGGTGGCCGCGCACTGCTCCCTGCTGCAGGGGAGTGGCAAGACCACTG 240

Db 181 ATGGGCAAGTGGTGGCCGCCACTGCTTCCCTGCTGCAGGGGAGTGGCAAGACCAACGTG 240

241 GCGCTTCTGGAGACCAGCAGACTCTGCTATGAAGACACTCAGGAACAGATGGGCAAG 300

Db 241 GCGCTTCTGGAGACCACGACTCTGCTATGAGACACTCAGGAACAAGATGGCAAG 300

QY 301 TGGTCTGCCACTGCTTCCCCCTGCTGCAGGGGAGCGGCAAGAGCAAGGTGGCGCTTG 360

Db 301 TGGTGTGCCACTGCTTCCCTGCTGCAGGGGAGCGGCAAGAGCAAGGTGGCGCTTGG 360

QY 361 GGAGACTACGATGACAGTGCCTTCATGGAGGCCCAAGGTACCACGTCCTGGAGAAGATCTG 420

Db 361 GGAGACTACGATGACAGTGCCCTTCATGGAGGCCCAAGTACCACGTCCTGGAGAAGATCTG 420

421 GACAAGCTCCACAGAGCTGCCCTGGTAAAGTCCCCAGAAAGGATCTCATCGTCATG 480

Db 421 GACAAGCTCCACAGAGCTGCTGGGTAAAGTCCCGAGAAAGGATCTCATCGTCATG 480

QY 481 CTCAGGACACTGACGTGAACAAGAAGGACAAGCAAAGAGGACTGCTCTACATCTGCC 540

Db 481 CTCAGGACACTGACGTGAACAAGAAGGACAAGCAAAGAGGACTGCTCTACATCTGGCC 540

QY 541 TCTGCCAATGGGAATTCAGAAGTAGTAAACTCCTGCTGGACAGACGATGTCACCTTAAT 600

Db 541 TCTGCCAATGGGAATTCAGAAGTAGTAAACTCCCTGCTGGACAGACGATGTCACTTAAT 600

QY 601 GTCCCTGACACAAAGAAGAGGACAGCTCTGATAAAGGCCGTACATGCCAGGAAGATGAA 660

Db 601 GTCCCTGACACAAAGAGAGACAGCTCTGATAAAGGCCGTACATGCCAGGAAGATGAA 660

QY 661 TGTGGTTAATGTTGCTGGACATGGCACTGATCCAAATATTCAGATGAGTATGGAAT 720

Db 661 TGTGCGTTAATGTTGCTGGACATGGCACTGATCCAAATATTCAGATGAGTATGGAAT 720

QY 721 ACCACTCTGCACCTACGCTATCTATAATGAAGATAAATTATGGCCAAAGCACTGCTCTTA 780

Db 721 ACCACTCTGCACCTACGCTATCTATAATGAAGATAAATTAATGCCCAAGCACCTGCTCTTA 780

QY 781 TATGGTCTGATATCGAATCAAAAAACAAGCATGGCCTCACACCACCTGTTACTTGGTGA 840

Db 781 TATGGTCTGATATCGAATCAAAAAACAAGCATGGCCTCACACCACCTGTTACTTGGTGA 840

OY	841	CATGAGCAAAAACGCAAGTCGGGAATTTTTTAACTAACAAAAAAGCCGAATTTAAATCA	900
Dd	841	CATGAGCAAAAACGCAAGTCGGGAATTTTTTAACTAACAAAAAAGCCGAATTTAAATCA	900
OY	901	CTGGATGATATGTGAAGACTGCTCATACTCGTGATGTGTTGTGATCAGCAGATTA	960
Dd	901	CTGGATGATATGTGAAGACTGCTCATACTCGTGATGTGTTGTGATCAGCAGATTA	960
OY	961	GTCAGCCTTCTACTTGAGCAAATATTGATGTAATCTTCTCAAGATCTATCTGGACAGCG	1020
Dd	961	GTCAGCCTTCTACTTGAGCAAATATTGATGTAATCTTCTCAAGATCTATCTGGACAGCG	1020
OY	1021	GCCAGAGATGCTGCTTCTTACTGCATCATCATGTAAATTTGCCAGTTACTTTCTGCATCAC	1080
Dd	1021	GCCAGAGATGCTGCTTCTTACTGCATCATCATGTAAATTTGCCAGTTACTTTCTGCATCAC	1080
OY	1081	AAAGAAAAACAGATGCTAAAAATCTCTTGAAACACGAAATCCAGAACAAACTTAAAG	1140
Dd	1081	AAAGAAAAACAGATGCTAAAAATCTCTTGAAACACGAAATCCAGAACAAACTTAAAG	1140
OY	1141	CTGACATCAGAGAGAAGTCACAAGAGTTCAAAGGCAATGAAATATAGCCAGCCAGAGAAA	1200
Dd	1141	CTGACATCAGAGAGAAGTCACAAGAGTTCAAAGGCAATGAAATATAGCCAGCCAGAGAAA	1200
OY	1201	ATGTCCTCAAGAACAGAAATTAATTAAGATGATGATAGAGAGTTGAGAAACAAATTAAG	1260
Dd	1201	ATGTCCTCAAGAACAGAAATTAATTAAGATGATGATAGAGAGTTGAGAAACAAATTAAG	1260
OY	1261	AAGCATGAAATTAATATGTGGGATTAATCTGAAACCTGACTAATGTGTCACCTGAGC	1320
Dd	1261	AAGCATGAAATTAATATGTGGGATTAATCTGAAACCTGACTAATGTGTCACCTGAGC	1320
OY	1321	AATGGTGATTAATGATTAATTTCTCAAAGAGAGCAGAAACCTGAAATATCAGCAATTT	1380
Dd	1321	AATGGTGATTAATGATTAATTTCTCAAAGAGAGCAGAAACCTGAAATATCAGCAATTT	1380
OY	1381	CCTGACCAACGAAATGGAAGATACACAGAAATTTGGAAATTTAGTTCTGACATCAAAABA	1440
Dd	1381	CCTGACCAACGAAATGGAAGATACACAGAAATTTGGAAATTTAGTTCTGACATCAAAABA	1440
OY	1441	AAACGATGCCAAATATCTCTTGAAACACGCAACCAGAAACAAAGACTTAAAGCTGACA	1500
Dd	1441	AAACGATGCCAAATATCTCTTGAAACACGCAACCAGAAACAAAGACTTAAAGCTGACA	1500
OY	1501	TCAGAGAGAAGTCACAAAGGCTTGAAGGGCAGTGAATAATGGCCAGCCAGAGCTAGAAAAT	1560
Dd	1501	TCAGAGAGAAGTCACAAAGGCTTGAAGGGCAGTGAATAATGGCCAGCCAGAGCTAGAAAAT	1560
OY	1561	TTTATGAGCTATCGAAGAAATGAAGAACACGGAAGTACTCATGTGGATTTCCACAGAAAC	1620
Dd	1561	TTTATGAGCTATCGAAGAAATGAAGAACACGGAAGTACTCATGTGGATTTCCACAGAAAC	1620
OY	1621	CTGACTAATGCTGACCTGCTGGCAATGGTGAATGATGATTAATTCCTCCCAAGAAAGAGC	1680
Dd	1621	CTGACTAATGCTGACCTGCTGGCAATGGTGAATGATGATTAATTCCTCCCAAGAAAGAGC	1680
OY	1681	AGAACACCTGAAGCCAGCAATTTCTGACACTGAGAAATGAAGAGATACACAGTGACGAA	1740
Dd	1681	AGAACACCTGAAGCCAGCAATTTCTGACACTGAGAAATGAAGAGATACACAGTGACGAA	1740
OY	1741	CAAAATGATCTCGAAGCAATTTTGTGAAGAACACAAACACTGGAATATTACACATATAG	1800
Dd	1741	CAAAATGATCTCGAAGCAATTTTGTGAAGAACACAAACACTGGAATATTACACATATAG	1800
OY	1801	ATTCTGATTCATGAAGAAAGACAGATTAAGATGCTGTGAAGAAANTGAATCTGAGCTTCT	1860
Dd	1801	ATTCTGATTCATGAAGAAAGACAGATTAAGATGCTGTGAAGAAANTGAATCTGAGCTTCT	1860
OY	1861	CTTAGTTGTAAAGAAAGAAAGACATCTTGCAATGAAGAAATAGTACGTTGGGGAAACAAAT	1920
Dd	1861	CTTAGTTGTAAAGAAAGAAAGACATCTTGCAATGAAGAAATAGTACGTTGGGGAAACAAAT	1920
OY	1921	GCCATGCTAAGACTGAGCTAGACACATGAACATCAGAGCCAGCTAAAAAAAAAAAAA	1980

Dd	1972	GCCATGCTAGACTGGAGCTAGACCAATGAACAATCAGAGCGCAGCTAAAAAAAAAAAAA	1980
Oy	1981	AAAAAAAAAAAAAAAAAAAAA	2000
Dd	1981	AAAAAAAAAAAAAAAAAAAAA	2000
<p style="text-align:center;">RESULT 6 AAH02780 ID AAH02780 standard; cDNA; 2000 BP.</p>			
Nc	AAH02780;		
Dt	14-JUN-2001	(first entry)	
Xx	Prostate tumour antigen determined cDNA splice variant of B305D #9.		
Xx	Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;		
Kw	prostate cancer; immunogenic; cytostatic; vaccine; ss.		
Xx	Homo sapiens.		
Os	W0200125272-A2.		
Pn	12-APR-2001.		
Pf	04-OCT-2000; 2000WO-US27464.		
Pf	04-OCT-1999; 99US-0157455.		
Pr	(CORI-) CORIXA CORP.		
Pa	Xu J, Skeiky YAM, Reed SG, Cheever MA;		
Pi	MP1: 2001-245062/25.		
Dk	P-PSDB; AAB74816.		
Xx	Prostate specific protein and its encoding polynucleotide, useful for		
Pt	the treatment and diagnosis of prostate cancer -		
Xx	Claim 50; Page 232; 276pp; English.		
Ps	The present invention describes an isolated polypeptide (I) comprising		
Xx	at least an immunogenic portion of a prostate tumour antigen protein or		
Cc	its variant. (I) have cytostatic activity and can be used in vaccine		
Cc	production. (I), prostate tumour antigen polynucleotides, an antigen		
Cc	presenting cell (ApC e.g. a dendritic cell) that expresses (I), and a		
Cc	pharmaceutical composition containing (I) are useful for inhibiting the		
Cc	development of cancer in a patient. Antibodies specific for prostate		
Cc	specific proteins and oligonucleotides that hybridize to a		
Cc	polynucleotide that encodes a prostate specific protein are useful		
Cc	for detecting the presence or absence of a cancer or monitoring the		
Cc	progression of a cancer, especially prostate cancer.		
Cc	AAH02422 to AAH2772.AAB74798 to AAB74821 and AAB74830 are sequences		
Cc	used in the exemplification of the present invention.		
SQ	Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 other:		
<p style="text-align:center;">Query Match 100.0%; Score 2000; DB 22; Length 2000; Best Local Similarity 100.0%; Pred. No. 0; Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0</p>			
Oy	1	ATGTGTTTGGATTGCATTCATGCCGGCTGCTCTTGTAAGAAGCATTTGGTCTC	60
Dd	1	ATGTGTTTGGATTGCATTCATGCCGGCTGCTCTTGTAAGAAGCATTTGGTCTC	60
Oy	61	AGGACCAAGATGGGCAAGTGTGTCGCCCTTCCCTGCTGCAGAGGAGCGGCAAG	120
Dd	61	AGGACCAAGATGGGCAAGTGTGTCGCCCTTCCCTGCTGCAGAGGAGCGGCAAG	120
Oy	121	AGCAACGTGGGCACTTGTGGAGACCACGACGACTCTGCTATAAGACACTCAGAGCAAG	180
Dd	121	AGCAACGTGGGCACTTGTGGAGACCACGACGACTCTGCTATAAGACACTCAGAGCAAG	180

Db 121 AGCAACGTGGGCACTTCTGGAGACCAAGCACTCTCTATGTAAGACACTCAGAGCAAG 180
Oy 181 ATGGCAAGTGGTGGCGCCACTGTTCCCTGCTGAGGGGGAGTGGCAAGCAACGAG 240
Db 181 ATGGGCAAGTGGTGGCGCCACTGTTCCCTGCTGAGGGGGAGTGGCAAGCAACGAG 240
Oy 241 GGGGCTTCTGGAGACCAAGCACTCTGCTATGAAGACACTCAGAAACAAGATGGGCAAG 300
Db 241 GGGGCTTCTGGAGACCAAGCACTCTGCTATGAAGACACTCAGAAACAAGATGGGCAAG 300
Oy 301 TGGTCTGCACTGCTTCCCTGCTGAGGGGAGCGGCAAGCAAGTGGGCGCTTGG 360
Db 301 TGGTCTGCACTGCTTCCCTGCTGAGGGGAGCGGCAAGCAAGTGGGCGCTTGG 360
Oy 361 GGAGACTACGATGACAGTGGCTTCAATGAGCCAGGTACCAAGTCCGTGGAAGATCTGG 420
Db 361 GGAGACTACGATGACAGTGGCTTCAATGAGCCAGGTACCAAGTCCGTGGAAGATCTGG 420
Oy 421 GACAAGCTCCACAGAGCTGCTGTTGGGGTAAAGTCCCGAAGAGGATCTCATGCTATG 480
Db 421 GACAAGCTCCACAGAGCTGCTGTTGGGGTAAAGTCCCGAAGAGGATCTCATGCTATG 480
Oy 481 CTCAGGAGACCTGACGTGACAAAGAAAGCAAGCAAGAGAGAGCTGCTTACATCTGGCC 540
Db 481 CTCAGGAGACCTGACGTGACAAAGAAAGCAAGCAAGAGAGAGCTGCTTACATCTGGCC 540
Oy 541 TCTGCCAATGGGAATTCAGAAAGTAAACCTGCTGAGAGAGATGCACTTAACTTAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAACCTGCTGAGAGAGATGCACTTAACTTAT 600
Oy 601 GTCTCTGACAAACAAAAGAGACAGCTGATAAAGGCCGTACAAATGCCAGAGATGAA 660
Db 601 GTCTCTGACAAACAAAAGAGAGACAGCTGATAAAGGCCGTACAAATGCCAGAGATGAA 660
Oy 661 TGTGGGTATATGTTGCTGGACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGGGTATATGTTGCTGGACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
Oy 721 ACCACTCTGCACTAGCGTATCTATATGAAGATTAATTAATGGCCAAACACAGCTGCTTA 780
Db 721 ACCACTCTGCACTAGCGTATCTATATGAAGATTAATTAATGGCCAAACACAGCTGCTTA 780
Oy 781 TATGCTGCTGATATGCAATCAAAAAACAAGCATGGCTCACACCACTGTTACTTGGTGA 840
Db 781 TATGCTGCTGATATGCAATCAAAAAACAAGCATGGCTCACACCACTGTTACTTGGTGA 840
Oy 841 CATGAGCAAAAAACAGCAAGTCTGAATTTTAAATCAGAAAAAAGCGAATTTAAATGA 900
Db 841 CATGAGCAAAAAACAGCAAGTCTGAATTTTAAATCAGAAAAAAGCGAATTTAAATGA 900
Oy 901 CTGGATAGATATGAAGAGCTGCTCATACTGCTGATGTTGTTGGATCAGCAAGTATA 960
Db 901 CTGGATAGATATGAAGAGAGCTGCTCATACTGCTGATGTTGTTGGATCAGCAAGTATA 960
Oy 961 GTACAGCTTCTACTTGGAGCAAAATATGATATCTTCAAGATCTATCTGACAGAG 1020
Db 961 GTACAGCTTCTACTTGGAGCAAAATATGATATCTTCAAGATCTATCTGACAGAG 1020
Oy 1021 GCCAAGAGATATGCTGTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Db 1021 GCCAAGAGATATGCTGTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Oy 1081 AAGAAAAACAGATGCTAAATCTCTGTAAGCAAGAAATCCAGAAACAAGCTTTAAG 1140
Db 1081 AAGAAAAACAGATGCTAAATCTCTGTAAGCAAGAAATCCAGAAACAAGCTTTAAG 1140
Oy 1141 CTGACATCAGAGAGAGTCAAAAGTTCAAGGAGTGAAGAAATAGCAGCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTCAAAAGTTCAAGGAGTGAAGAAATAGCAGCAGAGAA 1200
Oy 1201 ATGTCTCAAGAACCAAAATTAATTAAGATGATAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAAATTAATTAAGATGATAGAGAGTTGAAGAAATGAAG 1260

Oy 1261 AAGCATGAAGTAAATATGTTGGGATTAATAGAAAACTGACATTAATGTGTCACCTGGC 1320
Db 1261 AAGCATGAAGTAAATATGTTGGGATTAATAGAAAACTGACATTAATGTGTCACCTGGC 1320
Oy 1321 AATGGTAAATGATTAATTCCTCAAAAGAGAGCAGAAACCTGGAATAGCAATTT 1380
Db 1321 AATGGTAAATGATTAATTCCTCAAAAGAGAGCAGAAACCTGGAATAGCAATTT 1380
Oy 1381 CCTGACACGAAAGTGAAGATATCAAGAAATTTGGCAATTAATTTCTGACTACAAAGA 1440
Db 1381 CCTGACACGAAAGTGAAGATATCAAGAAATTTGGCAATTAATTTCTGACTACAAAGA 1440
Oy 1441 AAACAGATGCCAAATATCTCTGTAAGCAAGAACCCGAAACAAACTTAAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATATCTCTGTAAGCAAGAACCCGAAACAAACTTAAAGCTGACA 1500
Oy 1501 TCAGAGGAAGAGTCAACAAAGGCTTGAAGGCAAGTGAAGATGGCCAGCAGAGTGAAGAT 1560
Db 1501 TCAGAGGAAGAGTCAACAAAGGCTTGAAGGCAAGTGAAGATGGCCAGCAGAGTGAAGAT 1560
Oy 1561 TTTATGCTATGAGAAATGAAGAAACGACGAGTACTCATGTGCGATTTCCAGAAAC 1620
Db 1561 TTTATGCTATGAGAAATGAAGAAACGACGAGTACTCATGTGCGATTTCCAGAAAC 1620
Oy 1621 CTGACTAATGGGCCACTGCTGGCAATGGTGAATGATGATTAATTTCTCCAGGAAGAGC 1680
Db 1621 CTGACTAATGGGCCACTGCTGGCAATGGTGAATGATGATTAATTTCTCCAGGAAGAGC 1680
Oy 1681 AGAACACCTGAAGAGCCAGCAATTTCTGACACTGAGAAATGAAGATATCAAGTACGAA 1740
Db 1681 AGAACACCTGAAGAGCCAGCAATTTCTGACACTGAGAAATGAAGATATCAAGTACGAA 1740
Oy 1741 CAAATGATATCTCAGAGCAATTTTGTGAAGAACAGAACTGGAATTTATACAGTGAAG 1800
Db 1741 CAAATGATATCTCAGAGCAATTTTGTGAAGAACAGAACTGGAATTTATACAGTGAAG 1800
Oy 1801 AATCTGATTCATGAAGAAAGAGATGAAGAGTGGTGAAGAAATGAATCTGAGCTTCT 1860
Db 1801 AATCTGATTCATGAAGAAAGAGATGAAGAGTGGTGAAGAAATGAATCTGAGCTTCT 1860
Oy 1861 CTAGTTGTAGAAAGAAAGAGACATCTTGCATGAAGAAATAGTACGTTGGGGAAAGAT 1920
Db 1861 CTAGTTGTAGAAAGAAAGAGACATCTTGCATGAAGAAATAGTACGTTGGGGAAAGAT 1920
Oy 1921 GCCATCTAAGACTGAGCTAGACACATGAATCAATCAGAGCCAGCTAAAAAAGAAAA 1980
Db 1921 GCCATCTAAGACTGAGCTAGACACATGAATCAATCAGAGCCAGCTAAAAAAGAAAA 1980
Oy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 7
AB195179
ID AB195179 standard; cDNA; 2000 BP.
XX
XX ABL95179;
XX
XX 19-JUL-2002 (first entry)
XX
XX Human B305D splice variant cDNA sequence SEQ ID NO 374.
XX
XX Human; cancer; prostate cancer; vaccine; cytosolic; immunostimulant;
KW gene therapy; gene; ss.
XX
XX Homo sapiens.
XX
XX US2002022248-A1.
XX
XX 21-FEB-2002.
XX


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Oy 1201 ATGTCACAGAACGACAAATAATAATAGATGCTGATAGAGGTTGAAGAAATGAAG 1260
    |||||||
Db 1201 ATGTCACAGAACGACAAATAATAATAGATGCTGATAGAGGTTGAAGAAATGAAG 1260
Oy 1261 AAGCATGAAAGTAATATATGTGGGATTACTAGAAAACCTGACTAATGTGTCTACTGTGCG 1320
    |||||||
Db 1261 AAGCATGAAAGTAATATATGTGGGATTACTAGAAAACCTGACTAATGTGTCTACTGTGCG 1320
Oy 1321 AATGTGTATATAGATTAATCTCTCAAGAGAGACAGAACCTGAAATATAGCAATTT 1380
    |||||||
Db 1321 AATGTGTATATAGATTAATCTCTCAAGAGAGAGACAGAACCTGAAATATAGCAATTT 1380
Oy 1381 CCTGACACGAAAGTAAGAGATATCACAGAAATTTGGAAATTTAGTTCTTCTACTACAAAGAA 1440
    |||||||
Db 1381 CCTGACACGAAAGTAAGAGATATCACAGAAATTTGGAAATTTAGTTCTTCTACTACAAAGAA 1440
Oy 1441 AAACAGATGCCAAATTAATCTCTTGAAAACAGCAACCCAGAAACAGACTTTAAAGCTGACA 1500
    |||||||
Db 1441 AAACAGATGCCAAATTAATCTCTTGAAAACAGCAACCCAGAAACAGACTTTAAAGCTGACA 1500
Oy 1501 TCAGAGGAAGAGTCAACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAGCTAGAAAAT 1560
    |||||||
Db 1501 TCAGAGGAAGAGTCAACAAAGGCTTGAGGGCAGTGAATAATGGCCAGAGCTAGAAAAT 1560
Oy 1561 TTTATGCGTATGAGAAATGAAGAACGACGGAAGTACTGATGCGGATTTCCAGAAAAC 1620
    |||||||
Db 1561 TTTATGCGTATGAGAAATGAAGAACGACGGAAGTACTGATGCGGATTTCCAGAAAAC 1620
Oy 1621 CTGACTAATGTGCGCACTGCTGGCAATGCTGATGATTAATTCCTCCAGAGAAAGAC 1680
    |||||||
Db 1621 CTGACTAATGTGCGCACTGCTGGCAATGCTGATGATTAATTCCTCCAGAGAAAGAC 1680
Oy 1681 AAGAACCTGAAAAGCCAGCAATTTCTGACACTGAGAAATGAAGAGATATCACAGTGCAGAA 1740
    |||||||
Db 1681 AAGAACCTGAAAAGCCAGCAATTTCTGACACTGAGAAATGAAGAGATATCACAGTGCAGAA 1740
Oy 1741 CAAATGATACTCAGAAAGCAATTTTGTGAAGAACAGAACACTGGAATTTTACACGATGAG 1800
    |||||||
Db 1741 CAAATGATACTCAGAAAGCAATTTTGTGAAGAACAGAACACTGGAATTTTACACGATGAG 1800
Oy 1801 AATTCGATTCATGAAGAAAGCAGATGAGAGTGGTTGAAAAATGAATTCGAGCTTTCT 1860
    |||||||
Db 1801 AATTCGATTCATGAAGAAAGCAGATGAGAGTGGTTGAAAAATGAATTCGAGCTTTCT 1860
Oy 1861 CTTAGCTGTGAAGAAAGAAAGACATCTTGCAATGAAATATAGTACGTTGGGGGAAAGAAAT 1920
    |||||||
Db 1861 CTTAGCTGTGAAGAAAGAAAGACATCTTGCAATGAAATATAGTACGTTGGGGGAAAGAAAT 1920
Oy 1921 GCCATGCTAAGACTGAGCTAGACACATGCAATGCAAGCCAGCTAAAAAAGAAAAA 1980
    |||||||
Db 1921 GCCATGCTAAGACTGAGCTAGACACATGCAATGCAAGCCAGCTAAAAAAGAAAAA 1980
Oy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
    |||||||
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

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RESULT 8
AAS99858
ID AAS99858 standard; cDNA; 2000 BP.

AC AAS99858;
XX 12-MAR-2002 (first entry)
DE Breast tumour-specific DNA B11a1 splice variant B11C-8.
XX
XX Human: breast cancer. PCR primer; ss; cytosolic; immunostimulant;
KW tumour; vaccine; immunogenic.
XX Homo sapiens.
OS
XX
PN WO200190152-A2.

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XX 29-NOV-2001.
PD
XX
PF 22-MAY-2001; 2001WO-US16776.
XX
XX 24-MAY-2000; 2000US-0577505.
PR 08-JUN-2000; 2000US-0590583.
PR 26-OCT-2000; 2000US-0699295.
PR 16-MAR-2001; 2001US-0810936.
XX
XX (CORI-) CORIXA CORP.
XX
PI Fruadakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
PI Wang A, Skelky YAM, Harlocker SL, Day CH;
XX
XX WPI: 2002-089919/12.
DR P-PSDB; AAU74378.
XX
XX New breast tumour proteins and polynucleotides encoding them, useful for
XX treating and/or preventing cancer, particularly breast cancer, and for
XX eliciting humoral and/or cellular immune response -
XX
XX Claim 1; Page 224; 245pp; English.
XX
XX The invention relates to novel breast tumour polynucleotides and
XX pharmaceutical compositions for treating and/or preventing cancer,
XX particularly breast cancer, and for eliciting an immune response,
XX particularly humoral and/or cellular immune response. The polynucleotides
XX may be used as probes or primers for nucleic acid hybridisation, in the
XX design and preparation of ribozyme molecules for inhibiting expression of
XX tumour polypeptides and proteins, and in recombinant DNA molecules to
XX direct expression of a polypeptide in host cells. AAS99570-AAS99888
XX represent novel human breast cancer protein coding sequences and
XX PCR primers of the invention.
XX
XX Sequence 2000 BP; 698 A; 388 C; 489 G; 425 T; 0 other:
XX
XX Query Match 100.0%; Score 2000; DB 24; Length 2000;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AATGCTGTGAGGTTGATTCATGCGGCTGCTTCTGTGAAGAACCATTTGGTCTC 60
    |||||||
Db 1 AATGCTGTGAGGTTGATTCATGCGGCTGCTTCTGTGAAGAACCATTTGGTCTC 60
Oy 61 AGGAGCAAGATGGGCAAGTGTGCTCCGTTGCTTCCCTGTCAGAGGACGGCAAG 120
    |||||||
Db 61 AGGAGCAAGATGGGCAAGTGTGCTCCGTTGCTTCCCTGTCAGAGGACGGCAAG 120
Oy 121 AGCAAGCTGGGCACTTCTGGAAGCAAGCAAGCACTGCTATGAAGACACTCAGAGCAAG 180
    |||||||
Db 121 AGCAAGCTGGGCACTTCTGGAAGCAAGCAAGCACTGCTATGAAGACACTCAGAGCAAG 180
Oy 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGTCAGAGGAGTGGCAAGCAACGTG 240
    |||||||
Db 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGTCAGAGGAGTGGCAAGCAACGTG 240
Oy 241 GGGGCTTGTGAGACACGACGACTGCTATGAAGCACTCAGAAACAAGATGGCAAG 300
    |||||||
Db 241 GGGGCTTGTGAGACACGACGACTGCTATGAAGCACTCAGAAACAAGATGGCAAG 300
Oy 301 TGGTGTGCGCACATGCTTCCCTGCTCAGAGGGGAGGGCAAGAGTGGGCGCTGG 360
    |||||||
Db 301 TGGTGTGCGCACATGCTTCCCTGCTCAGAGGGGAGGGCAAGAGTGGGCGCTGG 360
Oy 361 GGAGCTACAGATGACAGTGCCTTCATGAGACCAGATACCACTCCGTGAGAAATCTG 420
    |||||||
Db 361 GGAGCTACAGATGACAGTGCCTTCATGAGACCAGATACCACTCCGTGAGAAATCTG 420
Oy 421 GACAAAGCTCCACAGAGCTGCTGTGGGTTAAAGTCCCGAAGAAAGATCTCATGTCATG 480
    |||||||
Db 421 GACAAAGCTCCACAGAGCTGCTGTGGGTTAAAGTCCCGAAGAAAGATCTCATGTCATG 480

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QY	481	CTGAGGACACTGACGTGAACAAAGAGACAAAGACACGTCGTCTACATCTGGCC	540
Db	481	CTCAGGGACACTGACGTGAACAAAGAGAGCAAGCAAAAGAGACGTCTCATCTGGCC	540
QY	541	TCCTGCATATGGGAATTTCAGAAAGTAAATAAATCTCTGTCGACAGAGATGTCACCTTAAT	600
Db	541	TCCTGCATATGGGAATTTCAGAAAGTAAATAAATCTCTGTCGACAGAGATGTCACCTTAAT	600
QY	601	GTCCTTGACAAACAAAAGAGAGACGCTCTGATTAAGGCCGTACAATGCCAGGAAGATGA	660
Db	601	GTCCTTGACAAACAAAAGAGAGACGCTCTGATTAAGGCCGTACAATGCCAGGAAGATGA	660
QY	661	TGTGCGCTTAATGTCTGCGAACAATGGCAGCTGATCCAAATATTCAGAGATGATGTGAAT	720
Db	661	TGTGCGCTTAATGTCTGCGAACAATGGCAGCTGATCCAAATATTCAGAGATGATGTGAAT	720
QY	721	ACCACTCTGCACCTACGCTATCTTAATTAAGAAATTAATGAGCCAAAGACCTGCTCTTA	780
Db	721	ACCACTCTGCACCTACGCTATCTTAATTAAGAAATTAATGAGCCAAAGACCTGCTCTTA	780
QY	781	TATGGTCTGATATCGAATCAAAAACAAAGCATGGCCTCACACCACTGTACTGTGGTGA	840
Db	781	TATGGTCTGATATCGAATCAAAAACAAAGCATGGCCTCACACCACTGTACTGTGGTGA	840
QY	841	CATGAGCAAAAACAGCAAGTCGTGAAATTTTATACAGAAAAACCGAATTTAATGCA	900
Db	841	CATGAGCAAAAACAGCAAGTCGTGAAATTTTATACAGAAAAACCGAATTTAATGCA	900
QY	901	CTGATATGATATGGAAGACCTGCTCATACCTGCTATGTTGTGGATACAGCAAGTTA	960
Db	901	CTGATATGATATGGAAGACCTGCTCATACCTGCTATGTTGTGGATACAGCAAGTTA	960
QY	961	GTCAGCCTTCTACTTGAAGCAAAATATTTGATGTATCTTCAAGATCTATCTGACAGAG	1020
Db	961	GTCAGCCTTCTACTTGAAGCAAAATATTTGATGTATCTTCAAGATCTATCTGACAGAG	1020
QY	1021	GCCAGAGAGTATGCTGTTTCTTAAGTCATCATCATATTAATTTGCCAGTACTTTCGACTAC	1080
Db	1021	GCCAGAGAGTATGCTGTTTCTTAAGTCATCATCATATTAATTTGCCAGTACTTTCGACTAC	1080
QY	1081	AAAGAAAACAGATGCTTAATAATCTCTTGAAACACGAATCCAGAACAGACTTAAG	1140
Db	1081	AAAGAAAACAGATGCTTAATAATCTCTTGAAACACGAATCCAGAACAGACTTAAG	1140
QY	1141	CTGACATCAGAGGAAAGATCACAAGAGTTCAAAAGCAGTGAATAATAGCAGCAGAGAAA	1200
Db	1141	CTGACATCAGAGGAAAGATCACAAGAGTTCAAAAGCAGTGAATAATAGCAGCAGAGAAA	1200
QY	1201	ATGTCTCAGAACCAGAAATTAATTAAGATGGTATAGAGAGGTTGAAGAAATGAAG	1260
Db	1201	ATGTCTCAGAACCAGAAATTAATTAAGATGGTATAGAGAGGTTGAAGAAATGAAG	1260
QY	1261	AAGATCAAAAGTATAATGTGGGATTAACATAGAAAACCTGACTAATAGGTGTCACTGTGGC	1320
Db	1261	AAGATCAAAAGTATAATGTGGGATTAACATAGAAAACCTGACTAATAGGTGTCACTGTGGC	1320
QY	1321	AATGCTATATGATTAATTTCTCTCAAAAGAGAGCAGAACCTGGAATAATCAGCAATTT	1380
Db	1321	AATGCTATATGATTAATTTCTCTCAAAAGAGAGCAGAACCTGGAATAATCAGCAATTT	1380
QY	1381	CCTGACAACGAAGTGAAGATATCAGAAATTTGGCAATTAAGTTCTGACTACAAAGAA	1440
Db	1381	CCTGACAACGAAGTGAAGATATCAGAAATTTGGCAATTAAGTTCTGACTACAAAGAA	1440
QY	1441	AAACAGATGCCAAATATCTCTCTCGAAAAACAGAACCCAGAACAGACTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAATATCTCTCTCGAAAAACAGAACCCAGAACAGACTTAAAGCTGACA	1500
QY	1501	TCAGAGGAAGAGTCACAAAGGCTTGAAGGCACTGAAATAATGGCCAGCCAGACTGGAAT	1560
Db	1501	TCAGAGGAAGAGTCACAAAGGCTTGAAGGCACTGGAATAATGGCCAGCCAGACTGGAAT	1560

QY	1561	TTTATGGCTATCGAAGAAATGAAGAAGCAAGAACTACTCATATGTCGGATTTCCCAAGAAAC	1620
Db	1561	TTTATGGCTATCGAAGAAATGAAGAAGCAAGAACTACTCATATGTCGGATTTCCCAAGAAAC	1620
QY	1621	CTGACTAATGTGGCCACTGCTGGCAATGGTGTATGATGATTAAATTCCTCCAAGGAAGAGC	1680
Db	1621	CTGACTAATGTGGCCACTGCTGGCAATGGTGTATGATGATTAAATTCCTCCAAGGAAGAGC	1680
QY	1681	AGAACACTGGAAGGCCAGCAATTTCTCTGACACTGAGAAATGAAGATATCACAGTGAAGAA	1740
Db	1681	AGAACACTGGAAGGCCAGCAATTTCTCTGACACTGAGAAATGAAGATATCACAGTGAAGAA	1740
QY	1741	CAAAATGATACACAGAACCAATTTTGTGAGAACAGAACACTGGAATTTTACAGATGAG	1800
Db	1741	CAAAATGATACACAGAACCAATTTTGTGAGAACAGAACACTGGAATTTTACAGATGAG	1800
QY	1801	ATTCTGATTCATGAGAAAAGCAGATAGACAGTGGTTGAAAAATGAATTTCTGAGCTTCT	1860
Db	1801	ATTCTGATTCATGAGAAAAGCAGATAGACAGTGGTTGAAAAATGAATTTCTGAGCTTCT	1860
QY	1861	CTTAGTGTGAAGAAAAGAAAGACATCTTGCATGAAATATGATGATTCCGGGAAGAAATT	1920
Db	1861	CTTAGTGTGAAGAAAAGAAAGACATCTTGCATGAAATATGATGATTCCGGGAAGAAATT	1920
QY	1921	GCCATGCTAAGACTGGAGCTAGACACAATGAAACATCAGAGCCAGCTTAAAAA	1980
Db	1921	GCCATGCTAAGACTGGAGCTAGACACAATGAAACATCAGAGCCAGCTTAAAAA	1980
QY	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAAA 2000	

RESULT 9
AAA06599

ID AAA06599 standard; cDNA; 2000 BP.

AA
AC AAA06599;

DT 13-JUN-2000 (first entry)

AA	DE	Human immunogenic prostate tumour protein cDNA sequence	SEQ ID NO:374.
AA	DE	Human immunogenic prostate tumour protein cDNA sequence	SEQ ID NO:374.

Human; prostate cancer; tumour; gene therapy; detection;

KW immunogenic; cytostatic; vaccine; ss.

Homo sapiens

AA WO200004149-A2.
PN

PD 27-JAN-2000.

AA 14-JUL-1999; 99WO-US15838.
PF

XX
PR 14-JUL-1998; 98US-0115453.

PR	14-JUL-1998;	98US-0116134.
PR	23-SEP-1998;	98US-0159812.

PR	23-SEP-1998;	9805-0159822.
PR	15-JAN-1999;	9905-0232149.

PR	15-JAN-1999;	99US-0232880.
PR	09-APR-1999;	99US-0288946.

XX (CORT-) CORTXA CORP.
PA

XX
PI
Pillion DC. Harlocker SL. Y

XX WPT: 2000-171268/15
DB

XX New polynitride useful for t

PT comprises an immunogenic por-

PS Claim 50; Page 222-223; 263p
yy

Dillon DC, Harlocker SL, Yagiu J, Xu J, Mitcham JL; WPI; 2000-171268/15.

New polypeptide useful for treating and diagnosing prostate cancer comprises an immunogenic portion of prostate tumor protein -

Claim 50: Page 222-223; 263bp; English.

Db 1861 CTTAGTCTAGAGAAAAGACATCTTCATGAAATAGTACGTCGGGAGCAATT 1920
QY 1921 GCCATGCTAGACCTGAGCTAGACCAATGAAACATCGAGCCGCTAAAAA 1980
Db 1921 GCCATGCTAGACCTGAGCTAGACCAATGAAACATCGAGCCGCTAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 10
AAC81013
ID AAC81013 standard; cDNA; 2040 BP.
XX AAC81013;
AC AAC81013;
XX 13-FEB-2001 (first entry)
XX Human B11A91 antigen splice isoform B11C-9-16 cDNA.
DE Human; breast tumour-specific antigen; cytostatic; vaccine;
KM Human; breast tumour-specific antigen; cytostatic; vaccine;
KM breast cancer; B18A91, B11A91, B15A91, ss.
XX Homo sapiens.
XX WO200061753-A2.
XX 19-OCT-2000.
XX 07-APR-2000; 2000WO-US09312.
XX 09-APR-1999; 99US-0289198.
PR 28-OCT-1999; 99US-0429755.
PR 23-MAR-2000; 2000US-0534825.
XX (CORI-) CORIXA CORP.
XX Frudakis TN, Smith JM, Reed SG, Misher LE, Retter MW, Dillon DC;
XX WPI: 2000-628403/60.
DR P-PSDB; AAB28630.
XX An isolated polypeptide comprising an immunogenic portion of a breast
PT tumor protein used for inhibiting the development of cancer, especially
PT breast cancer, and monitoring cancer progression in a patient -
XX Claim 4; Page 178; 187pp; English.

XX The present sequence is given in a specification relating to compositions
CC and methods for the treatment and diagnosis of breast cancer. Nucleotide
CC sequences that are preferentially expressed in breast tumour tissue, and
CC the polypeptides encoded by such nucleotide sequences, are used in
CC compositions and vaccines to inhibit the development of cancer,
CC especially breast cancer. The progression of a cancer may be monitored by
CC carrying out detection of tumour-specific antigens at subsequent time
CC points and comparing the results from the different time points.
CC C4+ and/or CD8+ T-Cells isolated from the cancer patient may be treated
CC with tumour-specific polypeptides, polynucleotides encoding the
CC polypeptides or antigen presenting cells expressing the polypeptides. The
CC cells are then administered to the patient to inhibit development of
CC cancer.

XX Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 other;
SQ

Query Match 77.5%; Score 1551; DB 21; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTTGAGTTGATTCATCGCGCTGCTTCTGTGAAGAGCATTTGGTCTC 60
Db 1 ATGTGTTGAGTTGATTCATCGCGCTGCTTCTGTGAAGAGCATTTGGTCTC 60

QY 61 AGAGCAAGATGGCAAGTGTGCTGCCGTTGCTTCCCTCTGTCAGAGGAGAGGGCAAG 120
Db 61 AGAGCAAGATGGCAAGTGTGCTGCCGTTGCTTCCCTCTGTCAGAGGAGAGGGCAAG 120
QY 121 AGCAAGCTGGGCACTTCTGGAGACACAGAGCACTCTGTTATGAAGACACTGAGAGCAAG 180
Db 121 AGCAAGCTGGGCACTTCTGGAGACACAGAGCACTCTGTTATGAAGACACTGAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCCGCTGCTTCCCTGCTGTCAGAGGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGGTGGCCGCTGCTTCCCTGCTGTCAGAGGGGAGTGGCAAGCAAGCTG 240
QY 241 GCGGCTTGGAGACACAGAGCACTCTGTTATGAAGACACTGAGAGCAAG 300
Db 241 GCGGCTTGGAGACACAGAGCACTCTGTTATGAAGACACTGAGAGCAAG 300
QY 301 TGGTGGCTGCACTGCTTCCCTGCTGTCAGAGGGGAGGAGGCAAGAGTGGGCGCTGG 360
Db 301 TGGTGGCTGCACTGCTTCCCTGCTGTCAGAGGGGAGGAGGCAAGAGTGGGCGCTGG 360
QY 361 GGAGACTAGATGACAGAGTGGCTTCATGAGAGCCAGAGTACCAAGTCCGTCGAGAGATCTG 420
Db 361 GGAGACTAGATGACAGAGTGGCTTCATGAGAGCCAGAGTACCAAGTCCGTCGAGAGATCTG 420
QY 421 GACAAAGCTCCACAGAGCTGCTGGTGGGTAAGTCCCAAGAAAGATCTCATGCTCATG 480
Db 421 GACAAAGCTCCACAGAGCTGCTGGTGGGTAAGTCCCAAGAAAGATCTCATGCTCATG 480
QY 481 CTCAGGGGACAGTACGTGCAAGAAAGAGCAAGAAAGAGAGCTGCTCATCTGCGCC 540
Db 481 CTCAGGGGACAGTACGTGCAAGAAAGAGCAAGAAAGAGAGCTGCTCATCTGCGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTGCTGTCAGAGAGATGCTCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTGCTGTCAGAGAGATGCTCAACTTAAT 600
QY 601 GTCTTGACAAACAAAAGAGAGAGAGCTGTATTAAGGCGCTACATGCGCAAGAGATGA 660
Db 601 GTCTTGACAAACAAAAGAGAGAGAGCTGTATTAAGGCGCTACATGCGCAAGAGATGA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGGGCACTGATCCAAATATTCAGAGATATGGAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGGGCACTGATCCAAATATTCAGAGATATGGAAT 720
QY 721 ACCACTGCACTAGCTATCTATTAATGAAGATTAATGAGCAAGCAAGCTGCTCTTA 780
Db 721 ACCACTGCACTAGCTATCTATTAATGAAGATTAATGAGCAAGCAAGCTGCTCTTA 780
QY 781 TATGCTGATATGCAATCAAAAACAGCATGGGCTCACACCACTGTTACTTGGTCTA 840
Db 781 TATGCTGATATGCAATCAAAAACAGCATGGGCTCACACCACTGTTACTTGGTCTA 840
QY 841 CATAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAGCAAAATTTAAATGA 900
Db 841 CATAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAGCAAAATTTAAATGA 900
QY 901 CTGATAGATATGAAGAGAGCTCTCATCTGCTGATTTGGATCGAGCAAGATATA 960
Db 901 CTGATAGATATGAAGAGAGCTCTCATCTGCTGATTTGGATCGAGCAAGATATA 960
QY 961 GTCAAGCTTCTAGTGAACAAAATATGATGATCTTCTCAAGATCTATCGACAGAGC 1020
Db 961 GTCAAGCTTCTAGTGAACAAAATATGATGATCTTCTCAAGATCTATCGACAGAGC 1020
QY 1021 GCCAGAGATATGCTGTTCTAGTCAATCATGATTAATTTGCGAGTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTCTAGTCAATCATGATTAATTTGCGAGTACTTCTGACTAC 1080
QY 1081 AAGAGAAAACAGATGTAAATAATCTTTCTGAAGAACAGCAATCGAGAAAGACTTAAAG 1140
Db 1081 AAGAGAAAACAGATGTAAATAATCTTTCTGAAGAACAGCAATCGAGAAAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAGGAGTGAATAATAGCCAGAGAGAAA 1200


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QY 781 TATGTCGTATATGATCAATCAAAAAACAGCATGCGCTCACACACTGTACTTGGTGA 840
    |||||||
Db 781 TATGTCGTATATGATCAATCAAAAAACAGCATGCGCTCACACACTGTACTTGGTGA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
    |||||||
Db 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATGATATGAGAGAGCTGCTCATCTACTGCTGATATGTTGGATTCAGCAAGTATA 960
    |||||||
Db 901 CTGATGATATGAGAGAGCTGCTCATCTACTGCTGATATGTTGGATTCAGCAAGTATA 960
QY 961 GTACAGCTTCTACTGTAGCAAAATATGATGATATCTTCTCAAGATCTATCTGAGACAGC 1020
    |||||||
Db 961 GTACAGCTTCTACTGTAGCAAAATATGATGATATCTTCTCAAGATCTATCTGAGACAGC 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
    |||||||
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
QY 1081 AAAAGAAAAAGCATGCTAAAAATCTCTCTGAAAAACGACATCCAGAAACAAGACTTAAG 1140
    |||||||
Db 1081 AAAAGAAAAAGCATGCTAAAAATCTCTCTGAAAAACGACATCCAGAAACAAGACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGTCAAAAAGTTTCAAAAGCAGTGAATAATAGCCACGACAGAGAA 1200
    |||||||
Db 1141 CTGACATCAGAGAGAGTCAAAAAGTTTCAAAAGCAGTGAATAATAGCCACGACAGAGAA 1200
QY 1201 ATGTCCTCAAGAACCAAGAAATTAATAGAGTGTGATAGAGAGTTGAAGAAATGAG 1260
    |||||||
Db 1201 ATGTCCTCAAGAACCAAGAAATTAATAGAGTGTGATAGAGAGTTGAAGAAATGAG 1260
QY 1261 AAGCATGAAATTAATATGTTGGATTTACTAGAAAACCTGACTAATGTTGCTACTGCTGC 1320
    |||||||
Db 1261 AAGCATGAAATTAATATGTTGGATTTACTAGAAAACCTGACTAATGTTGCTACTGCTGC 1320
QY 1321 AATGCTGTAATGATTAATTTCTCTCAAGAGAGCAGAACCTGGAATAATCAGCAATTT 1380
    |||||||
Db 1321 AATGCTGTAATGATTAATTTCTCTCAAGAGAGCAGAACCTGGAATAATCAGCAATTT 1380
QY 1381 CCTGACAAACGAAATGAAAGATATCACAGAAATTTGCCAATTAAGTTTCTGACTACAAAGAA 1440
    |||||||
Db 1381 CCTGACAAACGAAATGAAAGATATCACAGAAATTTGCCAATTAAGTTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCAAAATACTCTTCTGAAAACAGCAACCAGAACAGACTTAAAGCTGACA 1500
    |||||||
Db 1441 AAACAGATGCAAAATACTCTTCTGAAAACAGCAACCAGAACAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGGAGAGAGTCAAAAAGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551
    |||||||
Db 1501 TCAGAGGAGAGAGTCAAAAAGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551

RESULT 12
AAS63809 standard; cDNA; 2040 BP.
XX
AC AAS63809;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human prostate cDNA clone B305D splice variant #10.
XX
KM Human; prostate cancer; ss; cytosolic; immunostimulant; tumour.
XX
OS Homo sapiens.
XX
PN W0200173032-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-0509919.
XX
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PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX
XX (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MM, Stolk JA, Day CH, Vedvyck NS, Carter D;
PI Li SX, Wang A, Skeiky YAM, Hepler WT, Henderson RA;
XX
XX WPI: 2001-639232/73.
XX
XX P-PSDB: AAU69779.
XX
PT New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
XX Claim 1; Page 350; 579pp; English.
XX
XX The invention relates to isolated prostate-specific
XX polypeptides, polypeptides, fusion proteins of the polypeptides,
XX antibodies raised against the polypeptides (or antigenic epitopes
XX derived from them) and antigen-presenting cells expressing the
XX polypeptides. The antibodies are useful for detecting the presence of
XX cancer, especially prostate cancer. The polypeptides, polynucleotides and
XX the antigen-presenting cells are useful for stimulating and/or expanding
XX T cells specific for a tumour protein, and for inhibiting the development
XX of cancer especially prostate cancer. Compositions comprising the
XX polynucleotide and/or polypeptide are useful for stimulating an immune
XX response, and for treating cancer. The oligonucleotide is useful for
XX detecting cancer. The present sequence is a prostate specific
XX polynucleotide of the invention.
XX
XX Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 other;
XX
XX Query Match 77.5%; Score 1551; DB 22; Length 2040;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ATGTCGTGAGTGGATTCATCCGCGCTGCTCTTCTGAGAAAGCCATTGGCTC 60
XX |||||||
Db 1 ATGTCGTGAGTGGATTCATCCGCGCTGCTCTTCTGAGAAAGCCATTGGCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGCCTGCTTCCCTGCTGAGGAGAGCGCAAG 120
XX |||||||
Db 61 AGGAGCAAGATGGGCAAGTGGTGCCTGCTTCCCTGCTGAGGAGAGCGCGCAAG 120
QY 61 AGGAGCAAGATGGGCAAGTGGTGCCTGCTTCCCTGCTGAGGAGAGCGCGCAAG 120
XX |||||||
Db 61 AGGAGCAAGATGGGCAAGTGGTGCCTGCTTCCCTGCTGAGGAGAGCGCGCAAG 120
QY 121 AGCAAGTGGGCACTTGTGAGACACGACACTCTGCTATGAAGACACTCAGAGCAAG 180
XX |||||||
Db 121 AGCAAGTGGGCACTTGTGAGACACGACACTCTGCTATGAAGACACTCAGAGCAAG 180
QY 121 AGCAAGTGGGCACTTGTGAGACACGACACTCTGCTATGAAGACACTCAGAGCAAG 180
XX |||||||
Db 121 AGCAAGTGGGCACTTGTGAGACACGACACTCTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
XX |||||||
Db 181 ATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
QY 241 GGGCTTCTGGAGACACGAGACTGCTGTGAAGACACTCAGAGCAAGATGGGCAAG 300
XX |||||||
Db 241 GGGCTTCTGGAGACACGAGACTGCTGTGAAGACACTCAGAGCAAGATGGGCAAG 300
QY 301 TGTGTCGCACTGCTTCCCTGCTGCAAGGGGAGCGCAAGAGAGTGGGCTTGG 360
XX |||||||
Db 301 TGTGTCGCACTGCTTCCCTGCTGCAAGGGGAGCGCAAGAGAGTGGGCTTGG 360
QY 361 GGAGACTACGATGACAGTGGCTTATGAGAGCCAGGTRACAGCTGCTGGAGAGATCTG 420
XX |||||||
Db 361 GGAGACTACGATGACAGTGGCTTATGAGAGCCAGGTRACAGCTGCTGGAGAGATCTG 420
XX
```



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Qy 181 ATGGCAAGTGGTCCGCACTGCTCCCTGCTGACGGGGAGTGGCAAGACGCTG 240
    |||||
Db 181 ATGGGCAAGTGGTCCGCACTGCTCCCTGCTGACGGGGAGTGGCAAGACGCTG 240
Qy 241 GGGGCTTCTGGAGACGACGACTGCTATGAAGACACTCAGGAACAAGTGGGCAAG 300
    |||||
Db 241 GGGGCTTCTGGAGACGACGACTGCTATGAAGACACTCAGGAACAAGTGGGCAAG 300
Qy 301 TGGTGGTCCCACTGCTCCCTGCTGACGGGGAGCGGCAAGGACAGTGGGGCTTGG 360
    |||||
Db 301 TGGTGGTCCCACTGCTCCCTGCTGACGGGGAGCGGCAAGGACAGTGGGGCTTGG 360
Qy 361 GGAGACTACGATGACAGTGGCTTCATGAGACCCAGTACACGCTCCGTGAGAAAGTCTG 420
    |||||
Db 361 GGAGACTACGATGACAGTGGCTTCATGAGACCCAGTACACGCTCCGTGAGAAAGTCTG 420
Qy 421 GACAAAGCTCCACAGAGCTGGCTGGTGGGTAAAGTCCCGAAGAAAGATCTCATGTCATG 480
    |||||
Db 421 GACAAAGCTCCACAGAGCTGGCTGGTGGGTAAAGTCCCGAAGAAAGATCTCATGTCATG 480
Qy 481 CTCAGGACACTGACGTGAACAGAAAGAGACAGAAAGAGACTGCTTACATCTGGCC 540
    |||||
Db 481 CTCAGGACACTGACGTGAACAGAAAGAGACAGAAAGAGACTGCTTACATCTGGCC 540
Qy 541 TCTGCCAATGGAAATTCAGAAATAGTAAAACTCCTGCTGACAGACAGATGTCACATTAA 600
    |||||
Db 541 TCTGCCAATGGAAATTCAGAAATAGTAAAACTCCTGCTGACAGACAGATGTCACATTAA 600
Qy 601 GTCTCTGACAAACAAAAGAGACAGCTCTGTATTAAGGCCCTGACAAATCCAGAAAGTAA 660
    |||||
Db 601 GTCTCTGACAAACAAAAGAGACAGCTCTGTATTAAGGCCCTGACAAATCCAGAAAGTAA 660
Qy 661 TGTGCTTAATGTGTGCGAATGGCACTGATCCAAATATTCAGATGGATGTAAGTAAT 720
    |||||
Db 661 TGTGCTTAATGTGTGCGAATGGCACTGATCCAAATATTCAGATGGATGTAAGTAAT 720
Qy 721 ACCACTCTGCACTACGCTATCTATATATGAATTAATGAGCAAGCAAGCACTGCTTAA 780
    |||||
Db 721 ACCACTCTGCACTACGCTATCTATATATGAATTAATGAGCAAGCAAGCACTGCTTAA 780
Qy 781 TATGCTCTGATATCGAATCAAAAACAGCAGTGGCTCACACGCTGTTACTTGGTGTGA 840
    |||||
Db 781 TATGCTCTGATATCGAATCAAAAACAGCAGTGGCTCACACGCTGTTACTTGGTGTGA 840
Qy 841 CATGAGCAAAAACAGCAGTGGCTGTAATTTTATCAAGAAAGAAAGGAATTTAAATGCA 900
    |||||
Db 841 CATGAGCAAAAACAGCAGTGGCTGTAATTTTATCAAGAAAGAAAGGAATTTAAATGCA 900
Qy 901 CTGGATAGATATGAGAGAGACTGCTCATACTGCTGATGTTGTTGATGTCAGCAAGTATA 960
    |||||
Db 901 CTGGATAGATATGAGAGAGACTGCTCATACTGCTGATGTTGTTGATGTCAGCAAGTATA 960
Qy 961 GTGACGCTTCTACTTGGAGCAAAATATGATGTTCTCAAGATCTATCTGACAGACAG 1020
    |||||
Db 961 GTGACGCTTCTACTTGGAGCAAAATATGATGTTCTCTCAAGATCTATCTGACAGACAG 1020
Qy 1021 GCCAGAGAGTATGCTGTTTCTAGTCATCATCATGTAATTTTCCAGTTACTTTCGACATC 1080
    |||||
Db 1021 GCCAGAGAGTATGCTGTTTCTAGTCATCATCATGTAATTTTCCAGTTACTTTCGACATC 1080
Qy 1081 AAAAGAAAAACAGATGCTAAAAATCTCTTGTGAAAACAGCAATCCAGAACAGACTTAAAG 1140
    |||||
Db 1081 AAAAGAAAAACAGATGCTAAAAATCTCTTGTGAAAACAGCAATCCAGAACAGACTTAAAG 1140
Qy 1141 CTGACATCAGAGAGAGTCCAAAGGTTCAAAGGCAAGTGAATAATGACCCAGAGAAA 1200
    |||||
Db 1141 CTGACATCAGAGAGAGTCCAAAGGTTCAAAGGCAAGTGAATAATGACCCAGAGAAA 1200
Qy 1201 ATGTCTCAAGAGACGAAATTAATTAAGATGCTATAGAGAGGTTGAAGAAATGAAG 1260
    |||||
Db 1201 ATGTCTCAAGAGACGAAATTAATTAAGATGCTATAGAGAGGTTGAAGAAATGAAG 1260

```

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Qy 1261 AAGCATGAAGTAAATAATGTGGATTACTAGAAAACCTGACTAATGTGTCTACTGCGC 1320
    |||||
Db 1261 AAGCATGAAGTAAATAATGTGGATTACTAGAAAACCTGACTAATGTGTCTACTGCGC 1320
Qy 1321 AATGCTATTAATGATTAATTTCTCTCAAGAGACGAAACACTGGAATAATCGCAATT 1380
    |||||
Db 1321 AATGCTATTAATGATTAATTTCTCTCAAGAGACGAAACACTGGAATAATCGCAATT 1380
Qy 1381 CCGACACAGCAAGTGAAGATATACAGAAATTTGCAATTTAGTTTCTGACTACAAAGAA 1440
    |||||
Db 1381 CCGACACAGCAAGTGAAGATATACAGAAATTTGCAATTTAGTTTCTGACTACAAAGAA 1440
Qy 1441 AAACAGATGCCAAATATCTTCTGAAAACAGCAACCCAGACAGACTTAAAGCTGACA 1500
    |||||
Db 1441 AAACAGATGCCAAATATCTTCTGAAAACAGCAACCCAGACAGACTTAAAGCTGACA 1500
Qy 1501 TCAGAGAGAAAGTCCAAAGGCTTGGAGGAGAGTGAATAATGGCCAGCCAGAG 1551
    |||||
Db 1501 TCAGAGAGAAAGTCCAAAGGCTTGGAGGAGAGTGAATAATGGCCAGCCAGAG 1551

RESULT 14
AAH85030
AAH85030 standard; cDNA; 2040 BP.
XX
XX AAH85030;
XX
XX 25-SEP-2001 (first entry)
XX
XX Human prostate-specific cDNA sequence B305D splice variant #10.
DE
XX Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
KW chromosome 22q11.2; prostate-specific protein; chromosome 1;
KW prostate specific antigen; PSA; ss.
XX
XX Homo sapiens.
OS
XX
XX NC200134802-A2.
XX
XX 17-MAY-2001.
XX
XX 09-NOV-2000; 2000MO-US30904.
XX
XX 12-NOV-1999; 99US-0439313.
XX
XX 18-NOV-1999; 99US-0443686.
XX
XX (CORI-) CORIXA CORP.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Retler MW, Stolk JA, Day CH, Skeiky YAW, Wang A;
DR WPI; 2001-308785/32.
XX
XX Isolated polypeptide comprising at least an immunogenic portion of a
PT prostate-specific protein, useful in the diagnosis and therapy of a
PI prostate cancer -
XX
XX Claim 31; Page 248; 325pp; English.
XX
XX The present invention describes an isolated polypeptide (P1) comprising
CC at least an immunogenic portion of a prostate-specific protein, or its
CC variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
CC (N1) have cytostatic activity and can be used in vaccine production.
CC The polypeptides, nucleic acids and antibodies from the present
CC invention are useful in the diagnosis and therapy of prostate cancer.
CC Prostate specific genes P704P, P712P, P774P, P775P and B305D are located
CC in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
CC region. Prostate specific antigen (PSA) P501S was located on
CC chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent
CC polynucleotide and polypeptide sequences used in the exemplification
CC of the present invention.
XX
XX Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 other;
SQ

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Query Match 77.5%; Score 1551; DB 22; Length 2040;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGTGGTTGAGCTGATTCCATGCCGGCTGCTCTTCTGTGAAGAAGCCATTGGTCTC 60
DB 1 ATGTGGTTGAGCTGATTCCATGCCGGCTGCTCTTCTGTGAAGAAGCCATTGGTCTC 60
QY 61 AGGACCAAGATGGGCAAGTGGTCCCTTCTTCCCTGCTGCGAGGAGAGCCGCAAG 120
DB 61 AGGACCAAGATGGGCAAGTGGTCCCTTCTTCCCTGCTGCGAGGAGAGCCGCAAG 120
QY 121 ACCAAGTGGGCACTTCTGAGACCAAGCAAGCTGCTATGAAGCACTCAGAGCAAG 180
DB 121 ACCAAGTGGGCACTTCTGAGACCAAGCAAGCTGCTATGAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGAGGAGAGTGGCAAGCAAGCTG 240
DB 181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGAGGAGAGTGGCAAGCAAGCTG 240
QY 241 GGGCGTTCTGGAGACGACGACGACCTCTGATGAAGACACTCAGGAACAAGTGGCAAG 300
DB 241 GGGCGTTCTGGAGACGACGACGACCTCTGATGAAGACACTCAGGAACAAGTGGCAAG 300
QY 301 TGGTCTGCACTGCTGCTCCCTGCTGCAAGGGGAGGGCAAGCAAGTGGGCGCTTG 360
DB 301 TGGTCTGCACTGCTGCTCCCTGCTGCAAGGGGAGGGCAAGCAAGTGGGCGCTTG 360
QY 361 GGAGACTACGATGACAGTCCCTTCAATGAGCCAGGTACACAGTCCGTGGAGAAGTCTG 420
DB 361 GGAGACTACGATGACAGTCCCTTCAATGAGCCAGGTACACAGTCCGTGGAGAAGTCTG 420
QY 421 GACAAGCTCCACAGAGCTCCCTGCTGGGTTAAAGTCCCGAAGAGATCTCATCTCATG 480
DB 421 GACAAGCTCCACAGAGCTCCCTGCTGGGTTAAAGTCCCGAAGAGATCTCATCTCATG 480
QY 481 CTCAGGACACTGAGCTGTAACAAGAGCAAGCAAAAGAGAGTCTTACATCTGGCC 540
DB 481 CTCAGGACACTGAGCTGTAACAAGAGCAAGCAAAAGAGAGTCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGGAGAGAGATGCACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGGAGAGAGATGCACTTAAT 600
QY 601 GTCCCTTGACAAACAAAGAGGACAGCTCTGATAAAGCCGTACAATGCCAGGAAGTGA 660
DB 601 GTCCCTTGACAAACAAAGAGGAGGACAGCTCTGATAAAGCCGTACAATGCCAGGAAGTGA 660
QY 661 TGTGGCTTAATGTGCTGGAAACATGGCACTGATCCAAATATCCAGATGATGGAAT 720
DB 661 TGTGGCTTAATGTGCTGGAAACATGGCACTGATCCAAATATCCAGATGATGGAAT 720
QY 721 ACCACTCTGCACTAGCTATCTATATGAAGATAATTAATGAGCAAGCACTGCTTA 780
DB 721 ACCACTCTGCACTAGCTATCTATATGAAGATAATTAATGAGCAAGCACTGCTTA 780
QY 781 TATGTGCTGATATGGAATCAAAAAACAAGCATGGCTCACACCACTGTTACTGGTGA 840
DB 781 TATGTGCTGATATGGAATCAAAAAACAAGCATGGCTCACACCACTGTTACTGGTGA 840
QY 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTAATGA 900
DB 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTAATGA 900
QY 901 CTGATATATATGAAGAGACTGCTCTCATCTGATGATGTTGGATCAGCAAGTATA 960
DB 901 CTGATATATATGAAGAGACTGCTCTCATCTGATGATGTTGGATCAGCAAGTATA 960
QY 961 GTCAACCTTTCTACTGAGCAAAATTTGATGATCTTCTCAAGATCTATCTGAGACAG 1020
DB 961 GTCAACCTTTCTACTGAGCAAAATTTGATGATCTTCTCAAGATCTATCTGAGACAG 1020

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QY 1021 GCCAGAGATATGCTGTTCTATGATCATCATGTAATTTGGCAGTTACTTTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTCTATGATCATCATGTAATTTGGCAGTTACTTTGACTAC 1080
QY 1081 AAAGAAAACAGATGCTAAAAATCTCTTCTGAAAACAGCAATTCAGAACAGCTTAAAG 1140
DB 1081 AAAGAAAACAGATGCTAAAAATCTCTTCTGAAAACAGCAATTCAGAACAGCTTAAAG 1140
QY 1141 CTGACATTCAGAGAGAGTCAACAAAGTTCAAAAGGAGTGAAGAAATGCCAGCAAGAA 1200
DB 1141 CTGACATTCAGAGAGAGTCAACAAAGTTCAAAAGGAGTGAAGAAATGCCAGCAAGAA 1200
QY 1201 ATGTCTCAAGAACCAAAATTAATAGATGGATGATAGAGAGTGAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACCAAAATTAATAGATGGATGATAGAGAGTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATGATGAGTACTTACTAGAAAACCTGACTAATGTTGCTGCTG 1320
DB 1261 AAGCATGAAGATTAATGATGAGTACTTACTAGAAAACCTGACTAATGTTGCTGCTG 1320
QY 1321 AATGTGATATGATTAATTCCTCAAGGAAGAGCAGAACCTGGAATAATGCAATTT 1380
DB 1321 AATGTGATATGATTAATTCCTCAAGGAAGAGCAGAACCTGGAATAATGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTGAAGATATACAGAAATTTGGAAATTTGTTCTGACTACAAAGAA 1440
DB 1381 CCTGACAAAGAAAGTGAAGATATACAGAAATTTGGAAATTTGTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAATACTCTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
DB 1441 AAACAGATGCCAAATACTCTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGAAAGTCAACAAAGGCTTGAGGGCACTGAAAATGGCCAGCCAGAG 1551
DB 1501 TCAGAGAAAGTCAACAAAGGCTTGAGGGCACTGAAAATGGCCAGCCAGAG 1551

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RESULT 15
 AAH02781
 ID AAH02781 standard; cDNA, 2040 BP.
 AC AAH02781;
 XX
 AC
 XX
 DT 14-JUN-2001 (first entry)
 XX
 DE Prostate tumour antigen determined cDNA splice variant of B305D #10.
 XX
 KW Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
 XX prostate cancer; immunogenic; cytostatic; vaccine; ss.
 XX
 OS Homo sapiens.
 XX
 OS
 XX
 PN WO200125272-A2.
 XX
 PD 12-APR-2001.
 XX
 PF 04-OCT-2000; 2000WO-US27464.
 XX
 PR 04-OCT-1999; 99US-0157455.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Skeiky YAM, Reed SC, Cheever MA;
 XX
 DR WPI; 2001-245062/25.
 XX
 DR P-PSDB; AAB74817.
 XX
 PT Prostate specific protein and its encoding polynucleotide, useful for
 XX the treatment and diagnosis of prostate cancer -
 XX
 PS Claim 50; Page 233; 276pp; English.
 XX
 CC The present invention describes an isolated polypeptide (I) comprising

at least an immunogenic portion of a prostate tumour antigen protein or its variant. (I) have cytostatic activity and can be used in vaccine production. (I), prostate tumour antigen polynucleotides, an antigen presenting cell (Apc e.g. a dendritic cell) that expresses (I), and a pharmaceutical composition containing (I) are useful for inhibiting the development of cancer in a patient. Antibodies specific for prostate specific proteins and oligonucleotides that hybridise to a polynucleotide that encodes a prostate specific protein are useful for detecting the presence or absence of a cancer or monitoring the progression the progression of a cancer. especially prostate cancer. AAH02442 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences used in the exemplification of the present invention.

50 Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 other;

Query Match	77.5%;	Score 1551;	DB 22;	Length 2040;
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Best Local Similarity 100.0%; Pred. No. 0;

Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	1	ATGAGGTTGAGGTTGATTCATCCCGGCTGCTCTCTGTAAGAAAGCATTTGGCTC	60
Db	1	ATGGGTGTGAGGTTGATTCATCCCGGCTGCTCTCTGTAAGAAAGCATTTGGCTC	60
OY	61	AGGACCAAGATGGGCAAGTGTGCTGGCTTGTCTCCCTGCTCAGAGGAGGGGCAAG	120
Db	61	AGGACCAAGATGGGCAAGTGTGCTGGCTTGTCTCCCTGCTCAGAGGAGGGGCAAG	120
OY	121	AGCAACGTGGGCACTTCTGGAGACCAGACGACTCTGCTATGAAGACCTCAGAGCAAG	180
Db	121	AGCAACGTGGGCACTTCTGGAGACCAGACGACTCTGCTATGAAGACCTCAGAGCAAG	180
OY	181	ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCGAGGGGGAGTGGCAAGCAAGCTG	240
Db	181	ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCGAGGGGGAGTGGCAAGCAAGCTG	240
OY	241	GGGCGTTTGTGAGACACACGACGACTCTGCTATGAAGACTCAGAGCAAGATGGGCAAG	300
Db	241	GGCGTTTGTGAGACACACGACGACTCTGCTATGAAGACTCAGAGCAAGATGGGCAAG	300
OY	301	TGTGCTGCTCACTGCTTCCCTGCTGTCAGGGGGAGCGGCAAGCAAGGTGGCGCTTGG	360
Db	301	TGTGCTGCTCACTGCTTCCCTGCTGTCAGGGGGAGCGGCAAGCAAGGTGGCGCTTGG	360
OY	361	GGAAGCTACGATGACAGTGCCTTATGGAAGCCAGATGCCAGCTGCTGGAGAAATCTG	420
Db	361	GGAAGCTACGATGACAGTGCCTTATGGAAGCCAGATGCCAGCTGCTGGAGAAATCTG	420
OY	421	GACAGCTCCACAGAGCTGCGTGGGGGTAAAGCCCGAAGAAAGATTCATGTCATG	480
Db	421	GACAGCTCCACAGAGCTGCGTGGGGGTAAAGCCCGAAGAAAGATTCATGTCATG	480
OY	481	CTCAGGGACACTGACGTGACAAAGAGCAAGCAAGCAAGAGACTGCTACATCTGGCC	540
Db	481	CTCAGGGACACTGACGTGACAAAGAGCAAGCAAGCAAGAGACTGCTACATCTGGCC	540
OY	541	TCTGCCAATGGGAATTCAAGAGTGTAAACTCTGCTGACAGACGATGCACTTAAT	600
Db	541	TCTGCCAATGGGAATTCAAGAGTGTAAACTCTGCTGACAGACGATGCACTTAAT	600
OY	601	GTCCTTGACACAAAGAGAGACGCTGTGTAAGAGCCGACAAATCCACGAAGATGAA	660
Db	601	GTCCTTGACACAAAGAGAGACGCTGTGTAAGAGCCGACAAATCCACGAAGATGAA	660
OY	661	TGTGCTTAATGTGCTGGAACTGGCACTATGCCAAATATTCCAGATGAGTATGAAAT	720
Db	661	TGTGCTTAATGTGCTGGAACTGGCACTATGCCAAATATTCCAGATGAGTATGAAAT	720
OY	721	ACCACCTGACACTACGCTATCTAATATGAAATTAATATGATGAGCAAGCACTGCTTA	780
Db	721	ACCACCTGACACTACGCTATCTAATATGAAATTAATATGATGAGCAAGCACTGCTTA	780
OY	781	TATGCTGCTATATGAATCAAAAAACAAGATGGCTCACACCACTGTTACTTGGTGTGA	840

Db	781	TATGGTGGTGAATTCGAATCAAAAACAAAGCATGGCTCACACACAGCTGTA	84
Qy	841	CATGAGCAAAAAACGCAAGTGGTAATTTTATTCAGAAAAAAGGAATTTAAATGCA	900
Db	841	CATGGCGCAAAAAACGCAAGTGGTAATTTTATTCAGAAAAAAGGAATTTAAATGCA	900
Qy	901	CTGGATTACATATGGAAGAGCTGCTCTCATCTTCTGTATGTTGGATAGCAAGTATA	960
Db	901	CTGGATTACATATGGAAGAGCTGCTCTCATCTTCTGTATGTTGGATAGCAAGTATA	960
Qy	961	GTCAAGCTTCTACTTGGACAAAATATTGATGATCTTCTCAAGATCATCTGGACAGAG	102
Db	961	GTCAAGCTTCTACTTGGACAAAATATTGATGATCTTCTCAAGATCATCTGGACAGAG	102
Qy	1021	GCCAGAGAGTATGCTGTTTCTAGTCATCATGTAAATTTGCCAGTTACTTTTGACTAC	108
Db	1021	GCCAGAGAGTATGCTGTTTCTAGTCATCATGTAAATTTGCCAGTTACTTTTGACTAC	108
Qy	1081	AAAGAAAAACGATGCTTAAAAATCTCTTCGAAAAACAGCAATCCAGAACAACTTAAG	114
Db	1081	AAAGAAAAACGATGCTTAAAAATCTCTTCGAAAAACAGCAATCCAGAACAACTTAAG	114
Qy	1141	CTGACATCAGAGGAAGAGTCACAAAGGTTCAAAGGAGTAAAAATAGCCAGCAGAGAAA	120
Db	1141	CTGACATCAGAGGAAGAGTCACAAAGGTTCAAAGGAGTAAAAATAGCCAGCAGAGAAA	120
Qy	1201	ATGTCTCAAGAACCCAGAAATTAATTAAGATGATGATAGAGAGTGAAGAAAGTAAG	126
Db	1201	ATGTCTCAAGAACCCAGAAATTAATTAAGATGATGATAGAGAGTGAAGAAAGTAAG	126
Qy	1261	AAGCATGGAAGTAATTAATGTTGGATTAAGTAAGAACTGACTAATGTTGACTGTCGC	132
Db	1261	AAGCATGGAAGTAATTAATGTTGGATTAAGTAAGAACTGACTAATGTTGACTGTCGC	132
Qy	1321	AATGTTGATTAATGATTAATTCCTCAAGGAAGAGCAGAACCTGAAAAATCAGCAATTT	138
Db	1321	AATGTTGATTAATGATTAATTCCTCAAGGAAGAGCAGAACCTGAAAAATCAGCAATTT	138
Qy	1381	CCTGCAACGAAAGTGAAGAGTATCACAGAAATTTGCCAATTAAGTTTGTGACTACAAAGAA	144
Db	1381	CCTGCAACGAAAGTGAAGAGTATCACAGAAATTTGCCAATTAAGTTTGTGACTACAAAGAA	144
Qy	1441	AAACGATGCCAAAATACTCTTCGAAAAACGCAACCCAGAACAGACTTAAAGCTGACA	150
Db	1441	AAACGATGCCAAAATACTCTTCGAAAAACGCAACCCAGAACAGACTTAAAGCTGACA	150
Qy	1501	TCAGAGGAAGATCCAAAGGCTTGAGGGCAGTGAATAATGCGCCAGCCAGAG	1551
Db	1501	TCAGAGGAAGATCCAAAGGCTTGAGGGCAGTGAATAATGCGCCAGCCAGAG	1551
RESULT 16			
ABL95180			
ID	ABL95180	standard; cDNA; 2040 BP.	
XX	ABL95180;		
AC			
XX			
DT	19-JUL-2002	(first entry)	
XX			
DE	Human B305D splice variant cDNA sequence SEQ ID NO 375.		
XX			
XX	Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;		
KW	gene therapy; gene; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	US2002022248-A1.		
XX			
PD	21-FEB-2002.		
XX			
PF	12-JAN-2001; 2001US-0759143.		
XX			
PR	25-FEB-1997; 97US-0806099.		

PR 01-AUG-1997; 97US-0904804.
 PR 09-FEB-1998; 98US-0020956.
 PR 25-FEB-1998; 98US-0030607.
 PR 14-JUL-1998; 98US-0115453.
 PR 23-SEP-1998; 98US-0159812.
 PR 15-JAN-1999; 99US-0232149.
 PR 09-APR-1999; 99US-0288946.
 PR 13-JUL-1999; 99US-0352616.
 PR 12-NOV-1999; 99US-0439313.
 PR 18-NOV-1999; 99US-0443686.
 PR 14-JAN-2000; 2000US-0483672.
 PR 27-MAR-2000; 2000US-0536857.
 PR 09-MAY-2000; 2000US-0568100.
 PR 12-MAY-2000; 2000US-0570737.
 PR 13-JUN-2000; 2000US-0593793.
 PR 27-JUN-2000; 2000US-0605783.
 PR 10-AUG-2000; 2000US-0636215.
 PR 29-AUG-2000; 2000US-0651236.
 PR 06-SEP-2000; 2000US-0657279.
 PR 02-OCT-2000; 2000US-0679426.
 PR 10-OCT-2000; 2000US-0685166.
 XX
 PA (XUJ/) XU J.
 PA (DILL/) DILLON D C.
 PA (MITC/) MITCHAM J L.
 PA (HARL/) HARLOCKER S L.
 PA (JIAN/) JIANG Y.
 PA (KALO/) KALOS M D.
 PA (FANG/) FANGER G R.
 PA (RETT/) RETTER M W.
 PA (STOL/) STOLK J A.
 PA (DAYC/) DAY C H.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (LISX/) LI S X.
 PA (WANG/) WANG A.
 PA (SKEI/) SKEIKY Y A W.
 PA (HEPL/) HEPLER W T.
 PA (HEND/) HENDERSON R A.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
 XX
 DR WPI: 2002-255649/30.
 XX
 PT New prostate-specific polynucleotides for diagnosing and treating
 PT diseases, in particular prostate cancer, and as markers for the
 PT progression of cancer -
 XX
 PS Claim 1: SEQ ID NO 375; 87pp: English.
 XX
 CC The present invention provides prostate-specific coding sequences and
 CC their encoded proteins. These can be used in the diagnosis and treatment
 CC of cancers, particularly prostate cancer. The present sequence is a cDNA
 CC described in the invention.
 XX
 SQ Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 other:
 Query Match 77.5%; Score 1551; DB 24; Length 2040;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 121 AGCAAGCTGGGCACTTCTGAGACACAGAGACTGTGCTATGAAGACTACAGAGCAAG 180
 QY 181 ATGGGCAATGATGATGCGCCCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAACGTG 240
 Db 181 ATGGGCAATGATGATGCGCCCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAACGTG 240
 QY 241 GGGGCTTGGAGACACAGAGCACTGCTATGAAGCACTGAGAAAGATGGGCAAG 300
 Db 241 GGGGCTTGGAGACACAGAGCACTGCTATGAAGCACTGAGAAAGATGGGCAAG 300
 QY 301 TGGTGTGCACTGCTTCCCTGCTGACAGGGGAGGCAAGCAAGGTGGGCGCTTG 360
 Db 301 TGGTGTGCACTGCTTCCCTGCTGACAGGGGAGGCAAGCAAGGTGGGCGCTTG 360
 QY 361 GGAGACTAGAGTACAGTGTGCTTATGAGAGCCAGGTACCAGTCCGTGGAGAACTG 420
 Db 361 GGAGACTAGAGTACAGTGTGCTTATGAGAGCCAGGTACCAGTCCGTGGAGAACTG 420
 QY 421 GACAACTGCACAGAGCTGCTGGGGTAAAGTCCCCAGAAAGATGTCATGCTCATG 480
 Db 421 GACAACTGCACAGAGCTGCTGGGGTAAAGTCCCCAGAAAGATGTCATGCTCATG 480
 QY 481 CTCAGGAGACACTGACGTGAACAAGAGCAAGAGAGACTGCTACATCTGGCC 540
 Db 481 CTCAGGAGACACTGACGTGAACAAGAGCAAGAGAGACTGCTACATCTGGCC 540
 QY 541 TCTGCCAATGGGAATTCAGAAATGTAATTAATCTCTGCTGACAGAGATGTAATTAAT 600
 Db 541 TCTGCCAATGGGAATTCAGAAATGTAATTAATCTCTGCTGACAGAGATGTAATTAAT 600
 QY 601 GTCCCTGACAAACAAAAGAGAGAGAGCTGATTAAGAGCCGTACAAATGAGCAAGATGA 660
 Db 601 GTCCCTGACAAACAAAAGAGAGAGAGCTGATTAAGAGCCGTACAAATGAGCAAGATGA 660
 QY 661 TGTGCGTTAATGTTGCTGGAACATGACACTGATCAAAATTTCCAGATGATGGAAT 720
 Db 661 TGTGCGTTAATGTTGCTGGAACATGACACTGATCAAAATTTCCAGATGATGGAAT 720
 QY 721 ACCACTGTGACATGACCTATCTAATGAAGATTAATTAATGGCCAAAGACATGCTCTTA 780
 Db 721 ACCACTGTGACATGACCTATCTAATGAAGATTAATTAATGGCCAAAGACATGCTCTTA 780
 QY 781 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
 Db 781 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
 QY 841 CATGACCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGA 900
 Db 841 CATGACCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGA 900
 QY 901 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
 Db 901 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
 QY 961 GTGAGCTTCTACTTATGAGCAAAATATTGATGATGATGATGATGATGATGATGATG 1020
 Db 961 GTGAGCTTCTACTTATGAGCAAAATATTGATGATGATGATGATGATGATGATGATG 1020
 QY 1021 GCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
 Db 1021 GCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
 QY 1081 AAAGAAAAACAGATGCTTAAATCTTCTGAAAACAGCAATTCAGAAAGCTTAAAG 1140
 Db 1081 AAAGAAAAACAGATGCTTAAATCTTCTGAAAACAGCAATTCAGAAAGCTTAAAG 1140
 QY 1141 CTGACATCAGAGAGAAAGTACAAAGGTTCAAGGCAAGTGAAGTGAAGTGAAGTGAAG 1200
 Db 1141 CTGACATCAGAGAGAAAGTACAAAGGTTCAAGGCAAGTGAAGTGAAGTGAAGTGAAG 1200
 QY 1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGATGATGATGATGATGATGATGATG 1260
 Db 1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGATGATGATGATGATGATGATGATG 1260

Qy	1261	AAGCATGAAAGTATATATGTGGGATTA	CTCTAC	TAC	TGAAACCTG	TAC	TAT	ATG	GTGT	CAC	TG	CGC	1320
Db	1261	AAGCATGAAAGTATATATGTGGGATTA	CTCTAC	TAC	TGAAACCTG	TAC	TAT	ATG	GTGT	CAC	TG	CGC	1320
Qy	1321	AATGGTATATGATTAATTCCTCA	AAAGAGAC	GACA	CAACCTG	TA	AAATCAG	CAATTT					1380
Db	1321	AATGGTATATGATTAATTCCTCA	AAAGAGAG	GACAGACA	CACTG	AAATCAG	CAATTT						1380
Qy	1381	CCTTACCAACGAAGTGAAGGTT	CTCACA	GATTTTGG	CAATTTGG	TTCTTG	CTG	ACT	CA	AGAA			1440
Db	1381	CCTTACCAACGAAGTGAAGGTT	CTCACA	GATTTTGG	CAATTTGG	TTCTTG	CTG	ACT	CA	AGAA			1440
Qy	1441	AAACAGATGCCAAATATCTTTCT	GTGAAAAC	CAGCAAC	CCAGACA	AGACTT	AAAGCTG	ACA					1500
Db	1441	AAACAGATGCCAAATATCTTTCT	GTGAAAAC	CAGCAAC	CCAGACA	AGACTT	AAAGCTG	ACA					1500
Qy	1501	TCAAGAGAAAGTCTACAAAGGCTT	GAGGCG	CAGTGA	AAATG	CCAGCC	ACG	AG					1551
Db	1501	TCAAGAGAAAGTCTACAAAGGCTT	GAGGCG	CAGTGA	AAATG	CCAGCC	ACG	AG					1551

RESULT 17

ID AAS99859 standard; cDNA; 2040 BP.

AC AAS99859;

DT 12-MAR-2002 (first entry)

DE Breast tumour-specific DNA B11a1 splice variant B11c-9,16.

KW Human; breast cancer; PCR primer; ss; cytostatic; immunostimulant;

KW tumour; vaccine; immunogenic.

..... Homo sapiens

PN WO200190152-A2.

PD 29-NOV-2001.

PF 22-MAY-2001; 2001WO-US16776.

PR	24-MAY-2000; 2000US-0577505.
PR	08-JUN-2000; 2000US-0580583

PR	26-OCT-2000; 2000US-0699295.
PR	16-MAR-2001; 2001US-0810936

XX
PA (CORT-) CORTXA CORP.

AA Frudakis TN, Reed SG, Smith

XX
XX
XX

many a, every law

XX
XX
XX

DR P-PSDB; AAU74379.

PT New breast tumour proteins and polynucleotides

PT eliciting humoral an

PS Claim 1; Page 224

CC The invention relates to novel breast

pharmaceutical compositions for treating and/or preventing cancer

CC particularly humoral and/or cellular immune response. The polynucleotides

design and preparation of ribozyme moi-

CC direct expression of a polypeptide in host cells. AAS99570-AAS99888
CC represent novel human breast cancer protein coding sequences and

CC PCR primers of the invention.

Sequence 2040 BP; 716 A; 392 C; 500 G; 432 T; 0 other;
SQ

Query Match	77.58;	Score 1551;	DB 24;	Length 2040;
-------------	--------	-------------	--------	--------------

Matches 1551; Conservative 0; Mismatches

QY 1 ATGGTGGTGAGGTTGATTCATGCCGGCTGCCCTCTTCTGTGAGAGGCCATTGGTCTC 60

Oy	1	ATGGGGGTTGAGGTTGAAATTCATCCGGCGTCTCTTGTAAGAAAGCAATTTGGTCTC	60
Oy	1	ATGGGGGTTGAGGTTGAAATTCATCCGGCGTCTCTTGTAAGAAAGCAATTTGGTCTC	60
Db	1	ATGGGGGTTGAGGTTGAAATTCATCCGGCGTCTCTTGTAAGAAAGCAATTTGGTCTC	60
Oy	61	AGGAGCAAGATGGCCAAAGTGGTGTGCTTTCCTTCCTGTCGAGGAGAGCGGCAAG	120
Oy	61	AGGAGCAAGATGGCCAAAGTGGTGTGCTTTCCTTCCTGTCGAGGAGAGCGGCAAG	120
Db	61	AGGAGCAAGATGGCCAAAGTGGTGTGCTTTCCTTCCTGTCGAGGAGAGCGGCAAG	120
Oy	121	AGCAACGCGGGCACTTCTGGGAGACCAAGACACTGCTATGAAGAACTCTCAGAGCAAG	180
Oy	121	AGCAACGCGGGCACTTCTGGGAGACCAAGACACTGCTATGAAGAACTCTCAGAGCAAG	180
Db	121	AGCAACGCGGGCACTTCTGGGAGACCAAGACACTGCTATGAAGAACTCTCAGAGCAAG	180
Oy	181	ATGGGCAAGTGGTCCCGCCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGACAGTG	240
Oy	181	ATGGGCAAGTGGTCCCGCCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGACAGTG	240
Db	181	ATGGGCAAGTGGTCCCGCCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGACAGTG	240
Oy	241	GCGCGCTTCTGGAGACCCAGACACTCTGCTATGAAGAACTCAGGAACAAGTGGGCAAG	300
Oy	241	GCGCGCTTCTGGAGACCCAGACACTCTGCTATGAAGAACTCAGGAACAAGTGGGCAAG	300
Db	241	GCGCGCTTCTGGAGACCCAGACACTCTGCTATGAAGAACTCAGGAACAAGTGGGCAAG	300
Oy	301	TGGTGTCCCACTCTTCCCTGCTGAGGGGGAGGCGCAAGAGTGGGCGCTTGG	360
Oy	301	TGGTGTCCCACTCTTCCCTGCTGAGGGGGAGGCGCAAGAGTGGGCGCTTGG	360
Db	301	TGGTGTCCCACTCTTCCCTGCTGAGGGGGAGGCGCAAGAGTGGGCGCTTGG	360
Oy	361	GGAGACTACGATGACAGTGCCTTTCATGAGAGCCAGGTACCAAGTCCGTGGAGAGTCTG	420
Oy	361	GGAGACTACGATGACAGTGCCTTTCATGAGAGCCAGGTACCAAGTCCGTGGAGAGTCTG	420
Db	361	GGAGACTACGATGACAGTGCCTTTCATGAGAGCCAGGTACCAAGTCCGTGGAGAGTCTG	420
Oy	421	GACAAGCTCCCAAGAGTGGCTGGTGGGGTAAAGTCCCAAGAAAGATCTCAATCGCATAG	480
Oy	421	GACAAGCTCCCAAGAGTGGCTGGTGGGGTAAAGTCCCAAGAAAGATCTCAATCGCATAG	480
Db	421	GACAAGCTCCCAAGAGTGGCTGGTGGGGTAAAGTCCCAAGAAAGATCTCAATCGCATAG	480
Oy	481	CTCAGGGACACTGACGTGAACACAGAAAGACCAAAAGAGAGCTGCTTACATCTGGCC	540
Oy	481	CTCAGGGACACTGACGTGAACACAGAAAGACCAAAAGAGAGCTGCTTACATCTGGCC	540
Db	481	CTCAGGGACACTGACGTGAACACAGAAAGACCAAAAGAGAGCTGCTTACATCTGGCC	540
Oy	541	TCTGTCCCATGGGAATTGAGAAAGTAAACTCTCTGTGACAGACGAGTCAACTTAAT	600
Oy	541	TCTGTCCCATGGGAATTGAGAAAGTAAACTCTCTGTGACAGACGAGTCAACTTAAT	600
Db	541	TCTGTCCCATGGGAATTGAGAAAGTAAACTCTCTGTGACAGACGAGTCAACTTAAT	600
Oy	601	GTCCTTGCACAAACAAAAGAGAGACGCTCTATAAAGGCGGTACAAATGCCAGGAATGAA	660
Oy	601	GTCCTTGCACAAACAAAAGAGAGACGCTCTATAAAGGCGGTACAAATGCCAGGAATGAA	660
Db	601	GTCCTTGCACAAACAAAAGAGAGACGCTCTATAAAGGCGGTACAAATGCCAGGAATGAA	660
Oy	661	TGTGCGTTAATGTTGCTGCGAACAATGGCAGCTGCACAAATTTCCAGATAGATGGAAAT	720
Oy	661	TGTGCGTTAATGTTGCTGCGAACAATGGCAGCTGCACAAATTTCCAGATAGATGGAAAT	720
Db	661	TGTGCGTTAATGTTGCTGCGAACAATGGCAGCTGCACAAATTTCCAGATAGATGGAAAT	720
Oy	721	ACCACTGTGCACCTACGCTATCTAATGAAGATAAATTAATGGCCAAACACTGCTCTTA	780
Oy	721	ACCACTGTGCACCTACGCTATCTAATGAAGATAAATTAATGGCCAAACACTGCTCTTA	780
Db	721	ACCACTGTGCACCTACGCTATCTAATGAAGATAAATTAATGGCCAAACACTGCTCTTA	780
Oy	781	TATGTGCTGTATATCGAATCAAAAACCAAGCAATGGCCTCACACACTGTTACTTGGTGA	840
Oy	781	TATGTGCTGTATATCGAATCAAAAACCAAGCAATGGCCTCACACACTGTTACTTGGTGA	840
Db	781	TATGTGCTGTATATCGAATCAAAAACCAAGCAATGGCCTCACACACTGTTACTTGGTGA	840
Oy	841	CATGAGCAAAAACAGCAAGTCGTGAATTTTAAACAAGAAAAAGCGAATTTAAATGCA	900
Oy	841	CATGAGCAAAAACAGCAAGTCGTGAATTTTAAACAAGAAAAAGCGAATTTAAATGCA	900
Db	841	CATGAGCAAAAACAGCAAGTCGTGAATTTTAAACAAGAAAAAGCGAATTTAAATGCA	900
Oy	901	CTGAGTATGATATGAAGAGACTGCTCTCATCTTGGCTGTATGTTGTGAGTACACAAAGTAA	960
Oy	901	CTGAGTATGATATGAAGAGACTGCTCTCATCTTGGCTGTATGTTGTGAGTACACAAAGTAA	960
Db	901	CTGAGTATGATATGAAGAGACTGCTCTCATCTTGGCTGTATGTTGTGAGTACACAAAGTAA	960
Oy	961	GTCAGCTTCTACTTGTAGCAAAATATATGATGATCTTCTCAAGATCTATCTGGACAGC	1020
Oy	961	GTCAGCTTCTACTTGTAGCAAAATATATGATGATCTTCTCAAGATCTATCTGGACAGC	1020
Db	961	GTCAGCTTCTACTTGTAGCAAAATATATGATGATCTTCTCAAGATCTATCTGGACAGC	1020

Db 961 GTCAACCTTCTACTTGACCAAAATATGATGATCTCTCAAGATCTATCTGACAGACG 1020
Oy 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGGCACTTCTCTGACATAC 1080
Db 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGGCACTTCTCTGACATAC 1080
Oy 1081 AAAGAAAACAGATGCTTAAAAATCTCTCTGAAAACAGCAATCCAGAACAGACTTAAAG 1140
Db 1081 AAAGAAAACAGATGCTTAAAAATCTCTCTGAAAACAGCAATCCAGAACAGACTTAAAG 1140
Oy 1141 CTGACATCAGAGAGAGAGTCAACAAAGTTCAAGGCACTGAAATAATAGCCAGCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGAGTCAACAAAGTTCAAGGCACTGAAATAATAGCCAGCAGAGAA 1200
Oy 1201 ATGTCTCAAGAACCGAAATTAATAGATGCTGATAGAGAGCTGAGAAAGAAATGSAAG 1260
Db 1201 ATGTCTCAAGAACCGAAATTAATAGATGCTGATAGAGAGCTGAGAAAGAAATGSAAG 1260
Oy 1261 AAGCATGAAGATTAATATGCTGGATTTACTAGAAAACCTGACTAATGTCTCACTGCTGC 1320
Db 1261 AAGCATGAAGATTAATATGCTGGATTTACTAGAAAACCTGACTAATGTCTCACTGCTGC 1320
Oy 1321 AATGCTGATTAATGATTAATCTCTCAAAAGAGACAGACACCTGAAAATCAGCAATTT 1380
Db 1321 AATGCTGATTAATGATTAATCTCTCAAAAGAGACAGACACCTGAAAATCAGCAATTT 1380
Oy 1381 CCTGCAACGAAAGAGAGATGATGCAAGAAATTTGCGAATTTGTTCTGACATCAAAAGAA 1440
Db 1381 CCTGCAACGAAAGAGAGATGATGCAAGAAATTTGCGAATTTGTTCTGACATCAAAAGAA 1440
Oy 1441 AAACAGATGCCAAATTAATCTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATTAATCTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Oy 1501 TCAGAGGAAAGTCAACAAAGCTTGAGGCACTGAAATGCGCCAGCCAGAG 1551
Db 1501 TCAGAGGAAAGTCAACAAAGCTTGAGGCACTGAAATGCGCCAGCCAGAG 1551

RESULT 18
ID AAA06600 standard; cDNA; 2040 BP.
XX
AC AAA06600;
XX
DE 13-JUN-2000 (first entry)
XX
DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:375.
XX
KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW immunogenic; cytostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200004149-A2.
XX
PD 27-JAN-2000.
XX
PF 14-JUL-1999; 99WO-US15838.
XX
PR 14-JUL-1998; 98US-0115453.
PR 14-JUL-1998; 98US-0116134.
PR 23-SEP-1998; 98US-0159812.
PR 23-SEP-1998; 98US-0159822.
PR 15-JAN-1999; 99US-0232149.
PR 15-JAN-1999; 99US-0232880.
PR 09-APR-1999; 99US-0288946.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Harlocker SL, Yuguu J, Xu J, Mitcham JL;
XX
DR WPI; 2000-171268/15.

XX
PT New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein -
XX
PS Claim 50; Page 223-224; 263pp; English.
XX
CC The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumor protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC the polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AA0641 to AA0651 and
CC AY82000 to AY82020 represent sequences used in the exemplification of
CC the present invention.
XX
SQ Sequence 2040 BP; 716 A; 393 C; 500 G; 431 T; 0 other:
Query Match 75.0%; Score 1500; DB 21; Length 2040;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1550; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 ATGTGCTTGAGCTTATGATTCATGCGGCTGCTCTCTGTAAGAACCATTTGCTTC 60
Db 1 ATGTGCTTGAGCTTATGATTCATGCGGCTGCTCTCTGTAAGAACCATTTGCTTC 60
Oy 61 AGAGCAAGATGGGCAAGGTGCTGCCCTTCCCTGCTGAGGAGGAGGCAAGCGCAAG 120
Db 61 AGAGCAAGATGGGCAAGGTGCTGCCCTTCCCTGCTGAGGAGGAGGCAAGCGCAAG 120
Oy 121 AGCAAGCTGGGCACTTCTGAGACCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAG 180
Db 121 AGCAAGCTGGGCACTTCTGAGACCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAG 180
Oy 181 ATGGGCAAGTGGTGGCGCCACGCTTCCCTGCTGAGGAGGAGGCAAGCAAGCGT 240
Db 181 ATGGGCAAGTGGTGGCGCCACGCTTCCCTGCTGAGGAGGAGGCAAGCAAGCGT 240
Oy 241 GGGCTTCTGAGACCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAGTGGGCAAG 300
Db 241 GGGCTTCTGAGACCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAGTGGGCAAG 300
Oy 301 TGGTGGTGGCACTGCTTCCCTGCTGAGGAGGAGGCAAGCAAGTGGGCGCTTGG 360
Db 301 TGGTGGTGGCACTGCTTCCCTGCTGAGGAGGAGGCAAGCAAGTGGGCGCTTGG 360
Oy 361 GGAGACTAGATGACAGTCCCTTCAAGGAGCCAGGTACACGCTCCGTGGAAGATCTG 420
Db 361 GGAGACTAGATGACAGTCCCTTCAAGGAGCCAGGTACACGCTCCGTGGAAGATCTG 420
Oy 421 GACAAGCTCCACAGAGCTCCGTGGGTTAAAGTCCCAAGAAAGATCTCATCTGCAAG 480
Db 421 GACAAGCTCCACAGAGCTCCGTGGGTTAAAGTCCCAAGAAAGATCTCATCTGCAAG 480
Oy 481 CTCAGGACACTGACGTGAACAAGAGCAAGCAAGAGAGACTGCTTACATCTGGCC 540
Db 481 CTCAGGACACTGACGTGAACAAGAGCAAGCAAGAGAGACTGCTTACATCTGGCC 540
Oy 541 TCTGCCAATGGGAATTCAGAAATGTAATAATCTGCTGAGACAGAGATGTAATTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATGTAATAATCTGCTGAGACAGAGATGTAATTAAT 600
Oy 601 GTCTTTGACAAACAAAAGAGACAGCTGATTAAGGCGGTCAATGCCAGAGAAATGAA 660
Db 601 GTCTTTGACAAACAAAAGAGACAGCTGATTAAGGCGGTCAATGCCAGAGAAATGAA 660
Oy 661 TGTGGTTAATGTTGCTGAGACATGGCACTGATCCAAATATTCAGATGATGTAAT 720
Db 661 TGTGGTTAATGTTGCTGAGACATGGCACTGATCCAAATATTCAGATGATGTAAT 720

QY 721 ACCACTCTGCATACGCTATCTATATGAAGATTAATTAATGAGCAAGCAGCTGCTTA 780
 DB 721 ACCACTCTGCATACGCTATCTATATGAAGATTAATTAATGAGCAAGCAGCTGCTTA 780
 QY 781 TATGTCCTCATATCATCAATCAAAAAACAGCAGTGGCTCACACCACTGTTACTTGGTGA 840
 DB 781 TATGTCCTCATATCATCAATCAAAAAACAGCAGTGGCTCACACCACTGTTACTTGGTGA 840
 QY 841 CATGAGCAAAAAACAGCAGTGGCTGTAATTTTAAATCAAGAAAAAGCAATTTTAAATGA 900
 DB 841 CATGAGCAAAAAACAGCAGTGGCTGTAATTTTAAATCAAGAAAAAGCAATTTTAAATGA 900
 QY 901 CTGATATGATATGGAAGAGCTGCTCATCTCTGCTATGTTGTTGATGATGATGATGATGAT 960
 DB 901 CTGATATGATATGGAAGAGCTGCTCATCTCTGCTATGTTGTTGATGATGATGATGATGAT 960
 QY 961 GTCAGCCTTCTACTTGAGCAAAATATTGATGATCTTCTCAAGATCTATCTGACAGAGC 1020
 DB 961 GTCAGCCTTCTACTTGAGCAAAATATTGATGATCTTCTCAAGATCTATCTGACAGAGC 1020
 QY 1021 GCCAGAGATATGCTGTTTCTAGCATCATGTAATTTGCCAGTACTTCTGACATAC 1080
 DB 1021 GCCAGAGATATGCTGTTTCTAGCATCATGTAATTTGCCAGTACTTCTGACATAC 1080
 QY 1081 AAAGAAAAACAGATGCTTAAATCTCTTCTGAAAAACAGCAATCCAGAAACAGATTAAAG 1140
 DB 1081 AAAGAAAAACAGATGCTTAAATCTCTTCTGAAAAACAGCAATCCAGAAACAGATTAAAG 1140
 QY 1141 CTGACATCAAGAGAGAGTACAAAGGTTCAAAAGGCTGAAAGTAAAGTAAAGTAAAG 1200
 DB 1141 CTGACATCAAGAGAGAGTACAAAGGTTCAAAAGGCTGAAAGTAAAGTAAAGTAAAG 1200
 QY 1201 ATGCTCTCAAGACAGAAATTAATTAAGATGATGATGATGATGATGATGATGATGATGAT 1260
 DB 1201 ATGCTCTCAAGACAGAAATTAATTAAGATGATGATGATGATGATGATGATGATGATGAT 1260
 QY 1261 AAGCATGAAGATTAATTAATGAGATTACTAGAAAAACCTGACTAATGCTGCTGCTGCTG 1320
 DB 1261 AAGCATGAAGATTAATTAATGAGATTACTAGAAAAACCTGACTAATGCTGCTGCTGCTG 1320
 QY 1321 AATGCTATTAATGATTAATTTCTCTCAAGAGAGAGCAACCTGAAATTAATTAATTAAT 1380
 DB 1321 AATGCTATTAATGATTAATTTCTCTCAAGAGAGAGCAACCTGAAATTAATTAATTAAT 1380
 QY 1381 CCTGACAAAGAGTGAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1440
 DB 1381 CCTGACAAAGAGTGAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1440
 QY 1441 AAACAGATGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1500
 DB 1441 AAACAGATGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1500
 QY 1501 TCAGAGGAAGAGTCAAAAGGCTTGAAGGCAAGTGAAGGCAAGGCAAGGCAAGGCAAG 1551
 DB 1501 TCAGAGGAAGAGTCAAAAGGCTTGAAGGCAAGTGAAGGCAAGGCAAGGCAAGGCAAG 1551

PN W0200061753-A2.
 XX 19-OCT-2000.
 PD 07-APR-2000; 2000MO-US09312.
 PF 09-APR-1999; 9905-0289198.
 PR 28-OCT-1999; 9905-0429755.
 PR 23-MAR-2000; 2000US-0534825.
 XX (CORI-) CORIXA CORP.
 XX Frudakis TN, Smith JM, Reed SG, Misher LE, Retter WM, Dillon DC;
 PI WPI: 2000-628403/60.
 DR P-PDB; AAB28628.
 PT An isolated polypeptide comprising an immunogenic portion of a breast
 PT tumor protein used for inhibiting the development of cancer, especially
 PT breast cancer, and monitoring cancer progression in a patient -
 XX
 PS Claim 4; Page 177; 187pp; English.
 CC The present sequence is given in a specification relating to compositions
 CC and methods for the treatment and diagnosis of breast cancer. Nucleotide
 CC sequences that are preferentially expressed in breast tumour tissue, and
 CC the polypeptides encoded by such nucleotide sequences, are used in
 CC compositions and vaccines to inhibit the development of cancer.
 CC especially breast cancer. The progression of a cancer may be monitored by
 CC carrying out detection of tumour-specific antigens at subsequent time
 CC points and comparing the results from the different time points.
 CC CD4+ and/or CD8+ T-Cells isolated from the cancer patient may be treated
 CC with tumour-specific polypeptides, polynucleotides encoding the
 CC polypeptides or antigen presenting cells expressing the polypeptides. The
 CC cells are then administered to the patient to inhibit development of
 CC cancer.
 XX
 SO Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;
 Query Match 56.4%; Score 1128; DB 21; Length 1155;
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Gaps 0;
 Matches 1128; Conservative 0; Indels 0; Gaps 0;
 QY 1 ATGCTGTTAGAGTGAATTCATGCGCTGCTCTCTGTAAGAACCATTTGGTCTC 60
 DB 1 ATGCTGTTAGAGTGAATTCATGCGCTGCTCTCTGTAAGAACCATTTGGTCTC 60
 QY 61 AGGAGCAAGATGGGCAAGTGGTGGTCTGCTCTCTGTAAGAACCATTTGGTCTC 120
 DB 61 AGGAGCAAGATGGGCAAGTGGTGGTCTGCTCTCTGTAAGAACCATTTGGTCTC 120
 QY 121 AGCAAGTGGGCACTTGTGAGACCAAGAGACTCTGTAAGAACCATTTGGTCTC 180
 DB 121 AGCAAGTGGGCACTTGTGAGACCAAGAGACTCTGTAAGAACCATTTGGTCTC 180
 QY 181 ATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
 DB 181 ATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
 QY 241 GGGGCTTCTGAGACCAAGAGACTCTGTAAGAACCATTTGGTGGTGGTGGTGGTGGTGG 300
 DB 241 GGGGCTTCTGAGACCAAGAGACTCTGTAAGAACCATTTGGTGGTGGTGGTGGTGGTGG 300
 QY 301 TGGGCTGCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
 DB 301 TGGGCTGCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
 QY 361 GGAGACTACGATGACATGCTTCAATGAGCCAGATACAGCTCCGTGAGAGATCTG 420
 DB 361 GGAGACTACGATGACATGCTTCAATGAGCCAGATACAGCTCCGTGAGAGATCTG 420
 QY 421 GACAGCTCCAGAGAGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
 DB 421 GACAGCTCCAGAGAGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480

Db 421 GACAACTCCACAGAGCTGCTGGTGGGTAAGTCCCGAAGAAAGATCTCATGTCATG 480
 Qy 481 CTCAGGAGACCTGAGCTGAACAAGAGAGCAAGCAAAAGAGAGCTGCTACATCTGGCC 540
 Db 481 CTCAGGAGACCTGAGCTGAACAAGAGAGCAAGCAAAAGAGAGCTGCTACATCTGGCC 540
 Qy 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGGACAGAGATGCACTTAAT 600
 Db 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGGACAGAGATGCACTTAAT 600
 Qy 601 GTCTCTGACAAACAAAAGAGAGAGAGCTGATTAAGAGCCGTACAAATGCCAGAAATGAA 660
 Db 601 GTCTCTGACAAACAAAAGAGAGAGAGCTGATTAAGAGCCGTACAAATGCCAGAAATGAA 660
 Qy 661 TGTGCTTATATGTTGGTGAACATGGACATGATCCAAATTTCCAGATGATGGAAT 720
 Db 661 TGTGCTTATATGTTGGTGAACATGGACATGATCCAAATTTCCAGATGATGGAAT 720
 Qy 721 ACCACTCTGACATGACCTATCTATTAATGAAGATAAATTAATGGCAAGACATGCTCTTA 780
 Db 721 ACCACTCTGACATGACCTATCTATTAATGAAGATAAATTAATGGCAAGACATGCTCTTA 780
 Qy 781 TATGGTGTGATATCCATTAACAAAACAGAGAGAGAGCTGACACCACTGTTACTTGGTGA 840
 Db 781 TATGGTGTGATATCCATTAACAAAACAGAGAGAGAGCTGACACCACTGTTACTTGGTGA 840
 Qy 841 CATGAGCAAAAACAGCAAGTCTGAAATTTTATCAAGAAAAGGAATTTAAATGCA 900
 Db 841 CATGAGCAAAAACAGCAAGTCTGAAATTTTATCAAGAAAAGGAATTTAAATGCA 900
 Qy 901 CTGGATAGATATGGAAGAGAGCTGCTCATCTACTGCTGATGTTGGATCAGCAAGTATA 960
 Db 901 CTGGATAGATATGGAAGAGAGAGCTGCTCATCTACTGCTGATGTTGGATCAGCAAGTATA 960
 Qy 961 GTGACCTTCTACTTGAAGCAAAATATTGATGATCTTCTCAAGATCTATCTGACAGAGC 1020
 Db 961 GTGACCTTCTACTTGAAGCAAAATATTGATGATCTTCTCAAGATCTATCTGACAGAGC 1020
 Qy 1021 GCCAGAGATGCTGTTTACTGATCATCATGATTAATTTGCCAGTACTTCTGACTAC 1080
 Db 1021 GCCAGAGATGCTGTTTACTGATCATCATGATTAATTTGCCAGTACTTCTGACTAC 1080
 Qy 1081 AAGAAACAGATGCTAAATCTCTTCTGAAAACAGCAATCCAGAA 1128
 Db 1081 AAGAAACAGATGCTAAATCTCTTCTGAAAACAGCAATCCAGAA 1128
 RESULT 20
 ID AAA06598 standard; cdna; 1155 BP.
 AC AAA06598:
 XX
 DE 13-JUN-2000 (first entry)
 XX
 DE Human immunogenic prostate tumour protein cdna sequence SEQ ID NO:373.
 KW Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
 KW Immunogenic; cytostatic; vaccine; ss.
 OS Homo sapiens.
 OS
 PN MO200004149-A2.
 PD 27-JAN-2000.
 PD
 PF 14-JUL-1999; 99MO-US15838.
 PR 14-JUL-1998; 98US-0115453.
 PR 14-JUL-1998; 98US-0116134.
 PR 23-SEP-1998; 98US-0159812.
 PR 23-SEP-1998; 98US-0159822.
 PR 15-JAN-1999; 99US-0232149.

PR 15-JAN-1999; 99US-0232880.
 PR 09-APR-1999; 99US-0288946.
 XX
 PA (CORI-) CORIXA CORP.
 PI Dillon DC, Harlocker SL, Yung J, Xu J, Mitcham JL;
 DR WPI; 2000-171268/15.
 XX
 PT New polypeptide useful for treating and diagnosing prostate cancer
 PT comprises an immunogenic portion of prostate tumor protein -
 PS
 XX
 XX
 CC Claim 50; Page 222; 263pp; English.
 CC The present invention describes isolated polypeptides, comprising an
 CC immunogenic portion of a prostate tumour protein (PTP). The polypeptides
 CC and polynucleotides encoding them have cytostatic activity and can be
 CC used in vaccines and in gene therapy. The polypeptides and
 CC polynucleotides encoding them, antigen presenting cells which express
 CC the polypeptides, antibodies against the polypeptides and vaccines
 CC comprising them can be used for inhibiting the development of prostate
 CC cancer in a patient. The polypeptides can be used to generate antibodies
 CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
 CC the polynucleotides encoding the polypeptides can be used as a probe or
 CC to modulate the expression of the polypeptides. AAA06241 to AAA06591 and
 CC AAY82000 to AAY82020 represent sequences used in the exemplification of
 CC the present invention.
 CC
 XX
 SQ Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;
 Query Match 56.4%; Score 1128; DB 21; Length 1155;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATGTGTTAGGTTGATTCATGCGGCTGCTCTTCTGTAAGAAAGCATTTGCTCTC 60
 Db 1 ATGTGTTAGGTTGATTCATGCGGCTGCTCTTCTGTAAGAAAGCATTTGCTCTC 60
 Qy 61 AGGAGCAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
 Db 61 AGGAGCAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
 Qy 121 AGCAACGTGGGCACTTCTGAGACACAGAGAGCTCTGTAAGAGACTCAGAGAGCAAG 180
 Db 121 AGCAACGTGGGCACTTCTGAGACACAGAGAGCTCTGTAAGAGACTCAGAGAGCAAG 180
 Qy 181 ATGGGCAAGTGGTGGGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGAGCACTG 240
 Db 181 ATGGGCAAGTGGTGGGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGAGCACTG 240
 Qy 241 GCGGCTTCTGAGACACAGAGAGCTGTAAGAGACTCAGAGAGCAAGATGGGCAAG 300
 Db 241 GCGGCTTCTGAGACACAGAGAGCTGTAAGAGACTCAGAGAGCAAGATGGGCAAG 300
 Qy 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGGGAGGCAAGAGAGAGTGGGCTTGG 360
 Db 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGGGAGGCAAGAGAGAGTGGGCTTGG 360
 Qy 361 GGAGACTACGATGACAGTGGCTTCTGAGAGCCAGTACACAGCTCCCTGGAGAGATCTG 420
 Db 361 GGAGACTACGATGACAGTGGCTTCTGAGAGCCAGTACACAGCTCCCTGGAGAGATCTG 420
 Qy 421 GACAAGCTCCACAGAGTGGCTGGTGGGTAAGTCCCGAAGAAAGATCTCATGCTATG 480
 Db 421 GACAAGCTCCACAGAGTGGCTGGTGGGTAAGTCCCGAAGAAAGATCTCATGCTATG 480
 Qy 481 CTCAGGAGACCTGAGCTGAACAAGAGAGCAAGCAAAAGAGAGCTGCTACATCTGGCC 540
 Db 481 CTCAGGAGACCTGAGCTGAACAAGAGAGCAAGCAAAAGAGAGCTGCTACATCTGGCC 540
 Qy 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGGACAGAGATGCACTTAAT 600
 Db 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGGACAGAGATGCACTTAAT 600

QY 601 GTCTTGACAAACAAAGAGAGAGAGCTCTGTATAAGGCCGTACATGCGCAGAGATGAA 660
 Db 601 GTCTTGACAAACAAAGAGAGAGAGCTCTGTATAAGGCCGTACATGCGCAGAGATGAA 660
 QY 661 TGTGCGTTAAAGTTCGTCGGAACATGCGCAGCTATCCAAATATTCAGATGATGAAAT 720
 Db 661 TGTGCGTTAAAGTTCGTCGGAACATGCGCAGCTATCCAAATATTCAGATGATGAAAT 720
 QY 721 ACCACTGTGACACTACGCTATCTATATGAAGATAAATTAATGCGCAAGACTGCTTTA 780
 Db 721 ACCACTGTGACACTACGCTATCTATATGAAGATAAATTAATGCGCAAGACTGCTTTA 780
 QY 781 TATGCGCTGATATGCAATCAAAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
 Db 781 TATGCGCTGATATGCAATCAAAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
 QY 841 CATGAGCAAAAACAG 900
 Db 841 CATGAGCAAAAACAG 900
 QY 901 CTGATGATATGAG 960
 Db 901 CTGATGATATGAG 960
 QY 961 GTGAGCTTCTACTTGAAGCAAAATATTTGATGATCTTCTCAAGATCTATGAGAGAG 1020
 Db 961 GTGAGCTTCTACTTGAAGCAAAATATTTGATGATCTTCTCAAGATCTATGAGAGAG 1020
 QY 1021 GCCAGAGAGTATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTATCTTCTGAC 1080
 Db 1021 GCCAGAGAGTATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTATCTTCTGAC 1080
 QY 1081 AAG 1128
 Db 1081 AAG 1128

RESULT 21
 ID AAI67211 standard; cDNA; 1155 BP.
 XX AAI67211;

DT 11-FEB-2002 (first entry)
 XX B305D isoform C splice variant 1 encoding cDNA.

KW Genetic substructure: DNA microarray analysis: polymerase chain reaction;
 KW cancer: B305D; ss.

XX Homo sapiens.

FT Key 1.1155
 FT CDS /product= "B305D isoform C splice variant"

PN MO200175171-A2.

PD 11-OCT-2001.

PF 02-APR-2001; 2001MO-US10631.

PR 03-APR-2000; 2000US-194241P.

PR 20-JUL-2000; 2000US-219862P.

PR 27-JUL-2000; 2000US-221300P.

PR 18-DEC-2000; 2000US-256592P.

PA (CORI-) CORIXA CORP.
 XX Houghton RL, Dillon DC, Molesh DA, Xu J, Zehentner B, Persing DH;
 XX

DR WPI: 2001-626449/72.
 DR P-PSDB: AAG65976.
 XX
 PT Identifying tissue (tumour)-specific polynucleotides overexpressed in
 PT tissue of interest as compared to control tissue, for detecting cancer
 PT cells in patient, comprises DNA microarray analysis or quantitative
 PT polymerase chain reaction -
 XX
 PS Claim 4: Page 93-94; 127pb: English.
 XX
 CC The invention relates to identifying tissue-specific polynucleotides (P)
 CC from tissue of interest (TI), performing DNA microarray analysis to
 CC identify first subset of polynucleotides (SPI) at least 2-fold over
 CC expressed in TI, and performing quantitative polymerase chain reaction
 CC (PCR) analysis on SPI to identify second subset of (P). The method is
 CC useful for determining the presence or absence of a cancer cell in a
 CC patient, monitoring the progression of cancer in a patient using a
 CC biological sample such as blood, serum, lymph nodes, bone marrow, sputum,
 CC urine or a tumour biopsy sample. The methods are useful for determining
 CC the presence or absence of or monitoring progression of prostate, breast,
 CC colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver,
 CC gastric, kidney, bladder, pancreatic or endometrial cancer. The present
 CC sequence represents a cDNA encoding a B305D isoform C splice variant.
 XX
 SQ Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;

Query Match 56.4%; Score 1128; DB 22; Length 1155;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTGAAGTGTGATTCATGCGCGCTGCTCTCTGTGAAGAGAGCCATTTGGTCTC 60
 Db 1 ATGGTGGTGAAGTGTGATTCATGCGCGCTGCTCTCTGTGAAGAGAGCCATTTGGTCTC 60
 QY 61 AGAGCAAGATGAG 120
 Db 61 AGAGCAAGATGAG 120
 QY 121 AGCAAGCTGGGACCTTCTGAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
 Db 121 AGCAAGCTGGGACCTTCTGAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
 QY 181 ATGGGCAAGTGGTCCGCCACTGCTCCCTGCTGACAGAGAGAGAGAGAGAGAGAGAG 240
 Db 181 ATGGGCAAGTGGTCCGCCACTGCTCCCTGCTGACAGAGAGAGAGAGAGAGAGAGAG 240
 QY 241 GCGCCTTCTGAGAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 Db 241 GCGCCTTCTGAGAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
 QY 301 TGGTGTGCGCCACTGCTCCCTGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
 Db 301 TGGTGTGCGCCACTGCTCCCTGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
 QY 361 GGAGACTACGATGACAG 420
 Db 361 GGAGACTACGATGACAG 420
 QY 421 GACAAAGCTCCACAG 480
 Db 421 GACAAAGCTCCACAG 480
 QY 481 CTGAGGAGACAG 540
 Db 481 CTGAGGAGACAG 540
 QY 541 TCTGCAATGAG 600
 Db 541 TCTGCAATGAG 600
 QY 601 GTCTTGACAAACAAAGAGAGAGAGCTCTGTATAAGGCCGTACATGCGCAGAGATGAA 660
 Db 601 GTCTTGACAAACAAAGAGAGAGAGCTCTGTATAAGGCCGTACATGCGCAGAGATGAA 660

Db 601 GTCCTTGACACAAAAAGAGACAGCTCTGATAAAGCCGCTACAAATGCCAGAGATGAA 660
QY 661 TGTGGTTAATGTTGCTGGAACATGCGACTGATCCAAATATCCAGATAGATGAAT 720
Db 661 TGTGGTTAATGTTGCTGGAACATGCGACTGATCCAAATATCCAGATAGATGAAT 720
QY 721 ACCACTGTCAGTACGCTATCTATATGAAGATTAATATATGCGCAACAGCTGCTTA 780
Db 721 ACCACTGTCAGTACGCTATCTATATGAAGATTAATATATGCGCAACAGCTGCTTA 780
QY 781 TATGCTGCTGATATGGAATCAAAAAACAAGATGCGCTCACACCAGTGTACTGGTGA 840
Db 781 TATGCTGCTGATATGGAATCAAAAAACAAGATGCGCTCACACCAGTGTACTGGTGA 840
QY 841 CATGAGCAAAACAGCAATCGTGAATTTTAAATCAAAAAAAGCGAATTAATGA 900
Db 841 CATGAGCAAAACAGCAATCGTGAATTTTAAATCAAAAAAAGCGAATTAATGA 900
QY 901 CTGATATGATATGAAGAGACTGCTCATACTTGTGATGTTGATGATCAGCAATATA 960
Db 901 CTGATATGATATGAAGAGACTGCTCATACTTGTGATGTTGATGATCAGCAATATA 960
QY 961 GTCAGCCTTCTACTGAGCAAAATATGATATCTTCAAGATCTATCTGAGACAG 1020
Db 961 GTCAGCCTTCTACTGAGCAAAATATGATATCTTCAAGATCTATCTGAGACAG 1020
QY 1021 GCCAAGAGATATGCTTTCTAGTCAATCATGTAATTTGCCAGTACTTCTGACTAC 1080
Db 1021 GCCAAGAGATATGCTTTCTAGTCAATCATGTAATTTGCCAGTACTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAATAATCTTCTGAAAAACAGCAATCCAGAA 1128
Db 1081 AAGAAAAACAGATGCTAAATAATCTTCTGAAAAACAGCAATCCAGAA 1128

RESULT 22
AAS63807
ID AAS63807 standard; cDNA; 1155 BP.

AC AAS63807;
DT 29-JAN-2002 (first entry)
XX Human prostate cDNA clone B305D splice variant #8.
DE Human prostate cancer; ss; cytosolic; immunostimulant; tumour.
XX Homo sapiens.
OS WO200173032-A2.
PN 04-OCT-2001.
PD 27-MAR-2001; 2001WO-US09919.
PF 27-MAR-2001; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679426.
PR 10-OCT-2000; 2000US-0685166.
XX (CORI-) CORIXA CORP.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Reiter KM, Stolk JA, Day CH, Vedicick TS, Carter D;
PI Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;
XX WPI; 2001-639232/73.

DR P-PSDB; AAU69777.
XX New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
XX
XX
PS Claim 1; Page 349; 579pp; English.

The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific polynucleotide of the invention.

SQ Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;

Query Match 56.4%; Score 1128; DB 22; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTGTTGAGTTGATTCATGCCGCTCCTCTTGTGTAAGAACCATTTGGTCTC 60
Db 1 ATGTGTGTTGAGTTGATTCATGCCGCTCCTCTTGTGTAAGAACCATTTGGTCTC 60
QY 61 AGGAGCAATATGGGCAAGTGTGCTGCTTCCCTGCTGCGAGGAGAGCGGCAAG 120
Db 61 AGGAGCAATATGGGCAAGTGTGCTGCTTCCCTGCTGCGAGGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACCAAGAGACTGCTATGAAAGCACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACCAAGAGACTGCTATGAAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGAGGAGGAGTGGCAAGCTTG 240
Db 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGAGGAGGAGTGGCAAGCTTG 240
QY 241 GGGGCTTGTGAGACCAAGAGACTGCTATGAAAGCACTCAGAGCAAGTGGCAAG 300
Db 241 GGGGCTTGTGAGACCAAGAGACTGCTATGAAAGCACTCAGAGCAAGTGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGAGGAGGAGCGCAAGAGTGGGCGCTTG 360
Db 301 TGGTGTGCACTGCTTCCCTGCTGAGGAGGAGCGCAAGAGTGGGCGCTTG 360
QY 361 GGAGACTACGATGACAGTGCCTTCATGAGCCAGGTACCAAGCTCGTGAGAAATCTG 420
Db 361 GGAGACTACGATGACAGTGCCTTCATGAGCCAGGTACCAAGCTCGTGAGAAATCTG 420
QY 421 GACAAGCTCAGACAGCTGCTGTTGAGTAAAGTCCCAAGAAAGATTCATCGTCAG 480
Db 421 GACAAGCTCAGACAGCTGCTGTTGAGTAAAGTCCCAAGAAAGATTCATCGTCAG 480
QY 481 CTCAGGACACTGACGTGTAACAAGAGCAAGCAAAAGAGCACTCTACATCGGCC 540
Db 481 CTCAGGACACTGACGTGTAACAAGAGCAAGCAAAAGAGCACTCTACATCGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAACTGTAAGAACTCTCTGAGACGAGTCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAACTGTAAGAACTCTCTGAGACGAGTCAACTTAAT 600
QY 601 GTCCTTGACAAAAAGAGAGAGCTGATGAAGGCGGTCAAGGCCAGGAAGTGA 660
Db 601 GTCCTTGACAAAAAGAGAGAGCTGATGAAGGCGGTCAAGGCCAGGAAGTGA 660
QY 661 TGTGCTTAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATAGATGAAT 720
Db 661 TGTGCTTAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATAGATGAAT 720

Db 661 TGTGCGTTAATGTTGCTGGAAACATGCGATGCCAATATATTCAGATGAGTATGGAAT 720
Qy 721 ACCACTGTGACACTGCGTATCATATGAGATGAATTAATGCGCAAGCACTGCTCTTA 780
Db 721 ACCACTGTGACACTGCGTATCATATGAGATGAATTAATGCGCAAGCACTGCTCTTA 780
Qy 781 TATGCTGTATATGATGCAATCAAAAAACAGAGCTGGCTCACACCACTGTTACTTGCTGA 840
Db 781 TATGCTGTATATGATGCAATCAAAAAACAGAGCTGGCTCACACCACTGTTACTTGCTGA 840
Qy 841 CATGAGCAAAAAACAGCAAGTGTGTAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTGTGTAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
Qy 901 CTGATGATGATGAGAGAGACTGCTCATACTGCTGATGTTGGATCGCAAGTATA 960
Db 901 CTGATGATGATGAGAGAGACTGCTCATACTGCTGATGTTGGATCGCAAGTATA 960
Qy 961 GTGAGCTTCTACTTGGAGCAAAATATTTGATGATCTTCTCAAGATCTATCGACAGACG 1020
Db 961 GTGAGCTTCTACTTGGAGCAAAATATTTGATGATCTTCTCAAGATCTATCGACAGACG 1020
Qy 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTTCTGACTAC 1080
Db 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTTCTGACTAC 1080
Qy 1081 AAGAAAAACAGATGCTAAATAATCTCTTGAAACAGCAATCCAGAA 1128
Db 1081 AAGAAAAACAGATGCTAAATAATCTCTTGAAACAGCAATCCAGAA 1128

RESULT 23
AAH93714
ID AAH93714 standard; cDNA; 1155 BP.
XX

XX AAH93714;

XX 04-OCT-2001 (first entry)

DE Human prostate-specific cDNA sequence B305D splice variant #8.

KW Human: prostate cancer; prostate-specific; diagnosis; vaccine;
cytostatic; gene therapy; metastasis; ss.

OS Homo sapiens.

PN M0200151633-A2.

PD 19-JUL-2001.

PF 16-JAN-2001; 2001MO-US01574.

PR 14-JAN-2000; 2000US-0483672.

XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kelos MD, Fanger GR, Day CH, Retter MM, Stolk JA, Skelky YAW;
PI Wang A, Mesgher MJ;

XX WPI; 2001-425873/45.

DR

XX New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -

XX Claim 1; Page 347; 543pp; English.

XX The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used treat cancer in a patient.

CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH0115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.

XX Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;

Query Match 56.4%; Score 1128; DB 22; Length 1155;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTTGTTGAGTTGATTCATGCGGCTGCTCTTCTGTGAAGAACCTTTGGTCTC 60
Db 1 ATGTTGTTGAGTTGATTCATGCGGCTGCTCTTCTGTGAAGAACCTTTGGTCTC 60
Qy 61 AGGAGCAAGATGGGCAAGTGGTGGCTGGCTTCCCTGCTGAGGAGAGGCGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGGTGGCTGGCTTCCCTGCTGAGGAGAGGCGCAAG 120
Qy 121 AGCAAGCTGGGCACTTGTGAGACCAAGCACTCTCTATGAAGACATCAGAGCAAG 180
Db 121 AGCAAGCTGGGCACTTGTGAGACCAAGCACTCTCTATGAAGACATCAGAGCAAG 180
Qy 181 ATGGGCAAGTGGTGGGCACTTGTGAGACCAAGCACTCTCTATGAAGACATCAGAGCAAG 240
Db 181 ATGGGCAAGTGGTGGGCACTTGTGAGACCAAGCACTCTCTATGAAGACATCAGAGCAAG 240
Qy 241 GGGCTTCTGGAGACCAAGCACTTGTGAGACCAAGCACTTGTGAGACCAAGCACTTGTGAGACCAAG 300
Db 241 GGGCTTCTGGAGACCAAGCACTTGTGAGACCAAGCACTTGTGAGACCAAGCACTTGTGAGACCAAG 300
Qy 301 TGTGCTGCGCACTGCTTCCCTGCTGCAAGGGGAGGCGCAAGAGTGGCGCTTGG 360
Db 301 TGTGCTGCGCACTGCTTCCCTGCTGCAAGGGGAGGCGCAAGAGTGGCGCTTGG 360
Qy 361 GGAACATACATGACATGCTTATGAGAGCCCAAGATACACATGCTTGTGAGAGATCTG 420
Db 361 GGAACATACATGACATGCTTATGAGAGCCCAAGATACACATGCTTGTGAGAGATCTG 420
Qy 421 GACAAGCTCCACAGAGTGGCTGCTGCAAGGGGAGGCGCAAGAGTGGCGCTTGG 480
Db 421 GACAAGCTCCACAGAGTGGCTGCTGCAAGGGGAGGCGCAAGAGTGGCGCTTGG 480
Qy 481 CTCAGGACACTGACGTGAACCAAGAGACCAAGAGAGTGGCTTACATCTGGCC 540
Db 481 CTCAGGACACTGACGTGAACCAAGAGACCAAGAGAGTGGCTTACATCTGGCC 540
Qy 541 TCTGCAATGGGAATTCAGAAATCTCTGCTGGACAGACATGCAACTTAAT 600
Db 541 TCTGCAATGGGAATTCAGAAATCTCTGCTGGACAGACATGCAACTTAAT 600
Qy 601 GTCTTGAACAACAAAAGAGAGAGCTGCTGTAAGAGCCGTAACATGCAAGATGAA 660
Db 601 GTCTTGAACAACAAAAGAGAGAGCTGCTGTAAGAGCCGTAACATGCAAGATGAA 660
Qy 661 TGTGCGTTAATGTTGCTGGAACATGCAAGTGAATTTCCAGATGATGAAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGCAAGTGAATTTCCAGATGATGAAAT 720
Qy 721 ACCACTGTGACACTGCGTATCATATGAGATGAATTAATGCGCAAGCACTGCTCTTA 780
Db 721 ACCACTGTGACACTGCGTATCATATGAGATGAATTAATGCGCAAGCACTGCTCTTA 780
Qy 781 TATGCTGTATATGATGCAATCAAAAAACAGAGCTGGCTCACACCACTGTTACTTGCTGA 840
Db 781 TATGCTGTATATGATGCAATCAAAAAACAGAGCTGGCTCACACCACTGTTACTTGCTGA 840
Qy 841 CATGAGCAAAAAACAGCAAGTGTGTAATTTTATCAAGAAAAAGCAATTTAAATGCA 900

|||||
Db 841 CATGAGCAAAAACAGCAAGTCTGAAATTTTAATCAAGAAAAAGCGAATTTAAATGCA 900
Qy 901 CTGGATATATATGGAAGAGCTCTCATACTTGTCTGTATGTTGGATCAGCAATATA 960
Db 901 CTGGATATATGGAAGAGCTCTCATACTTGTCTGTATGTTGGATCAGCAATATA 960
Qy 961 GTCAACCTTCTACTGAGCAAAATATGATGTATCTTCAAGATCTATCTGAGACAGC 1020
Db 961 GTCAACCTTCTACTGAGCAAAATATGATGTATCTTCAAGATCTATCTGAGACAGC 1020
Qy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Qy 1081 AAGAAAAACAGATCTAAAAATCTCTTCTGAAACAGCAATCCAGAA 1128
Db 1081 AAGAAAAACAGATCTAAAAATCTCTTCTGAAACAGCAATCCAGAA 1128

RESULT 24

AAH85028
ID AAH85028 standard; cDNA; 1155 BP.

XX AAH85028;

XX 25-SEP-2001 (first entry)

DE Human prostate-specific cDNA sequence B305D splice variant #8.

KW Human; prostate cancer; therapy; diagnosis; cat eye syndrome;

KM Chromosome 22q11.2; prostate-specific protein; chromosome 1;

KW prostate specific antigen; PSA; ss.

OS Homo sapiens.

XX WO200134802-A2.

XX 17-MAY-2001.

XX 09-NOV-2000; 2000WO-US30904.

XX 12-NOV-1999; 99US-0439313.

XX 18-NOV-1999; 99US-0443686.

XX (CORI-) CORIXA CORP.

XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;

PI Kalos MD, Reltter MW, Stolk JA, Day CH, Skelky YAW, Wang A;

XX WPI; 2001-308785/32.

PS Claim 31; Page 246-247; 325pp; English.

CC The present invention describes an isolated polypeptide (P1) comprising
CC at least an immunogenic portion of a prostate-specific protein, or its
CC variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
CC (N1) have cytostatic activity and can be used in vaccine production.
CC The polypeptides, nucleic acids and antibodies from the present
CC invention are useful in the diagnosis and therapy of prostate cancer.
CC Prostate specific genes P704P, P712P, P774P, P775P and B305D are located
CC in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
CC region. Prostate specific antigen (PSA) P501S was located on
CC chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent
CC polynucleotide and polypeptide sequences used in the exemplification
CC of the present invention.

XX Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;

Query Match 56.4%; Score 1128; DB 22; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGCTTGGAGTGTGATTCATGCCGCTGCTTCTGTGAAGAGCCATTGGTCTC 60
Db 1 ATGTGCTTGGAGTGTGATTCATGCCGCTGCTTCTGTGAAGAGCCATTGGTCTC 60
Qy 61 AAGAGCAATATGGGCAAGGTGTGCTGCTTCCCTGCTGCGAGGAGGCGGCAAG 120
Db 61 AAGAGCAATATGGGCAAGGTGTGCTGCTTCCCTGCTGCGAGGAGGCGGCAAG 120
Qy 121 ACCAAGTGGGCACTTCTGAGACACGACGACTGCTATGAAGCACTCAGAGCAAG 180
Db 121 ACCAAGTGGGCACTTCTGAGACACGACGACTGCTATGAAGCACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGTGCCGCACTGCTTCCCTGCTGCGAGGAGGAGTGGCAAGCAAGT 240
Db 181 ATGGGCAAGTGTGCCGCACTGCTTCCCTGCTGCGAGGAGGAGTGGCAAGCAAGT 240
Qy 241 GGCGCTTCTGGAGACACGACGACTGCTATGAAGCACTCAGAGCAAGTGGGCAAG 300
Db 241 GGCGCTTCTGGAGACACGACGACTGCTATGAAGCACTCAGAGCAAGTGGGCAAG 300
Qy 301 TGTGCTGCTGACCTGCTTCCCTGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Db 301 TGTGCTGCTGACCTGCTTCCCTGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Qy 361 GGAGACTATGATGACAGTGCCTTCTCATGAGCCAGGTACACGCTCCGTGGAGAGTCTG 420
Db 361 GGAGACTATGATGACAGTGCCTTCTCATGAGCCAGGTACACGCTCCGTGGAGAGTCTG 420
Qy 421 GACAAGCTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421 GACAAGCTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Qy 481 CTCAGGACACTGACGTGTAACAAGAGCAAGCAAGAGCAAGCAAGCAAGCAAGCAAG 540
Db 481 CTCAGGACACTGACGTGTAACAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
Qy 541 TCTGCCAATGGGAATTCAGAGTATGTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 541 TCTGCCAATGGGAATTCAGAGTATGTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Qy 601 GTGCTGGAACAAGAAAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 601 GTGCTGGAACAAGAAAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Qy 661 TGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 661 TGTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Qy 721 ACCACTCTGCACTAGCTATCTATATGAAGTAATTAATGAGCCAAAGCAAGCTGCTTA 780
Db 721 ACCACTCTGCACTAGCTATCTATATGAAGTAATTAATGAGCCAAAGCAAGCTGCTTA 780
Qy 781 TATGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 781 TATGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Qy 841 CATGAGCAAAAACAGCAAGTCTGTAATTTTAATCAAGAAAAAGCGAATTTAAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGTCTGTAATTTTAATCAAGAAAAAGCGAATTTAAATGCA 900
Qy 901 CTGGATATATGGAAGAGCTCTCATACTTGTCTGTATGTTGGATCAGCAATATA 960
Db 901 CTGGATATATGGAAGAGCTCTCATACTTGTCTGTATGTTGGATCAGCAATATA 960
Qy 961 GTCAACCTTCTACTGAGCAAAATATGATGTATCTTCAAGATCTATCTGAGACAGC 1020
Db 961 GTCAACCTTCTACTGAGCAAAATATGATGTATCTTCAAGATCTATCTGAGACAGC 1020
Qy 1021 GCCAGAGTATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080

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Db 1021 GCCGAGAGTATGCTTTCTAGTCATCATATGTAATTTGCCAGTACTTTCTGACTAC 1080
Qy 1081 AAAGAAAAAGATGCTAAAAATCTCTTGTGAAACAGCAATCCAGAA 1128
Db 1081 AAAGAAAAAGATGCTAAAAATCTCTTGTGAAACAGCAATCCAGAA 1128
RESULT 25
AAH02779
ID AAH02779 standard; cDNA; 1155 BP.
XX AAH02779;
AC AAH02779;
XX
XX 14-JUN-2001 (first entry)
DE Prostate tumour antigen determined cDNA splice variant of B305D #8.
XX
XX
KW Human: prostate tumour antigen; prostate tumour; therapy; diagnosis;
KM prostate cancer; immunogenic; cytostatic; vaccine; ss.
XX Homo sapiens.
OS
XX W0200125272-A2.
PN 12-APR-2001.
PD
XX 04-OCT-2000; 2000MO-US27464.
PF
XX 04-OCT-1999; 99US-0157455.
PR
XX (CORI-) CORIXA CORP.
PA
PI Xu J, Skeiky YAM, Reed SG, Cheever MA;
XX WPI: 2001-245062/25.
DR P-PSDB; AAB74815.
XX
XX Prostate specific protein and its encoding polynucleotide, useful for
PT the treatment and diagnosis of prostate cancer -
XX
PS Claim 50; Page 231-232; 276pp; English.
XX
XX The present invention describes an isolated polypeptide (I) comprising
CC at least an immunogenic portion of a prostate tumour antigen protein or
CC its variant. (I) have cytostatic activity and can be used in vaccine
CC production. (I), prostate tumour antigen polynucleotides, an antigen
CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a
CC pharmaceutical composition containing (I) are useful for inhibiting the
CC development of cancer in a patient. Antibodies specific for prostate
CC specific proteins and oligonucleotides that hybridise to a
CC polynucleotide that encodes a prostate specific protein are useful
CC for detecting the presence or absence of a cancer or monitoring the
CC progression of a cancer, especially prostate cancer.
CC AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences
CC used in the exemplification of the present invention.
XX
SQ Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;

Query Match 56.4%; Score 1128; DB 22; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGTGTTAGTGTATTCATCGCGTGCCTCTTGTGAAAGCAATTTGTTCTC 60
|||||
Db 1 ATGTGTGTTAGTGTATTCATCGCGTGCCTCTTGTGAAAGCAATTTGTTCTC 60
1 ATGTGTGTTAGTGTATTCATCGCGTGCCTCTTGTGAAAGCAATTTGTTCTC 60
Qy 61 AGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGACAGGAGCGGCAAG 120
|||||
Db 61 AGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGACAGGAGCGGCAAG 120
61 AGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGACAGGAGCGGCAAG 120
Qy 121 AGCAAGCTGGGCACTTGTGAGACAGAGACACTCTCTATGAAGACACTGAGGCAAG 180
|||||

Db 121 AGCAAGCTGGGCACTTGTGAGACAGAGACACTCTCTATGAAGACACTGAGGCAAG 180
Qy 181 ATGGGCAAGTGTGTCGCCGCACTGCTTCCCTGCTGTCAGAGGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGTGTCGCCGCACTGCTTCCCTGCTGTCAGAGGGGAGTGGCAAGCAAGCTG 240
Qy 241 GGGCTTCTGGAGACACAGAGACTTGTATGAAGACACTCAGGAACAGATGGGCAAG 300
Db 241 GGGCTTCTGGAGACACAGAGACTTGTATGAAGACACTCAGGAACAGATGGGCAAG 300
Qy 301 TGGTGTGCGCCACTTCCCTGCTGCGAGGGGGAGCGGCAAGCAAGTGGGCGCTTGG 360
Db 301 TGGTGTGCGCCACTTCCCTGCTGCGAGGGGGAGCGGCAAGCAAGTGGGCGCTTGG 360
Qy 361 GGAGACTACGATGACAGTGCCTTCATGAGAGCCAGTACACAGTCCGTGAGGAAGATCTG 420
Db 361 GGAGACTACGATGACAGTGCCTTCATGAGAGCCAGTACACAGTCCGTGAGGAAGATCTG 420
Qy 421 GACAAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCCAGAAAGATCTCATGTCATG 480
Db 421 GACAAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCCAGAAAGATCTCATGTCATG 480
Qy 481 CTCAGGGACACTGACGTGAACAGAGAGACAGCAAGAGAGACTGCTTACATCTGGCC 540
Db 481 CTCAGGGACACTGACGTGAACAGAGAGAGACAGCAAGAGAGACTGCTTACATCTGGCC 540
Qy 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCCTGCTGACAGACAGATGCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCCTGCTGACAGACAGATGCAACTTAAT 600
Qy 601 GTCTTGAACAACAAAAGAGAGACAGTGTGATAAGGCCGTACATGCGAGGAAGATGAA 660
Db 601 GTCTTGAACAACAAAAGAGAGACAGTGTGATAAGGCCGTACATGCGAGGAAGATGAA 660
Qy 661 TGTGCGTTAATGTTGCGGAACATGCGCATGATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGCGTTAATGTTGCGGAACATGCGCATGATCCAAATATTCAGATGATGGAAT 720
Qy 721 ACCACTGTGACACTGCTATCTATATGAAGATTAATGCGCAAGCAAGCTGCTCTTA 780
Db 721 ACCACTGTGACACTGCTATCTATATGAAGATTAATGCGCAAGCAAGCTGCTCTTA 780
Qy 781 TATGTGCTGATATGCAATCAAAAAACAGCATGGCTCACACCACTGTTACTTGGTGTGA 840
Db 781 TATGTGCTGATATGCAATCAAAAAACAGCATGGCTCACACCACTGTTACTTGGTGTGA 840
Qy 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAAGGAATTTAAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAAGGAATTTAAATGCA 900
Qy 901 CTGATAGATATGGAAGAGACTGCTCTCATCTTCTGTATGTTGGATGAGCAAGTATA 960
Db 901 CTGATAGATATGGAAGAGACTGCTCTCATCTTCTGTATGTTGGATGAGCAAGTATA 960
Qy 961 GTCAAGCTTCTACTTGAAGCAAAATATTGATGATCTTCAAGATCTATCTGACACAGC 1020
Db 961 GTCAAGCTTCTACTTGAAGCAAAATATTGATGATCTTCAAGATCTATCTGACACAGC 1020
Qy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATTAATTTGCCAGTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATTAATTTGCCAGTACTTCTGACTAC 1080
Qy 1081 AAAGAAAAAGATGCTAAAAATCTCTTGTGAAACAGCAATCCAGAA 1128
Db 1081 AAAGAAAAAGATGCTAAAAATCTCTTGTGAAACAGCAATCCAGAA 1128
RESULT 26
ABL95178
ID ABL95178 standard; cDNA; 1155 BP.
XX ABL95178;
XX

DT 19-JUL-2002 (first entry)
XX Human B3050 splice variant cDNA sequence SEQ ID NO 373.
DE Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
XX gene therapy; gene; ss.
KW Homo sapiens.
XX US2002022248-A1.
XX
XX 21-FEB-2002.
XX
XX 12-JAN-2001; 2001US-0759143.
XX
XX 25-FEB-1997; 97US-0806099.
XX 01-AUG-1997; 97US-0904804.
XX 09-FEB-1998; 98US-0020956.
XX 25-FEB-1998; 98US-0030607.
XX 14-JUL-1998; 98US-0115453.
XX 23-SEP-1998; 98US-0159812.
XX 15-JAN-1999; 99US-0232149.
XX 09-APR-1999; 99US-0288946.
XX 13-JUL-1999; 99US-0352616.
XX 12-NOV-1999; 99US-0439313.
XX 18-NOV-1999; 99US-0443686.
XX 14-JAN-2000; 2000US-0483672.
XX 27-MAR-2000; 2000US-0536857.
XX 09-MAY-2000; 2000US-0568100.
XX 12-MAY-2000; 2000US-0570737.
XX 13-JUN-2000; 2000US-0593793.
XX 27-JUN-2000; 2000US-0605783.
XX 10-AUG-2000; 2000US-0636215.
XX 29-AUG-2000; 2000US-0651236.
XX 06-SEP-2000; 2000US-0657279.
XX 02-OCT-2000; 2000US-0679426.
XX 10-OCT-2000; 2000US-0685166.
XX
XX (XUJ/) XU J.
XX (DILL/) DILLON D C.
XX (MITC/) MITCHAM J L.
XX (HARL/) HARLOCKER S L.
XX (JIAN/) JIANG Y.
XX (KALO/) KALOS M D.
XX (FANG/) FANGER G R.
XX (RETT/) RETTER M W.
XX (STOL/) STOLK J A.
XX (DAYC/) DAY C H.
XX (VEDV/) VEDVICK T S.
XX (CART/) CARTER D.
XX (LISX/) LI S X.
XX (WANG/) WANG A.
XX (SKET/) SKELKY Y A W.
XX (HEPL/) HEPLER W T.
XX (HEND/) HENDERSON R A.
XX
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD,
XX Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
XX Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;
XX WPI; 2002-255649/30.
XX
XX New prostate-specific polynucleotides for diagnosing and treating
XX diseases, in particular prostate cancer, and as markers for the
XX progression of cancer -
XX
XX Claim 1: SEQ ID NO 373; 87pp; English.
XX
XX The present invention provides prostate-specific coding sequences and
XX their encoded proteins. These can be used in the diagnosis and treatment
XX of cancers, particularly prostate cancer. The present sequence is a cDNA
XX described in the invention.

Sequence 1155 BP; 346 A; 253 C; 297 G; 259 T; 0 other;
Query Match 56.4%; Score 1128; DB 24; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTGTGAGTGTGATTCACATGCGGCTGCTTCTGTGAAGAACCATTTGGTCTC 60
DB 1 ATGGTGTGAGTGTGATTCACATGCGGCTGCTTCTGTGAAGAACCATTTGGTCTC 60
QY 61 AGAGCAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGAGAGCGGCAAG 120
DB 61 AGAGCAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACCAAGCAGACTGCTGTATGAAGCACTCAGGACAA 180
DB 121 AGCAAGTGGGCACTTCTGAGACCAAGCAGACTGCTGTATGAAGCACTCAGGACAA 180
QY 181 ATGGGCAAGTGGGCGCCACTGCTTCCCTGCTGCAAGAGAGAGTGGCAAGCACTG 240
DB 181 ATGGGCAAGTGGGCGCCACTGCTTCCCTGCTGCAAGAGAGAGTGGCAAGCACTG 240
QY 241 GGGGCTTCTGAGACCAAGCAGACTGCTGTATGAAGCACTCAGGACAAAGTGGCAAG 300
DB 241 GGGGCTTCTGAGACCAAGCAGACTGCTGTATGAAGCACTCAGGACAAAGTGGCAAG 300
QY 301 TGGTGTGCTGCTGCTTCCCTGCTGCAAGAGAGAGTGGGCGGCTTGG 360
DB 301 TGGTGTGCTGCTGCTTCCCTGCTGCAAGAGAGAGTGGGCGGCTTGG 360
QY 361 GGAGCTACAGTACAGTCTTCATGAGAGCCAGTACAGTCCGCTGGAGAGATCTG 420
DB 361 GGAGCTACAGTACAGTCTTCATGAGAGCCAGTACAGTCCGCTGGAGAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTCTGGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
DB 421 GACAAGCTCCACAGAGCTCTGGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
QY 481 CTCAGGACACTGACTGAAAGAGCAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 481 CTCAGGACACTGACTGAAAGAGCAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAAGTCTCTGAGAGAGATGTCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAAGTAAAGTCTCTGAGAGAGATGTCAACTTAAT 600
QY 601 GTCCCTTGACAAACAAAAGAGACAGCTGTGATTAAGGCGGTACATGCCAGAAATGA 660
DB 601 GTCCCTTGACAAACAAAAGAGAGAGCTGTGATTAAGGCGGTACATGCCAGAAATGA 660
QY 661 TGTGCTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
DB 661 TGTGCTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTGCACTACGCTATCTATGAAGATTAATGAGCCAAAGCACTGCTTAA 780
DB 721 ACCACTGCACTACGCTATCTATGAAGATTAATGAGCCAAAGCACTGCTTAA 780
QY 781 TATGCTGATGATGATCAATCAAAAAAAGCATGAGCTCACACCTGTACTTGGTGA 840
DB 781 TATGCTGATGATGATCAATCAAAAAAAGCATGAGCTCACACCTGTACTTGGTGA 840
QY 841 CATGACCAAAACAGCAAGTCTGAAATTTTAAATCAAAAAAGCAATTTTAAATGA 900
DB 841 CATGACCAAAACAGCAAGTCTGAAATTTTAAATCAAAAAAGCAATTTTAAATGA 900
QY 901 CTGATAGATATGAGAGAGAGTCTCATACTGCTGATGTTGTGATCAGCAATATA 960
DB 901 CTGATAGATATGAGAGAGAGTCTCATACTGCTGATGTTGTGATCAGCAATATA 960
QY 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAG 1020
DB 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAG 1020

AAS9869
ID AAS9869 standard: DNA; 1590 BP.
XX
AC AAS9869;
XX
DT 12-MAR-2002 (first entry)
XX
DE Breast tumour-specific gene B305D fusion construct.
XX
KM Human; breast cancer; PCR primer; ss; cytostatic; immunostimulant;
KM tumour; vaccine; immunogenic.
XX
OS Homo sapiens.
XX
PN W0200190152-A2.
XX
PD 29-NOV-2001.
XX
PF 22-MAY-2001; 2001WO-US16776.
XX
PR 24-MAY-2000; 2000US-0577505.
PR 08-JUN-2000; 2000US-0590583.
PR 26-OCT-2000; 2000US-0699295.
PR 16-MAR-2001; 2001US-0810936.
XX
PA (CORI-) CORIXA CORP.
XX
PI Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
PI Wang A, Skelky YAW, Harlocker SL, Day CH;
XX
DR WPI; 2002-089919/12.
XX
PT New breast tumour proteins and polynucleotides encoding them, useful for
PT treating and/or preventing cancer, particularly breast cancer, and for
PT eliciting humoral and/or cellular immune response
XX
PS Example 8; Page 235; 245bp; English.
XX
CC The invention relates to novel breast tumour polynucleotides and
CC polypeptides. The polypeptides and polynucleotides are useful in
CC pharmaceutical compositions for treating and/or preventing cancer,
CC particularly breast cancer, and for eliciting an immune response,
CC particularly humoral and/or cellular immune response. The polynucleotides
CC may be used as probes or primers for nucleic acid hybridisation, in the
CC design and preparation of ribozyme molecules for inhibiting expression of
CC tumour polypeptides and proteins, and in recombinant DNA molecules to
CC direct expression of a polypeptide in host cells. AAS9570-AAS9888
CC represent novel human breast cancer protein coding sequences and
CC PCR primers of the invention.
XX
SQ Sequence 1590 BP; 424 A; 403 C; 433 G; 329 T; 1 other:
Query Match 52.2%; Score 1044; DB 24; Length 1590;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1094; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 34 TCTTCTGTAAGAAGCCATTGCTCTCAGAGACAGATGGCAAGTGCTGCGCTTGC 93
DB 469 TCTTCTGTAAGAAGCCATTGCTCTCAGAGACAGATGGCAAGTGCTGCGCTTGC 528
QY 94 TTCCCTGCTGAGGAGAGCGGCAAGACAGTGGCACTTCTGAGACACGACGAC 153
DB 529 TTCCCTGCTGAGGAGAGCGGCAAGACAGTGGCACTTCTGAGACACGACGAC 588
QY 154 TCTGCTATGAGACACTCAGAGCAAGATGGCAAGTGCTGCGCACTTCCCTGC 213
DB 589 TCTGCTATGAGACACTCAGAGCAAGATGGCAAGTGCTGCGCACTTCCCTGC 648
QY 214 TGCAGGGGAGTGGCAAGCAACGTCGCTTCTGAGACACGACACTCTGTATG 273
DB 649 TGCAGGGGAGTGGCAAGCAACGTCGCTTCTGAGACACGACACTCTGTATG 708
QY 274 AAGACACTCAGAACACAGATGGCAAGTGCTGCTGCTTCCCTGCTGACAGGGG 333

DB 709 AAGACACTCAGAACACAGATGGGCAAGTGCTGCTGCTTCCCTGCTGACAGGGG 768
QY 334 AGCGGCAGAGCAAGTGGGCGCTTGGGAGACTACGATGACAGTGCCTTCAATGACGCC 393
DB 769 AGCGGCAGAGCAAGTGGGCGCTTGGGAGACTACGATGACAGTGCCTTCAATGACGCC 828
QY 394 AGGTACACGTCCTGAGAGAGATGTCGACAGCTCCACAGAGCTGCGTGGGGTAA 453
DB 829 AGGTACACGTCCTGAGAGAGATGTCGACAGCTCCACAGAGCTGCGTGGGGTAA 888
QY 454 GTCCCCAGAAAGATCTCATGCTCATGCTCAGGAGACTGACGTGAACAAGAGCAAG 513
DB 889 GTCCCCAGAAAGATCTCATGCTCATGCTCAGGAGACTGACGTGAACAAGAGCAAG 948
QY 514 CAAAAGAGCACTGCTTACATCTGGCTTGCCTGCAATGGCAATTCAGACTAGTAAACTC 573
DB 949 CAAAAGAGCACTGCTTACATCTGGCTTGCCTGCAATGGCAATTCAGACTAGTAAACTC 1008
QY 574 CTGCTGAGACAGAGATGTCACCTTAATGCTTGAACAAAAGAGACAGCTGAT 633
DB 1009 CTGCTGAGACAGAGATGTCACCTTAATGCTTGAACAAAAGAGACAGCTGAT 1068
QY 634 AAGCGCTCAATGCGCAGAGAGATGATGCTTAACTGCTGGAACATGCACTGAT 693
DB 1069 AAGCGCTCAATGCGCAGAGAGATGATGCTTAACTGCTGGAACATGCACTGAT 1128
QY 694 CCAATATTCAGAGATGATGGAATACCACCTGCTACCTATCTATATGAGAT 753
DB 1129 CCAATATTCAGAGATGATGGAATACCACCTGCTACCTATCTATATGAGAT 1188
QY 754 AATTAATGGCCAAAGCACTGCTTATATGCTGATGGAATCAAAAACAGAT 813
DB 1189 AATTAATGGCCAAAGCACTGCTTATATGCTGATGGAATCAAAAACAGAT 1248
QY 814 GGCTTCACACCACTGTTACTGCTGATGACAAAACAGCAAGTGTGAATTTTA 873
DB 1249 GGCTTCACACCACTGTTACTGCTGATGACAAAACAGCAAGTGTGAATTTTA 1308
QY 874 ATCAGAAAAAAGCCATTTAATGCTGATGATATGAGAGACTGCTCATACTT 933
DB 1309 ATCAGAAAAAAGCCATTTAATGCTGATGATATGAGAGACTGCTCATACTT 1368
QY 934 GCTGATGTTGGATGACCAAGTATGACGCTTCTGAGCAAAATATGATGA 993
DB 1369 GCTGATGTTGGATGACCAAGTATGACGCTTCTGAGCAAAATATGATGA 1428
QY 994 TCTTCAAGATCTATCTGACAGAGCGCCAGAGATGCTGTTCTAGTCATCAT 1053
DB 1429 TCTTCAAGATCTATCTGACAGAGCGCCAGAGATGCTGTTCTAGTCATCAT 1488
QY 1054 GTAATTTGCCAGTACTTCTGACTACAAAAGAAACAGATGCTAATCTCTTGA 1113
DB 1489 GTAATTTGCCAGTACTTCTGACTACAAAAGAAACAGATGCTAATCTCTTGA 1548
QY 1114 AACAGCAATCCAGAA 1128
DB 1549 AACAGCAATCCAGAA 1563
RESULT 29
AAS9872
ID AAS9872 standard: DNA; 1155 BP.
XX
AC AAS9872;
XX
DT 12-MAR-2002 (first entry)
XX
DE Breast tumour-specific gene B305D homologue #2.
XX
KM Human; breast cancer; PCR primer; ss; cytostatic; immunostimulant;
KM tumour; vaccine; immunogenic.
XX

OS Homo sapiens.
 XX WO200190152-A2.
 XX 29-NOV-2001.
 PD 22-MAY-2001; 2001WO-US16776.
 XX 24-MAY-2000; 2000US-0577505.
 PR 08-JUN-2000; 2000US-0590583.
 PR 26-OCT-2000; 2000US-0699295.
 PR 16-MAR-2001; 2001US-0810936.
 XX (CORI-) CORIXA CORP.
 PA Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
 PI Wang A, Skelky YAM, Harlocker SL, Day CH;
 DR WPI; 2002-089919/12.
 DR P-PSDB; AA074390.
 XX New breast tumour proteins and polynucleotides encoding them, useful for
 PT treating and/or preventing cancer, particularly breast cancer, and for
 PT eliciting humoral and/or cellular immune response
 XX Claim 1; Page 239; 245pp; English.
 PS The invention relates to novel breast tumour polynucleotides and
 CC polypeptides. The polypeptides and polynucleotides are useful in
 CC pharmaceutical compositions for treating and/or preventing cancer,
 CC particularly breast cancer, and for eliciting an immune response,
 CC particularly humoral and/or cellular immune response. The polynucleotides
 CC may be used as probes or primers for nucleic acid hybridisation, in the
 CC design and preparation of ribozyme molecules for inhibiting expression of
 CC tumour polypeptides and proteins, and in recombinant DNA molecules to
 CC direct expression of a polypeptide in host cells. AAS99570-AAS99888
 CC represent novel human breast cancer protein coding sequences and
 CC PCR primers of the invention.
 XX Sequence 1155 BP; 346 A; 253 C; 296 G; 260 T; 0 other;
 SO
 Query Match 48.8%; Score 975; DB 24; Length 1155;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1123; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 421 GACAAGCTCCACAGAGCTGCTGGGTAAAGTCCCCAGAAAGATCTTCATGTCATG 480
 |||||||
 Db 421 GACAAGCTCCACAGAGCTGCTGGGTAAAGTCCCCAGAAAGATCTTCATGTCATG 480
 QY 481 CTCAGGACATGACGTGAAACAAAGAGACAAAGAAAGAGACTGCTACATCTGCC 540
 |||||||
 Db 481 CTCAGGACATGACGTGAAACAAAGAGACAAAGAAAGAGACTGCTACATCTGCC 540
 QY 541 TCTCCAAATGGGAATTCAGAAATAGTAAACTCCTGCTGACAGACATGCAACTTAAT 600
 |||||||
 Db 541 TCTCCAAATGGGAATTCAGAAATAGTAAACTCCTGCTGACAGACATGCAACTTAAT 600
 QY 601 GTCTTGACAAACAAAGAGACAGCTGTGATAAGGCCCTGACATGCCAGGAAGTAA 660
 |||||||
 Db 601 GTCTTGACAAACAAAGAGACAGCTGTGATAAGGCCCTGACATGCCAGGAAGTAA 660
 QY 661 TGTGCGTTAATGTTGCTGGAACATGCGACATGCAATCAATATCCAGATGAGTAAAT 720
 |||||||
 Db 661 TGTGCGTTAATGTTGCTGGAACATGCGACATGCAATCAATATCCAGATGAGTAAAT 720
 QY 721 ACCACTGACACTACGCTATCTATATGAAGATTAATTAAGGCCAAAGCACTGCTCTTA 780
 |||||||
 Db 721 ACCACTGACACTACGCTATCTATATGAAGATTAATTAAGGCCAAAGCACTGCTCTTA 780
 QY 781 TATGTCCTGATATGCAATCAAAACAAAGCAGTGCCTACACCACTGTACTTGTGTGA 840
 |||||||
 Db 781 TATGTCCTGATATGCAATCAAAACAAAGCAGTGCCTACACCACTGTACTTGTGTGA 840
 QY 841 CATAGCAAAAACAGCAAGCTGTAATTTTATCAAGAAAGAAAGGAAATTTAAATGA 900
 |||||||
 Db 841 CATAGCAAAAACAGCAAGCTGTAATTTTATCAAGAAAGAAAGGAAATTTAAATGA 900
 QY 901 CTGATAGATATGGAAGAGACTGCTCTCATCTTCTGATGTTGTGATGACGAAGTATA 960
 |||||||
 Db 901 CTGATAGATATGGAAGAGACTGCTCTCATCTTCTGATGTTGTGATGACGAAGTATA 960
 QY 961 GTCAAGCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGACG 1020
 |||||||
 Db 961 GTCAAGCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGACG 1020
 QY 1021 GCCAGAGATATGCTGTTTATGATCATCATGATTAATTTGCGAGTACTTTCATGACTAC 1080
 |||||||
 Db 1021 GCCAGAGATATGCTGTTTATGATCATCATGATTAATTTGCGAGTACTTTCATGACTAC 1080
 QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGAAAAACAGCAATCCAGAA 1128
 |||||||
 Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGAAAAACAGCAATCCAGAA 1128
 RESULT 30
 AAV68995
 ID AAV68995 standard; DNA; 1512 BP.
 XX
 AC AAV68995;
 XX
 DT 22-JAN-1999 (first entry)
 XX
 DE DNA molecule encoding a breast tumour specific polypeptide #187.
 XX
 KW Human; breast cancer; breast tumour tissue; diagnosis; treatment;
 KW vaccine; epitope; endogenous; retroviral element; ss.
 OS Homo sapiens.
 OS
 XX
 PN WO9845328-A2.
 XX
 PD 15-OCT-1998.
 PD
 XX
 PF 09-APR-1998; 98MO-US06939.
 PF
 XX
 PR 11-DEC-1997; 97US-0991789.
 PR 09-APR-1997; 97US-0838762.
 XX

PA (CORI-) CORIXA CORP.
 XX
 PI Frudakis TN, Reed SG, Smith JM;
 XX
 DR WPI: 1998-557473/47.
 XX
 PT New DNA sequences isolated from endogenous human retroviral element
 PT - and related vectors, transformed cells, proteins and antibodies,
 PT useful for diagnosis, treatment and prevention of breast cancer
 XX
 PS Claim 1: Page 137-138; 173pp; English.
 XX
 CC AAV68800 to AAV68998 represent nucleotide sequences which encode human
 CC breast tumour specific polypeptides. Detection or measurement of
 CC human breast tumour specific polypeptides and nucleotide sequences,
 CC or the corresponding RNA in a sample, is used for diagnosis and
 CC monitoring of breast cancer. Human breast tumour specific polypeptides
 CC and nucleotide sequences, and the vectors containing the DNAs, are also
 CC useful in vaccines for inhibiting development (for prevention or
 CC therapy) of breast cancer. The polypeptides may also be used to
 CC raise monoclonal antibodies, used as immunosassay reagents.
 XX
 SQ Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;
 Query Match 24.6%; Score 491; DB 19; Length 1512;
 Best Local Similarity 99.4%; Pred. No. 4.4e-177;
 Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 34 TCTTGTGAAGAGCAATTTGGTCTCAGAGCAGATGGGCAAGTGTGCGCTTGC 93
 DB 256 TTTTCTGTGAAGAGCAATTTGGTCTCAGAGCAGATGGGCAAGTGTGCGCTTGC 315
 QY 94 TTCCCTGCTGCAGGAGAGCGGCAAGACAGTGGGCACTTCTGAGACCAAGACGAC 153
 DB 316 TTCCCTGCTGCAGGAGAGCGGCAAGACAGTGGGCACTTCTGAGACCAAGACGAC 375
 QY 154 TCTGCTATGAAGACACTCAGAGCAAGATGGCAAGTGGTCCGCCACTGCTTCCCTGC 213
 DB 376 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGTCCGCCACTGCTTCCCTGC 435
 QY 214 TGCAGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACAGACAGCTCTGTATG 273
 DB 436 TGCAGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACAGACAGCTCTGTATG 495
 QY 274 AAGACACTCAGAGCAAGATGGGCAAGTGGTCCGCCACTGCTTCCCTGCAGAGGG 333
 DB 496 AAGACACTCAGAGCAAGATGGGCAAGTGGTCCGCCACTGCTTCCCTGCAGAGGG 555
 QY 334 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGCACTACAGATGACAGTCCCTTATGAGCCC 393
 DB 556 AGCAGCAAGAGCAAGTGGGCGCTTGGGAGCACTACAGATGACAGTCCCTTATGAGCCC 615
 QY 394 AGTACACAGCTCCGTGGAGAGATCTGACAGCTCCACAGAGCTGCCGTGGGGGTAA 453
 DB 616 AGTACACAGCTCCGTGGAGAGATCTGACAGCTCCACAGAGCTGCCGTGGGGGTAA 675
 QY 454 GTCCCGAAGAGATCTCATCTGTCATGCTCAGGAGCACTAGAGTGAACAAGAGCAAG 513
 DB 676 GTCCCGAAGAGATCTCATCTGTCATGCTCAGGAGCACTAGAGTGAACAAGAGCAAG 735
 QY 514 CAAAAGAGAGCTGCTTACATCTGGCCCTTGGCAATGGGAATTCAGAGTAAACTTC 573
 DB 736 CAAAAGAGAGCTGCTTACATCTGGCCCTTGGCAATGGGAATTCAGAGTAAACTTC 795
 QY 574 CTGCTGAGACAGAGATGTCACCTTATGTCCTTGACAAACAAAAGAGGACAGCTCGATA 633
 DB 796 STGCTGAGACAGAGATGTCACCTTATGTCCTTGACAAACAAAAGAGGACAGCTCGATA 855
 QY 634 AAGGCGGTACAAATGCGCAGAGAGATGATGCTTAAATGTTCTGGAACATGGACATGAT 693
 DB 856 AAGGCGGTACAAATGCGCAGAGAGATGATGCTTAAATGTTCTGGAACATGGACATGAT 915
 QY 694 CCAAAATATTCAGATGATGATGAATAATACCACTCT 728

DB 916 CCAAAATATTCAGATGATGATGAATAATACCACTCT 950
 |||||||||||||||||||||||||||||||||||||||
 RESULT 31
 AAC81006
 ID AAC81006 standard; cDNA; 1512 BP.
 AC AAC81006;
 XX
 DT 13-FEB-2001 (first entry)
 XX
 DE Human B11Ag1 antigen protein coding exon cDNA SEQ ID NO: 294.
 XX
 KW Human; breast tumour-specific antigen; cytostatic; vaccine;
 KW breast cancer; B18Ag1; B11Ag1; B15Ag1; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO20061753-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 07-APR-2000; 2000WO-US09312.
 XX
 PR 09-APR-1999; 99US-0289198.
 PR 28-OCT-1999; 99US-0429755.
 PR 23-MAR-2000; 2000US-0534825.
 XX
 PA (CORI-) CORIXA CORP.
 PI Frudakis TN, Smith JM, Reed SG, Misher LE, Retter MW, Dillon DC;
 XX
 DR WPI: 2000-628403/60.
 XX
 PT An isolated polypeptide comprising an immunogenic portion of a breast
 PT tumor protein used for inhibiting the development of cancer, especially
 PT breast cancer, and monitoring cancer progression in a patient -
 XX
 PS Claim 4: Page 172; 187pp; English.
 XX
 CC The present sequence is given in a specification relating to compositions
 CC and methods for the treatment and diagnosis of breast cancer. Nucleotide
 CC sequences that are preferentially expressed in breast tumour tissue, and
 CC the polypeptides encoded by such nucleotide sequences, are used in
 CC compositions and vaccines to inhibit the development of cancer,
 CC especially breast cancer. The progression of a cancer may be monitored by
 CC carrying out detection of tumour-specific antigens at subsequent time
 CC points and comparing the results from the different time points.
 CC CD4+ and/or CD8+ T-Cells isolated from the cancer patient may be treated
 CC with tumour-specific polypeptides, polynucleotides encoding the
 CC polypeptides or antigen presenting cells expressing the polypeptides. The
 CC cells are then administered to the patient to inhibit development of
 CC cancer.
 XX
 SQ Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;
 Query Match 24.6%; Score 491; DB 21; Length 1512;
 Best Local Similarity 99.4%; Pred. No. 4.4e-177;
 Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 34 TCTTGTGAAGAGCAATTTGGTCTCAGAGCAGATGGGCAAGTGTGCGCTTGC 93
 DB 256 TCTTGTGAAGAGCAATTTGGTCTCAGAGCAGATGGGCAAGTGTGCGCTTGC 315
 QY 94 TTCCCTGCTGCAGGAGAGCGGCAAGACAGTGGGCACTTCTGAGACCAAGACGAC 153
 DB 316 TTCCCTGCTGCAGGAGAGCGGCAAGACAGTGGGCACTTCTGAGACCAAGACGAC 375
 QY 154 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGTCCGCCACTGCTTCCCTGC 213
 DB 376 TCTGCTATGAAGACACTCAGAGCAAGATGGGCAAGTGGTCCGCCACTGCTTCCCTGC 435

OY	214	TCGACGGGGAGTGGCACAAGACAACGTGGGGCGCTTCTGGAGAACCCAGCAGCACTCTGCTATG	273
Db	436	TCGACGGGGAGTGGCACAAGACAACGTGGGGCGCTTCTGGAGAACCCAGCAGCACTCTGCTATG	495
OY	274	AAGACACTCAGGAACAAGATGGGCAAGTGGTGTGCCACACTGCTTCCCTCTGCCAGGGGG	333
Db	496	AAGACACTCAGGAACAAGATGGGCAAGTGGTGTGCCACACTGCTTCCCTCTGCCAGGGGG	555
OY	334	AGCGGCAAGAGCAAGGTGGGCGCTTGGGGAGACTACGATACACAGTGCCTTTCATGGAGCCC	393
Db	556	AGCGGCAAGAGCAAGGTGGGCGCTTGGGGAGACTACGATACACAGTGCCTTTCATGGAGCCC	615
OY	394	AGGTACACACGTCCCTGGAGAAAGATCTTGGACAAGCTCCACAGAGCTCCTGTGGGGGTAA	453
Db	616	AGGTACACACGTCCCTGGAGAAAGATCTTGGACAAGCTCCACAGAGCTCCTGTGGGGGTAA	675
OY	454	GTCCCCAGAAAAGATCTTCATCTGTCATGCTCAGGGACACTGACGTGAACAAGAGCAAG	513
Db	676	GTCCCCAGAAAAGATCTTCATCTGTCATGCTCAGGGACACTGACGTGAACAAGAGCAAG	735
OY	514	CAAAAGAGAGCTGCTCTACATCTGGCCCTGTGCCAATGGGGAATTCAGAAAGTAAACATC	573
Db	736	CAAAAGAGAGCTGCTCTACATCTGGCCCTGTGCCAATGGGGAATTCAGAAAGTAAACATC	795
OY	574	CTGCTGGACAGACGATGTCAACTTAATGTCTTGCACAAACAAAAAGAGCAGCTCTGATA	633
Db	796	CTGCTGGACAGACGATGTCAACTTAATGTCTTGCACAAACAAAAAGAGCAGCTCTGATA	855
OY	634	AAGCGCGTACAAATGCCCAAGGAAGATGTGGCTTAATGTGTGTGGAACATGGCACTGAT	693
Db	856	AAGCGCGTACAAATGCCCAAGGAAGATGTGGCTTAATGTGTGTGGAACATGGCACTGAT	915
OY	694	CCAAATATTTCCAGATGAGTATGGAATATCACACTCT	728
Db	916	CCAAATATTTCCAGATGAGTATGGAATATCACACTCT	950
RESULT 32			
AAA06593	AAA06593 standard; cDNA; 1512 BP.		
AC	AAA06593:		
XX	13-JUN-2000 (first entry)		
DE	Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:368		
KW	Human; prostate cancer; diagnosis; tumour; gene therapy; detection;		
OS	immunogenic; cytosolic; vaccine; ss.		
XX	Homo sapiens.		
XX	MO200004149-A2.		
PD	27-JAN-2000.		
XX	14-JUL-1999; 99MO-US15838.		
PR	14-JUL-1998; 9805-0115453.		
PR	14-JUL-1998; 9805-0116134.		
PR	23-SEP-1998; 9805-0159812.		
PR	23-SEP-1998; 9805-0159822.		
PR	15-JAN-1999; 9805-0232149.		
PR	15-JAN-1999; 9805-0232880.		
PR	09-APR-1999; 9905-0288946.		
XX	(CORI-) CORIXA CORP.		
PI	Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL.		
DR	WPI: 2000-171268/15.		
XT	New polypeptide useful for treating and diagnosing prostate cancer		

PT comprises an immunogenic portion of prostate tumor protein -
XX
XX Claim 50; Page 219; 263pp; English.
XX
CC The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumour protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC the polypeptides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AA06241 to AA06691 and
CC AA982000 to AA982020 represent sequences used in the exemplification of
CC the present invention.
XX
SQ Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;

Query Match	24.6%	Score 491	DB 211	Length 1512
Best Local Similarity	99.4%	Pred. 14.4e-177		
Matches 691	Conservative	0	Mismatches 4	Indels 0
				Gaps 0
QY	34 TCTTGTGTAAAGGCATTGGTCTCAGACCAAGATGGCGAAGTGGTGTGCGCGTTGC	93		
DB	256 TCTTCTGTGTAAAGGCATTGGTCTCAGACCAAGATGGCGAAGTGGTGTGCGCGTTGC	315		
QY	94 TTCCCTGCTGCAGGAGAGCGCGCAAGCAACGTGGGCATTCTTGGAGACACGACAC	153		
DB	316 TTCCCTGCTGCAGGAGAGCGCGCAAGCAACGTGGGCATTCTTGGAGACACGACAC	375		
QY	154 TCTGCTATGAACACACTCGAGCAAGATGGGCAAGTGGTGGCGGCACATGCTCCCTGC	213		
DB	376 TCTGCTATGAACACACTCGAGCAAGATGGGCAAGTGGTGGCGGCACATGCTCCCTGC	435		
QY	214 TGCAGGGGGAGTGGCAAGCAACGTGGGCGCTTCTGAGACACAGACACTGTGTATG	273		
DB	436 TGCAGGGGGAGTGGCAAGCAACGTGGGCGCTTCTGAGACACAGACACTGTGTATG	495		
QY	274 AAGACACTGAGAACACAGATGGGCAAGTGGTCTGCTCCACTGTTCCCTGCTGCAGGGG	333		
DB	496 AAGACACTGAGAACACAGATGGGCAAGTGGTCTGCTCCACTGTTCCCTGCTGCAGGGG	555		
QY	334 ACCGGCAAGAGCAAGGTGGGCGCTTGGGGAGACTCGATGACAGTGCCTTCAATGAGCCC	393		
DB	556 ACCGGCAAGAGCAAGGTGGGCGCTTGGGGAGACTCGATGACAGTGCCTTCAATGAGCCC	615		
QY	394 AGGTACCAACGTCCTGTGAGAAAGATGTGGCAACGCTCCACAGACGTCGCTGTGGGGTAA	453		
DB	616 AGGTACCAACGTCCTGTGAGAAAGATGTGGCAACGCTCCACAGACGTCGCTGTGGGGTAA	675		
QY	454 GTCCCCAGAAAGATCTCATCTGCTCATGCTCAGGACACTGACGTGAACAGAGACAAG	513		
DB	676 GTCCCCAGAAAGATCTCATCTGCTCATGCTCAGGACACTGACGTGAACAGAGACAAG	735		
QY	514 CAAAGAGSACTGCTCTACATCTGGCCCTTGCCATTGGGAATTCAGAAATGATTAACAC	573		
DB	736 CAAAGAGSACTGCTCTACATCTGGCCCTTGCCATTGGGAATTCAGAAATGATTAACAC	795		
QY	574 CTGCTGAGACAGATGTCACCTTAATGCTCTTGACCAACAAAAAGAGACACTGTGATA	633		
DB	796 CTGCTGAGACAGATGTCACCTTAATGCTCTTGACCAACAAAAAGAGACACTGTGATA	855		
QY	634 AAGGCCGTACAAATGCCAGAGATGATGTGCGTTAATGTTGCTGGAACATGGCACTGAT	693		
DB	856 AAGGCCGTACAAATGCCAGAGATGATGTGCGTTAATGTTGCTGGAACATGGCACTGAT	915		
QY	694 CCAATATTCCAGATGATGATGGAATACCACTCT 728			
DB	916 CCAATATTCCAGATGATGGAATACCACTCT 950			

```
RESULT 33
AAS63802
ID AAS63802 standard; cDNA; 1512 BP.
XX
AC AAS63802;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human prostate cDNA clone B305D splice variant #3.
XX
KW Human; prostate cancer; ss: cytosstatic; immunostimulant; tumour.
XX
OS Homo sapiens.
XX
PN MO200173032-A2.
XX
PD 04-OCT-2001.
XX
PE 27-MAR-2001; 2001WO-US09919.
XX
PR 27-MAR-2000; 2000US-0536857.
PR 09-MAY-2000; 2000US-0568100.
PR 12-MAY-2000; 2000US-0570737.
PR 13-JUN-2000; 2000US-0593793.
PR 27-JUN-2000; 2000US-0605783.
PR 10-AUG-2000; 2000US-0636215.
PR 29-AUG-2000; 2000US-0651236.
PR 06-SEP-2000; 2000US-0657279.
PR 02-OCT-2000; 2000US-0679428.
PR 10-OCT-2000; 2000US-0685166.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stoik JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;
XX
DR WPI: 2001-639232/73.
XX
PT New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer -
XX
PS Claim 1: Page 345-346; 579pp; English.
XX
CC The invention relates to isolated prostate-specific
CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
CC antibodies raised against the polypeptides (or antigenic epitopes
CC derived from them) and antigen-presenting cells expressing the
CC polypeptides. The antibodies are useful for detecting the presence of
CC cancer, especially prostate cancer. The polypeptides, polynucleotides
CC and the antigen-presenting cells are useful for stimulating and/or
CC T cells specific for a tumor protein, and for inhibiting the development
CC of cancer especially prostate cancer. Compositions comprising the
CC polynucleotide and/or polypeptide are useful for stimulating an immune
CC response, and for treating cancer. The oligonucleotide is useful for
CC detecting cancer. The present sequence is a prostate specific
CC polynucleotide of the invention.
XX
SQ Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other:
Query Match 24.6%; Score 491; DB 22; Length 1512;
Best Local Similarity 99.4%; Pred. No. 4,4e-177;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
DB 376 TCTGCTATGAAAGACACTAGAGAGCAAGATGGCAAGTGGTGGCGGCACGTCTCCCTGAC 435
|||
OY 214 TGCAGGGGAGTGCGCAAGACAGCAAGCTGGCGCTTCTGGAGACCAGACAGACTCTGATG 273
|||
DB 436 TGCAGGGGAGTGCGCAAGAGCAAGCTGGCGCTTCTGGAGACCAGACAGACTCTGATG 495
|||
OY 274 AAGACACTCAGGACAAAGATGGGCAAGTGGTGGCTGCGCATGCTTCCCGCTGACGGGGG 333
|||
DB 496 AAGACACTCAGGACAAAGATGGGCAAGTGGTGGCTGCGCATGCTTCCCGCTGACGGGGG 555
|||
OY 334 ACGGCAAGAGCAAGCTGGGCGCTTGGGAGAGCACTAGATGACAGTGCCTTCAATGAGGCC 393
|||
DB 556 ACGRCAAGAGCAAGCTGGGCGCTTGGGAGAGCACTAGATGACAGTGCCTTCAATGAGGCC 615
|||
OY 394 ACGTACACAGCTCGTGAGAGACATCTGCACAGCTCCACAGAGCTGCTGGGGGTAA 453
|||
DB 616 AAGTACACAGCTCGTGAGAGACATCTGCACAGCTCCACAGAGCTGCTGGGGGTAA 675
|||
OY 454 GTCCCCAGAAAGATCTCATGTCATGCTCAGGAGCACTGAGCTGACAAAGAGCAAG 513
|||
DB 676 GTCCCCAGAAAGATCTCATGTCATGCTCAGGAGCACTGAGCTGACAAAGAGCAAG 735
|||
OY 514 CAAAAGAGGACTGCTCTACATCTGGCGCTTGCCTCAATGGGAATTGCAAGTAAACTC 573
|||
DB 736 CAAAAGAGGACTGCTCTACATCTGGCGCTTGCCTCAATGGGAATTGCAAGTAAACTC 795
|||
OY 574 CTGCTGAGACAGACATGTCACCTTAATGCTCTTGACACAAAAGAGACAGCTGATG 633
|||
DB 796 STGCTGAGACAGACATGTCACCTTAATGCTCTTGACACAAAAGAGACAGCTGATG 855
|||
OY 634 AAGGCCGTACATGGCAGAAATGATGATGGCTTAATGCTGGAACATGGCACTGAT 693
|||
DB 856 AAGGCCGTACATGGCAGAAATGATGATGGCTTAATGCTGGAACATGGCACTGAT 915
|||
OY 694 CCAATATTCAGATGAGTATGAAATACCACTCT 728
|||
DB 916 CCAATATTCAGATGAGTATGAAATACCACTCT 950
|||

RESULT 34
AAH93709
ID AAH93709 standard; cDNA; 1512 BP.
XX
AC AAH93709;
XX
DT 04-OCT-2001 (first entry)
XX
DE Human prostate-specific cDNA sequence B305D splice variant #3.
XX
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytosstatic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX
PN MO200151633-A2.
XX
PD 19-JUL-2001.
XX
PE 16-JAN-2001; 2001WO-US01574.
XX
PR 14-JAN-2000; 2000US-0483672.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stoik JA, Skelky YAW;
PI Wang A, Meagher MJ;
XX
DR WPI: 2001-425873/45.
XX
PT New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
```

PT for use in vaccines -
XX
XX
XX
Claim 1; Page 343-344; 543pp; English.
CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytosolic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used to treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
CC AAH01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX
XX
Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;

Query Match 24.6%; Score 491; DB 22; Length 1512;
Best Local Similarity 99.4%; Pred. No. 4.4e-177;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
QY 34 TCTTCTGTGAAGAGCCATTGCTCAGAGCAAGATGGGCAAGTGGCTGCGCTTGC 93
DB 256 TCTTCTGTGAAGAGCCATTGCTCAGAGCAAGATGGGCAAGTGGCTGCGCTTGC 315
QY 94 TTCCCTGCTGCGAGGAGCGGCAAGACACCTGGGCACTTGTGAGACACGACGAC 153
DB 316 TTCCCTGCTGCGAGGAGCGGCAAGACACCTGGGCACTTGTGAGACACGACGAC 375
QY 154 TCTGCTATGAAGACACACAGAGCAAGATGGGCAAGTGGGCGGCACTGCTCCCTGC 213
DB 376 TCTGCTATGAAGACACACAGAGCAAGATGGGCAAGTGGGCGGCACTGCTCCCTGC 435
QY 214 TGCAGGGGAGTGCCAAAGACACGTCGCTTCTGAGACACGACGACGATGCTATG 273
DB 436 TGCAGGGGAGTGCCAAAGACACGTCGCTTCTGAGACACGACGACGATGCTATG 495
QY 274 AAGACACTCAGGAACAAGATGGGCAAGTGGCTGCTGCACTGCTTCCCTGCTGAGGGG 333
DB 496 AAGACACTCAGGAACAAGATGGGCAAGTGGCTGCTGCACTGCTTCCCTGCTGAGGGG 555
QY 334 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTAGATGACATGCTGCTCATGGAGCC 393
DB 556 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTAGATGACATGCTGCTCATGGAGCC 615
QY 394 AGGTACCAAGTCCGTGGAGAAATCTGAGACACCTCCACAGAGCTGCTGGGGTAAA 453
DB 616 AGGTACCAAGTCCGTGGAGAAATCTGAGACACCTCCACAGAGCTGCTGGGGTAAA 675
QY 454 GTCCCCGAAGAAGATCTCATCTGTCATGCTCAGGACACTGACGTAACAAGAGACAA 513
DB 676 GTCCCCGAAGAAGATCTCATCTGTCATGCTCAGGACACTGACGTAACAAGAGACAA 735
QY 514 CAAAAGAGAGCTGCTACATCTGGCCTTGCCCAATGGGAATTCAGAAAGTAAACTC 573
DB 736 CAAAAGAGAGCTGCTACATCTGGCCTTGCCCAATGGGAATTCAGAAAGTAAACTC 795
QY 574 CTGTGACAGAGAGATGCACTTAATGCTCTTGACAACAAAAGAGAGACGCTGTATA 633
DB 796 STGTGAGAGAGAGATGCACTTAATGCTCTTGACAACAAAAGAGAGACGCTGTATA 855
QY 634 AAGGCGCTACAAATGCCAGGAAGATGAATGTCGTTAATGTTCTGGAACATGCACTGAT 693
DB 856 AAGGCGCTACAAATGCCAGGAAGATGAATGTCGTTAATGTTCTGGAACATGCACTGAT 915
QY 694 CCAAAATATTCAGATGATGTAATGAAATACACACT 728
DB 916 CCAAAATATTCAGATGATGTAATGAAATACACACT 950
```

RESULT 35
AAH85023
ID AAH85023 standard; cDNA; 1512 BP.
XX
XX
XX
AAH85023;
XX
XX
25-SEP-2001 (first entry)
XX
XX
Human prostate-specific cDNA sequence B305D splice variant #3.
DE
XX
XX
Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
KW chromosome 22q11.2; prostate-specific protein; chromosome 1;
KW prostate specific antigen; PSA; ss.
XX
OS Homo sapiens.
XX
PN W0200134802-A2.
XX
PD 17-MAY-2001.
XX
PE 09-NOV-2000; 2000MO-US30904.
XX
PR 12-NOV-1999; 9905-0439313.
XX
PR 18-NOV-1999; 9905-0443686.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Rietter MW, Stolk JA, Day CH, Skeiky YAM, Wang A;
XX
XX
WPI; 2001-308785/32.
XX
PT Isolated polypeptide comprising at least an immunogenic portion of a
PT prostate-specific protein, useful in the diagnosis and therapy of
PT prostate cancer -
XX
XX
Claim 31; Page 243-244; 325pp; English.
XX
XX
The present invention describes an isolated polypeptide (P1) comprising
CC at least an immunogenic portion of a prostate-specific protein, or its
CC variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
CC (N1) have cytosolic activity and can be used in vaccine production.
CC The polypeptides, nucleic acids and antibodies from the present
CC invention are useful in the diagnosis and therapy of prostate cancer.
CC Prostate specific genes P704P, P712P, P774P, P775P and B305D are located
CC in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
CC region. Prostate specific antigen (PSA) P501S was located on
CC chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent
CC polynucleotide and polypeptide sequences used in the exemplification
CC of the present invention.
XX
XX
Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;

Query Match 24.6%; Score 491; DB 22; Length 1512;
Best Local Similarity 99.4%; Pred. No. 4.4e-177;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
QY 34 TCTTCTGTGAAGAGCCATTGCTCAGAGCAAGATGGGCAAGTGGCTGCGCTTGC 93
DB 256 TCTTCTGTGAAGAGCCATTGCTCAGAGCAAGATGGGCAAGTGGCTGCGCTTGC 315
QY 94 TTCCCTGCTGCGAGGAGCGGCAAGACACCTGGGCACTTGTGAGACACGACGAC 153
DB 316 TTCCCTGCTGCGAGGAGCGGCAAGACACCTGGGCACTTGTGAGACACGACGAC 375
QY 154 TCTGCTATGAAGACACACAGAGCAAGATGGGCAAGTGGGCGGCACTGCTCCCTGC 213
DB 376 TCTGCTATGAAGACACACAGAGCAAGATGGGCAAGTGGGCGGCACTGCTCCCTGC 435
QY 214 TGCAGGGGAGTGCCAAAGACACGTCGCTTCTGAGACACGACGACGATGCTATG 273
DB 436 TGCAGGGGAGTGCCAAAGACACGTCGCTTCTGAGACACGACGACGATGCTATG 495
```

QY 274 AAGACTCAGAGAACAGATGGGCAAGTGGTCTGCACTGCTTCCCTGTCAGAGGG 333
DB 496 AAGACTCAGAGAACAGATGGGCAAGTGGTCTGCACTGCTTCCCTGTCAGAGGG 555
QY 334 ACGGCAAGAGCAAGTGGGCGCTTGGGAGACACAGATGACAGTGCCTTCATGAGCCC 393
DB 556 AGCAGCAAGAGCAAGTGGGCGCTTGGGAGACACAGATGACAGTGCCTTCATGAGCCC 615
QY 394 AGGTACACAGTCCGTCGAGAGATCTGACAGCTCCACAGAGCTCCCTGGGGTAA 453
DB 616 AGGTACACAGTCCGTCGAGAGATCTGACAGCTCCACAGAGCTCCCTGGGGTAA 675
QY 454 GTCCCAAGAGAGATCTGTCATGCTCAGGACACAGTGAACAAGAGCAAG 513
DB 676 GTCCCAAGAGAGATCTGTCATGCTCAGGACACAGTGAACAAGAGCAAG 735
QY 514 CAAAAGAGAGCTGCTACATCTGGCCCTCTGCAATGGGAATTCAGAACTGTAACCTC 573
DB 736 CAAAAGAGAGCTGCTACATCTGGCCCTCTGCAATGGGAATTCAGAACTGTAACCTC 795
QY 574 CTGCTGACAGACAGATGTAATGTCCTTGACACAAAAAGAGACAGCTGTA 633
DB 796 CTGCTGACAGACAGATGTAATGTCCTTGACACAAAAAGAGACAGCTGTA 855
QY 634 AAGCCGTCATGCGCAGAGAGATGATGCTTATGCTGAGACATGAGCACTGAT 693
DB 856 AAGCCGTCATGCGCAGAGAGATGATGCTTATGCTGAGACATGAGCACTGAT 915
QY 694 CCAAAATATTCAGATGATGTAATGTAATACCACTCT 728
DB 916 CCAAAATATTCAGATGATGTAATGTAATACCACTCT 950

RESULT 36

AAH02774 standard; cDNA: 1512 BP.

AAH02774:

14-JUN-2001 (first entry)

DE Prostate tumour antigen determined cDNA splice variant of B305D #3.
XX Prostate tumour antigen; prostate tumour; therapy; diagnosis;
KM prostate cancer; immunogenic; cytosolic; vaccine; ss.
XX

Homo sapiens.

WO200125272-A2.

12-APR-2001.

04-OCT-2000; 2000WO-US27464.

04-OCT-1999; 99US-0157455.

(CORI-) CORIXA CORP.

Xu J, Skelky YAW, Reed SG, Cheever MA;

WPI: 2001-245062/25.

PT Prostate specific protein and its encoding polynucleotide, useful for
PT the treatment and diagnosis of prostate cancer -

Claim 50; Page 229; 276pp; English.

CC The present invention describes an isolated polypeptide (I) comprising
CC at least an immunogenic portion of a prostate tumour antigen protein or
CC its variant. (I) have cytostatic activity and can be used in vaccine
CC production. (I), prostate tumour antigen polynucleotides, an antigen
CC presenting cell (APC e.g. a dendritic cell) that expresses (I), and a

CC pharmaceutical composition containing (I) are useful for inhibiting the
CC development of cancer in a patient. Antibodies specific for prostate
CC specific proteins and oligonucleotides that hybridise to a
CC polynucleotide that encodes a prostate specific protein are useful
CC for detecting the presence or absence of a cancer or monitoring the
CC progression the progression of a cancer, especially prostate cancer.
CC AAH02422 to AAH2872, AAB74798 to AAB74821 and AAB74830 are sequences
CC used in the exemplification of the present invention.

SQ Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other:

Query Match 24.6%; Score 491; DB 22; Length 1512;

Best Local Similarity 99.4%; Pred. No. 4,4e-177;

Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 34 TCTTCTGTAAAGAGCATTTGGTCTCAGAGACAGAAATGGGCAAGTGGTGGCGCTTGC 93
DB 256 TCTTCTGTAAAGAGCATTTGGTCTCAGAGACAGAAATGGGCAAGTGGTGGCGCTTGC 315
QY 94 TTCCCTGCTGCAAGGAGAGCGCAAGACCAAGTGGCACTTCTGAGACCAAGCAGAC 153
DB 316 TTCCCTGCTGCAAGGAGAGCGCAAGACCAAGTGGCACTTCTGAGACCAAGCAGAC 375
QY 154 TCTGCTATGAAGACACTCAGAGAGCAAGATGGCAAGTGGTCCCGCACTGCTTCCCTGC 213
DB 376 TCTGCTATGAAGACACTCAGAGAGCAAGATGGCAAGTGGTCCCGCACTGCTTCCCTGC 435
QY 214 TGCAGGGGGAGTGGCAAGAGCAACGTGGCGCTTCTGAGAGACACAGCACTTGTATG 273
DB 436 TGCAGGGGGAGTGGCAAGAGCAACGTGGCGCTTCTGAGAGACACAGCACTTGTATG 495
QY 274 AAGACACTCAGAGAAACAAGTGGGCAAGTGGTGGCACTGCTTCCCTGTCAGAGGG 333
DB 496 AAGACACTCAGAGAAACAAGTGGGCAAGTGGTGGCACTGCTTCCCTGTCAGAGGG 555
QY 334 AAGCGCAAGAGCAAGTGGGCGCTTGGGAGACATGATGACAGTGCCTTCATGAGCCC 393
DB 556 AAGCGCAAGAGCAAGTGGGCGCTTGGGAGACATGATGACAGTGCCTTCATGAGCCC 615
QY 394 AGGTACACAGTCCGTCGAGAGATCTGACAGCTCCACAGAGCTCCCTGGGGTAA 453
DB 616 AGGTACACAGTCCGTCGAGAGATCTGACAGCTCCACAGAGCTCCCTGGGGTAA 675
QY 454 GTCCCAAGAGAGATCTGTCATGCTCAGGACACAGTGAACAAGAGCAAG 513
DB 676 GTCCCAAGAGAGATCTGTCATGCTCAGGACACAGTGAACAAGAGCAAG 735
QY 514 CAAAAGAGAGCTGCTACATCTGGCCCTCTGCAATGGGAATTCAGAACTGTAACCTC 573
DB 736 CAAAAGAGAGCTGCTACATCTGGCCCTCTGCAATGGGAATTCAGAACTGTAACCTC 795
QY 574 CTGCTGACAGACAGATGTAATGTCCTTGACACAAAAAGAGACAGCTGTA 633
DB 796 CTGCTGACAGACAGATGTAATGTCCTTGACACAAAAAGAGACAGCTGTA 855
QY 634 AAGCCGTCATGCGCAGAGAGATGATGCTTATGCTGAGACATGAGCACTGAT 693
DB 856 AAGCCGTCATGCGCAGAGAGATGATGCTTATGCTGAGACATGAGCACTGAT 915
QY 694 CCAAAATATTCAGATGATGTAATGTAATACCACTCT 728
DB 916 CCAAAATATTCAGATGATGTAATGTAATACCACTCT 950

RESULT 37

ABL95173 standard; cDNA: 1512 BP.

ABL95173:

19-JUL-2002 (first entry)

DE Human B305D splice variant cDNA sequence SEQ ID NO 368.

XX Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX Homo sapiens.
XX US2002022248-A1.
XX 21-FEB-2002.
XX 12-JAN-2001. 2001US-0759143.
XX 25-FEB-1997. 97US-0806099.
XX 01-AUG-1997. 97US-0904804.
XX 09-FEB-1998. 98US-0020956.
XX 25-FEB-1998. 98US-0030607.
XX 14-JUL-1998. 98US-0115453.
XX 23-SEP-1998. 98US-0159812.
XX 15-JAN-1999. 99US-0232149.
XX 09-APR-1999. 99US-0288946.
XX 13-JUL-1999. 99US-0352616.
XX 12-NOV-1999. 99US-0439313.
XX 18-NOV-1999. 99US-0443686.
XX 14-JAN-2000. 2000US-0483672.
XX 27-MAR-2000. 2000US-0536857.
XX 09-MAY-2000. 2000US-0568100.
XX 12-MAY-2000. 2000US-0570737.
XX 13-JUN-2000. 2000US-0593793.
XX 27-JUN-2000. 2000US-0605783.
XX 10-AUG-2000. 2000US-0636215.
XX 29-AUG-2000. 2000US-0651236.
XX 06-SEP-2000. 2000US-0657279.
XX 10-OCT-2000. 2000US-0679426.
XX 10-OCT-2000. 2000US-0685166.
XX (XUJ/) XU J.
XX (DILL/) DILLON D C.
XX (MITC/) MITCHAM J L.
XX (HARL/) HARLOCKER S L.
XX (JIAN/) JIANG Y.
XX (KALO/) KALOS M D.
XX (FANG/) FANGER G R.
XX (RETT/) RETTER M W.
XX (STOL/) STOLK J A.
XX (DAYC/) DAY C H.
XX (VEDV/) VEDVICK T S.
XX (CART/) CARTER D.
XX (LISX/) LI S X.
XX (WANG/) WANG A.
XX (SKEI/) SKEIKY Y A W.
XX (HEPL/) HEPLER W T.
XX (HEND/) HENDERSON R A.
XX Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD,
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX WPI: 2002-255649/30.
XX New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer
XX Claim 1; SEQ ID NO 368; 87pp; English.
XX The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a CDNA
CC described in the invention.
XX Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other:
SO Query Match 24.6%; Score 491; DB 24; Length 1512;

Best Local Similarity 99.4%; Pred. No. 4,4e-177;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAGCCATTGGTCTCAGGAGCAAGATGGCAAGTGTGCTGCCCTGC 93
|||
Db 256 TCTTCTGTGAAGAGCCATTGGTCTCAGGAGCAAGATGGCAAGTGTGCTGCCCTGC 315
QY 94 TTCCCTGCTGCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 153
|||
Db 316 TTCCCTGCTGCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 375
QY 154 TCTGCTATGAAGACACTCAGAGAGCAAGATGGGCAAGTGTGCTGCCCACTGCTCCCTGC 213
|||
Db 376 TCTGCTATGAAGACACTCAGAGAGCAAGATGGGCAAGTGTGCTGCCCACTGCTCCCTGC 435
QY 214 TGCAGGGGAGATGGCAAGAGCAAGCTGGGCGCTTCTGAGACCAAGCACTGCTATG 273
|||
Db 436 TGCAGGGGAGATGGCAAGAGCAAGCTGGGCGCTTCTGAGACCAAGCACTGCTATG 495
QY 274 AAGCACTCAAGCAAGATGGGCAAGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 333
|||
Db 496 AAGCACTCAAGCAAGATGGGCAAGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 555
QY 334 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTACAGATGACAGTGCCTTCATGAGGCC 393
|||
Db 556 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTACAGATGACAGTGCCTTCATGAGGCC 615
QY 394 AGGTACCACTCGGTGAGAAAGATCTGAGACAGTCCACAGAGCTGCTGCTGCTGCTGCTGCTG 453
|||
Db 616 AGGTACCACTCGGTGAGAAAGATCTGAGACAGTCCACAGAGCTGCTGCTGCTGCTGCTGCTG 675
QY 454 GTCCCCAGAAAGATCTCATCTGATCTCAGGAGCACTGACGTAAGCAAGAGAGCAAG 513
|||
Db 676 GTCCCCAGAAAGATCTCATCTGATCTCAGGAGCACTGACGTAAGCAAGAGAGCAAG 755
QY 514 CAAAAGAGAGCTGCTACATCTGGCCTCTGCCAATGGAAATTCAGAAATGATGAAAATCTC 573
|||
Db 736 CAAAAGAGAGCTGCTACATCTGGCCTCTGCCAATGGAAATTCAGAAATGATGAAAATCTC 795
QY 574 CTGCTGACAGAGAGATGCTCAACTTAATGCTGCTGACAAACAAAAGAGAGAGCTGTATA 633
|||
Db 796 CTGCTGACAGAGAGATGCTCAACTTAATGCTGCTGACAAACAAAAGAGAGAGCTGTATA 855
QY 634 AAGGCCGTACAAATGCCAGAAATGAATGCGTTAATGTTGCTGGAACATGGCAGTAT 693
|||
Db 856 AAGGCCGTACAAATGCCAGAAATGAATGCGTTAATGTTGCTGGAACATGGCAGTAT 915
QY 694 CCAAAATATTCAGATGATGAAATACCACTCT 728
|||
Db 916 CCAAAATATTCAGATGATGAAATACCACTCT 950
RESULT 38
ABK46896
ID ABK46896 standard; DNA: 1512 BP.
XX ABK46896;
AC
XX
DT 05-JUN-2002 (first entry)
XX
DE Human breast tumour-specific DNA B11ag1, protein coding exon #3.
XX
XX Human: breast tumour-specific protein; vaccine; breast cancer;
KW gene; ds.
XX
XX Homo sapiens.
XX
XX US6344550-B1.
PN
XX
PD 05-FEB-2002.
XX
PF 17-APR-1998. 98US-0062451.
XX

.PR 01-JAN-1996; 96US-0585392.
PR 20-AUG-1996; 96US-0700014.
PR 10-JAN-1997; 97WO-US00485.
PR 09-APR-1997; 97US-0838762.
PR 11-DEC-1997; 97US-0991789.
XX
XX (CORI-) CORIXA CORP.
XX
XX Frudakis TN, Smith JM, Reed SG;
XX WPI: 2002-215084/27.
XX
XX Polynucleotide encoding breast-specific tumour polypeptides useful as
XX vaccine for preventing and treating breast cancer in a subject -
XX
XX Claim 1: Column 211-213; 128pp; English.
XX
XX The invention relates to an isolated DNA molecule (I) encoding breast-
XX tumour-specific polypeptides. (I) is useful as a vaccine for preventing
XX and treating breast cancer in a subject. The polypeptide encoded by (I)
XX is used for production of compounds such as antibodies useful in
XX diagnosing and monitoring the progression of breast cancer. ABK4614-
XX ABK4689 represent human breast tumour-specific coding sequences and
XX related PCR primers of the invention.
XX
XX Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;

Query Match 24.6%; Score 491; DB 24; Length 1512;
Best Local Similarity 99.4%; Pred. No. 4.4e-177;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 34 TCTTGTGTAAGAACCAATTTGCTCAGAGACAGATGGGCAAGTGGTGGCGGTGC 93
DB 256 TCTTGTGTAAGAACCAATTTGCTCAGAGACAGATGGGCAAGTGGTGGCGGTGC 315
OY 94 TTCCCTGCTGCAGGAGAGCGGCAAGACAGTGGCAGCTTGTGAGACCAGCAGAC 153
DB 316 TTCCCTGCTGCAGGAGAGCGGCAAGACAGTGGCAGCTTGTGAGACCAGCAGAC 375
OY 154 TCTGCTATGAGACACTCAGAGACAGATGGGCAAGTGGTGGCGGTGCCTTCCCTGC 213
DB 376 TCTGCTATGAGACACTCAGAGACAGATGGGCAAGTGGTGGCGGTGCCTTCCCTGC 435
OY 214 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTGTGAGACAGACAGCTCTGTATG 273
DB 436 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTGTGAGACAGACAGCTCTGTATG 495
OY 274 AAGACACTCAGAGACAGATGGGCAAGTGGTGGCAGCTCTTCCCTGCTGACAGGG 333
DB 496 AAGACACTCAGAGACAGATGGGCAAGTGGTGGCAGCTCTTCCCTGCTGACAGGG 555
OY 334 AGCGGCAAGAGCAGAGTGGGCGCTTGGGAGACTAGCATGACAGTGCCTTCATGAGCCC 393
DB 556 AGCRCACAGAGCAGAGTGGGCGCTTGGGAGACTAGCATGACAGTGCCTTCATGAGCCC 615
OY 394 AGGTACACAGTCCGCGGAGAGATCTGGACAGCTCCACAGAGTGGCGGTGGGTAA 453
DB 616 AGGTACACAGTCCGCGGAGAGATCTGGACAGCTCCACAGAGTGGCGGTGGGTAA 675
OY 454 GTCCCCAGAAAGATCTCATCTGCTCATGCTCAGGAGACAGTGAACAAGAGAGCAAG 513
DB 676 GTCCCCAGAAAGATCTCATCTGCTCATGCTCAGGAGACAGTGAACAAGAGAGCAAG 735
OY 514 CAAAAGAGAGCTGCTCATCATCTGGCCTCTGCGCAATGGGAATTCAGAACTAGTAAACTC 573
DB 736 CAAAAGAGAGCTGCTCATCATCTGGCCTCTGCGCAATGGGAATTCAGAACTAGTAAACTC 795
OY 574 CTGCTGAGAGAGCATGTCACCTTAATGCTTGAACAACAAAAGAGGACACTGCGATA 633
DB 796 STGCTGAGAGAGCATGTCACCTTAATGCTTGAACAACAAAAGAGGACACTGCGATA 855
OY 634 AAGGCCGTACATGCGCAGAGAGATGAATGTGCTTAATGTTCTGGAAACATGGCACTGAT 693
|||||

DB 856 AAGCCGTACATGCCAGAGATGAATGTGCTTAATGTTCTGGAAACATGGCACTGAT 915
OY 694 CCAATATATCCAGATGAGATGGAATACACTCT 728
DB 916 CCAATATATCCAGATGAGTATGGAATACCACTCT 950

RESULT 39
AAS99852
ID AAS99852 standard; cDNA; 1512 BP.
XX
XX AAS99852;
XX
XX AC
XX
XX 12-MAR-2002 (first entry)
XX
XX DE Breast tumour-specific DNA #225.
XX
XX DE Human; breast cancer; PCR primer; ss; cytosilic; immunostimulant;
XX
XX KW tumour; vaccine; immunogenic.
XX
XX OS Homo sapiens.
XX
XX PN WO200190152-A2.
XX
XX PD 29-NOV-2001.
XX
XX PF 22-MAY-2001; 2001WO-US16776.
XX
XX PR 24-MAY-2000; 2000US-0577505.
XX
XX PR 08-JUN-2000; 2000US-0590583.
XX
XX PR 26-OCT-2000; 2000US-0699295.
XX
XX PR 16-MAR-2001; 2001US-0810936.
XX
XX PA (CORI-) CORIXA CORP.
XX

Frudakis TN, Reed SG, Smith JM, Misher LE, Dillon DC, Retter MW;
Wang A, Skelky YAW, Harlocker SL, Day CH;
WPI: 2002-089919/12.

New breast tumour proteins and polynucleotides encoding them, useful for
treating and/or preventing cancer, particularly breast cancer, and for
eliciting humoral and/or cellular immune response -

Claim 1: Page 219; 245pp; English.

The invention relates to novel breast tumour polynucleotides and
polypeptides. The polypeptides and polynucleotides are useful in
pharmaceutical compositions for treating and/or preventing cancer,
particularly breast cancer, and for eliciting an immune response,
particularly humoral and/or cellular immune response. The polynucleotides
may be used as probes or primers for nucleic acid hybridisation. In the
design and preparation of ribozyme molecules for inhibiting expression of
cancer polypeptides and proteins, and in recombinant DNA molecules to
direct expression of a polypeptide in host cells. AAS99570-AAS99888
represent novel human breast cancer protein coding sequences and
PCR primers of the invention.

Sequence 1512 BP; 406 A; 301 C; 393 G; 399 T; 13 other;

Query Match 24.6%; Score 491; DB 24; Length 1512;
Best Local Similarity 99.4%; Pred. No. 4.4e-177;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 34 TCTTGTGTAAGAACCAATTTGCTCAGAGACAGATGGGCAAGTGGTGGCGGTGC 93
DB 256 TCTTGTGTAAGAACCAATTTGCTCAGAGACAGATGGGCAAGTGGTGGCGGTGC 315
OY 94 TTCCCTGCTGCAGGAGAGCGGCAAGACAGTGGCAGCTTGTGAGACCAGCAGAC 153
DB 316 TTCCCTGCTGCAGGAGAGCGGCAAGACAGTGGCAGCTTGTGAGACCAGCAGAC 375
OY 154 TCTGCTATGAGACACTCAGAGACAGATGGGCAAGTGGTGGCGGTGCCTTCCCTGC 213
|||||

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Db 376 TCTGCTATGAAAGACACACAGAGAGAGATGGGCAAGTGGGCCCGCCACTGCTCCCTGC 435
QY 214 TGCAGGGGAGTGGGACAGCAACGCTGGGCGCTTCTGGAGCCAGCGAGCTGTATG 273
Db 436 TGCAGGGGAGTGGGACAGCAACGCTGGGCGCTTCTGGAGCCAGCGAGTGTATG 495
QY 274 AAGACTCTCAGGAACAAGATGGGCAAGTGGTGTCTGCGACTGCTTCCCTGCGAGGGG 333
Db 496 AAGACTCTCAGGAACAAGATGGGCAAGTGGTGTCTGCGACTGCTTCCCTGCGAGGGG 555
QY 334 AGCGGCAAGCAAGAGTGGGCGCTTGGGAGACTACAGTACAGTGGCTTCTATGGAGCC 393
Db 556 AGCGGCAAGCAAGAGTGGGCGCTTGGGAGACTACAGTACAGTGGCTTCTATGGAGCC 615
QY 394 AGTACACACGCTCGTGAGAGATCTGACAGCTCCACAGAGCTGGTGGGTAAA 453
Db 616 AGTACACACGCTCGTGAGAGATCTGACAGCTCCACAGAGCTGGTGGGTAAA 675
QY 454 GTCCCGCAAGAGATCTCATCTCATCTCAGGACACTGACGTGAACAAGAGACAG 513
Db 676 GTCCCGCAAGAGATCTCATCTCATCTCAGGACACTGACGTGAACAAGAGACAG 735
QY 514 CAAAGAGGAGTCTCTACACTCTGCGCTTGGCAATGGGAATTCAGAGTAAACTC 573
Db 736 CAAAGAGGAGTCTCTACACTCTGCGCTTGGCAATGGGAATTCAGAGTAAACTC 795
QY 574 CTGTGACAGAGATCTCACTTAATGTCTTGACAAACAAAGAGAGAGCTGTATA 633
Db 796 STGTGACAGAGATCTCACTTAATGTCTTGACAAACAAAGAGAGAGCTGTATA 855
QY 634 AAGCCCTACAAATGCCAGAGATGAATGTGCTTAATGTCTGGAACATGCACTGAT 693
Db 856 AAGCCCTACAAATGCCAGAGATGAATGTGCTTAATGTCTGGAACATGCACTGAT 915
QY 694 CCAATATTCAGATGATGGAATGGAATACCACTCT 728
Db 916 CCAATATTCAGATGATGGAATGGAATACCACTCT 950

RESULT 40
AAV68996
ID AAV68996 standard; DNA: 1853 BP.
AC AAV68996;
XX
XX 22-JAN-1999 (first entry)
DE DNA molecule encoding a breast tumour specific polypeptide #188.
XX
XX Human; breast cancer; breast tumour tissue; diagnosis; treatment;
KW vaccine; epitope; endogenous; retroviral element; ss.
XX
OS Homo sapiens.
XX
XX WO9845328-A2.
XX
XX 15-OCT-1998.
XX
XX 09-APR-1998; 98MO-US06939.
XX
XX 11-DEC-1997; 97US-0991789.
XX
XX 09-APR-1997; 97US-0838762.
XX
XX (CORI-) CORIXA CORP.
XX
XX Frudakis TN, Reed SG, Smith JM;
XX
XX WPI; 1998-557473/47.
XX
XX New DNA sequences isolated from endogenous human retroviral element
PT - and related vectors, transformed cells, proteins and antibodies,
PT useful for diagnosis, treatment and prevention of breast cancer

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XX
XX Claim 1; Page 138-139; 173pp; English.
PS
XX AAV68800 to AAV68998 represent nucleotide sequences which encode human
CC breast tumour specific polypeptides. Detection or measurement of
CC human breast tumour specific polypeptides and nucleotide sequences,
CC or the corresponding RNA in a sample, is used for diagnosis and
CC monitoring of breast cancer. Human breast tumour specific polypeptides
CC and nucleotide sequences, and the vectors containing the DNAs, are also
CC useful in vaccines for inhibiting development (for prevention or
CC therapy) of breast cancer. The polypeptides may also be used to
CC raise monoclonal antibodies, used as immunoassay reagents.
XX
XX Sequence 1853 BP; 521 A; 381 C; 492 G; 431 T; 28 other;
SQ
Query Match 12.6%; Score 252; DB 19; Length 1853;
Best Local Similarity 99.7%; Pred. No. 2,4e-86;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 34 TCTTCTGTGAAGAACCCATTGCTCTCAGAGCAAGATGGGCAAGTGGTCTGCGCTTGC 93
Db 256 TCTTCTGTGAAGAACCCATTGCTCTCAGAGCAAGATGGGCAAGTGGTCTGCGCTTGC 315
QY 94 TTCCCTGCTGCGAGGAGACCGCAAGACAGCTGGGCACTTCTGAGACACAGACAGAC 153
Db 316 TTCCCTGCTGCGAGGAGACCGCAAGACAGCTGGGCACTTCTGAGACACAGACAGAC 375
QY 154 TCTGCTATGAAGACACTCAGAGACAGATGGGCAAGTGGTGGCGCCACTGCTTCCCTGC 213
Db 376 TCTGCTATGAAGACACTCAGAGACAGATGGGCAAGTGGTGGCGCCACTGCTTCCCTGC 435
QY 214 TGCAGGGGAGTGGGCAAGCAACGCTGGGCGCTTCTGGAACACAGACAGACTGTATG 273
Db 436 TGCAGGGGAGTGGGCAAGCAACGCTGGGCGCTTCTGGAACACAGACAGACTGTATG 495
QY 274 AAGACTCTCAGGAACAAGATGGGCAAGTGGTGTCTGCGACTGCTTCCCTGCGAGGGG 333
Db 496 AAGACTCTCAGGAACAAGATGGGCAAGTGGTGTCTGCGACTGCTTCCCTGCGAGGGG 555
QY 334 AGC 336
Db 556 AGC 558

RESULT 41
AAC81007
ID AAC81007 standard; cDNA; 1853 BP.
XX
XX AAC81007;
AC
XX 13-FEB-2001 (first entry)
DE Human B1Agl1 antigen protein coding exon cDNA SEQ ID NO: 295.
XX
XX Human; breast tumour-specific antigen; cytosolic; vaccine;
KW breast cancer; B1Bgl1; B1Agl1; B1Bgl1; ss.
XX
XX Homo sapiens.
XX
XX WO200061753-A2.
XX
XX 19-OCT-2000.
XX
XX 07-APR-2000; 2000MO-US09312.
XX
XX 09-APR-1999; 99US-0289198.
XX
XX 28-OCT-1999; 99US-0429755.
XX
XX 23-MAR-2000; 2000US-0534825.
XX
XX (CORI-) CORIXA CORP.
XX
XX Frudakis TN, Smith JM, Reed SG, Misher LE, Retter MW, Dillon DC;
XX
XX

```


DR WPI: 2000-628403/60.

XX An isolated polypeptide comprising an immunogenic portion of a breast
XX tumor protein used for inhibiting the development of cancer, especially
PT breast cancer, and monitoring cancer progression in a patient.
XX
XX
PS Claim 4: Page 172-173; 187pp; English.

XX The present sequence is given in a specification relating to compositions
CC and methods for the treatment and diagnosis of breast cancer. Nucleotide
CC sequences that are preferentially expressed in breast tumour tissue, and
CC the polypeptides encoded by such nucleotide sequences, are used in
CC compositions and vaccines to inhibit the development of cancer,
CC especially breast cancer. The progression of a cancer may be monitored by
CC carrying out detection of tumour-specific antigens at subsequent time
CC points and comparing the results from the different time points.
CC CD4+ and/or CD8+ T-cells isolated from the cancer patient may be treated
CC with tumour-specific polypeptides, polynucleotides encoding the
CC polypeptides or antigen presenting cells expressing the polypeptides. The
CC cells are then administered to the patient to inhibit development of
CC cancer.

SQ Sequence 1853 BP; 521 A; 381 C; 492 G; 431 T; 28 other:

Query Match 12.6%; Score 252; DB 21; Length 1853;
Best Local Similarity 99.7%; Pred. No. 2.4e-86;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAGAGCCATTGCTCTCAGAGCAAGTGGGCAAGTGTGCTGCCGTTGC 93
DB 256 TCTTCTGTGAGAGCCATTGCTCTCAGAGCAAGTGGGCAAGTGTGCTGCCGTTGC 315

QY 94 TTCCCTGTGTGAGGAGGCGGCAAGCAAGTGGGCAAGTGTGCTGCCGTTGCAGCAGC 153
DB 316 TTCCCTGTGTGAGGAGGCGGCAAGCAAGTGGGCAAGTGTGCTGCCGTTGCAGCAGC 375

QY 154 TCTGCTATGAGACACTCAGAGCAAGTGGGCAAGTGGGCAAGTGTGCTGCCGTTGC 213
DB 376 TCTGCTATGAGACACTCAGAGCAAGTGGGCAAGTGGGCAAGTGTGCTGCCGTTGC 435

QY 214 TGCAGGGGAGTGGCAAGCAAGTGGGCTTCTGAGACCAAGAGCAGTCTGTCTATG 273
DB 436 TGCAGGGGAGTGGCAAGCAAGTGGGCTTCTGAGACCAAGAGCAGTCTGTCTATG 495

QY 274 AAGACACTCAGAGCAAGTGGGCAAGTGGGCTTCTGAGACCAAGAGCAGTCTGTCTATG 333
DB 496 AAGACACTCAGAGCAAGTGGGCAAGTGGGCTTCTGAGACCAAGAGCAGTCTGTCTATG 555

QY 334 AGC 336
DB 556 AGC 558

RESULT 42
ID AAA06594 standard; cDNA; 1853 BP.

XX AAA06594;
XX
DT 13-JUN-2000 (first entry)

DE Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:369.
XX
XX Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW immunogenic; cytostatic; vaccine; ss.
XX
OS Homo sapiens.
XX
XX WO200004149-A2.
XX
XX 27-JAN-2000.
PD
XX 14-JUL-1999; 99WO-US15838.
PF

XX 14-JUL-1998; 98US-0115453.
PR 14-JUL-1998; 98US-0116134.
PR 23-SEP-1998; 98US-0159812.
PR 23-SEP-1998; 98US-0159822.
PR 15-JAN-1999; 99US-0232149.
PR 15-JAN-1999; 99US-0232880.
PR 09-APR-1999; 99US-0288946.

XX (CORI-) CORIXA CORP.
XX
XX Dillon DC, Harlocker SL, Yugu J, Xu J, Mitcham JL;
PI WPI: 2000-171268/15.

DR New polypeptide useful for treating and diagnosing prostate cancer
PT comprises an immunogenic portion of prostate tumor protein -
XX
XX
PS Claim 50; Page 219-220; 263pp; English.

XX The present invention describes isolated polypeptides, comprising an
CC immunogenic portion of a prostate tumour protein (PTP). The polypeptides
CC and polynucleotides encoding them have cytostatic activity and can be
CC used in vaccines and in gene therapy. The polypeptides and
CC polynucleotides encoding them, antigen presenting cells which express
CC the polypeptides, antibodies against the polypeptides and vaccines
CC comprising them can be used for inhibiting the development of prostate
CC cancer in a patient. The polypeptides can be used to generate antibodies
CC or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC the polynucleotides encoding the polypeptides can be used as a probe or
CC to modulate the expression of the polypeptides. AAA06241 to AAA06691 and
CC AA82000 to AA82020 represent sequences used in the exemplification of
CC the present invention.

SQ Sequence 1853 BP; 521 A; 381 C; 492 G; 431 T; 28 other:

Query Match 12.6%; Score 252; DB 21; Length 1853;
Best Local Similarity 99.7%; Pred. No. 2.4e-86;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAGAGCCATTGCTCTCAGAGCAAGTGGGCAAGTGTGCTGCCGTTGC 93
DB 256 TCTTCTGTGAGAGCCATTGCTCTCAGAGCAAGTGGGCAAGTGTGCTGCCGTTGC 315

QY 94 TTCCCTGTGTGAGGAGGCGGCAAGCAAGTGGGCAAGTGTGCTGCCGTTGCAGCAGC 153
DB 316 TTCCCTGTGTGAGGAGGCGGCAAGCAAGTGGGCAAGTGTGCTGCCGTTGCAGCAGC 375

QY 154 TCTGCTATGAGACACTCAGAGCAAGTGGGCAAGTGGGCAAGTGTGCTGCCGTTGC 213
DB 376 TCTGCTATGAGACACTCAGAGCAAGTGGGCAAGTGGGCAAGTGTGCTGCCGTTGC 435

QY 214 TGCAGGGGAGTGGCAAGCAAGTGGGCTTCTGAGACCAAGAGCAGTCTGTCTATG 273
DB 436 TGCAGGGGAGTGGCAAGCAAGTGGGCTTCTGAGACCAAGAGCAGTCTGTCTATG 495

QY 274 AAGACACTCAGAGCAAGTGGGCAAGTGGGCTTCTGAGACCAAGAGCAGTCTGTCTATG 333
DB 496 AAGACACTCAGAGCAAGTGGGCAAGTGGGCTTCTGAGACCAAGAGCAGTCTGTCTATG 555

QY 334 AGC 336
DB 556 AGC 558

RESULT 43
ID AAS63803 standard; cDNA; 1853 BP.

XX AAS63803;
XX
DT 29-JAN-2002 (first entry)
XX

DE Human prostate cDNA clone B305D splice variant #4.
 XX
 KM Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
 XX
 OS Homo sapiens.
 XX
 PN WO200173032-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001MO-US09919.
 XX
 PR 27-MAR-2000; 2000US-0536857.
 PR 09-MAY-2000; 2000US-0568100.
 PR 12-MAY-2000; 2000US-0570737.
 PR 13-JUN-2000; 2000US-0593793.
 PR 27-JUN-2000; 2000US-0605783.
 PR 10-AUG-2000; 2000US-0636215.
 PR 29-AUG-2000; 2000US-0651236.
 PR 06-SEP-2000; 2000US-0657279.
 PR 02-OCT-2000; 2000US-0679426.
 PR 10-OCT-2000; 2000US-0685166.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
 PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
 PI Li SX, Wang A, Skelky YAM, Hepler WT, Henderson RA;
 XX
 DR WPI; 2001-639232/73.
 XX
 PT New human prostate-specific polypeptides and polynucleotides useful for
 PT the diagnosis and treatment of cancer, especially prostate cancer -
 PS Claim 1; Page 346-347; 579pp; English.
 XX
 CC The invention relates to isolated prostate-specific
 CC polynucleotides, polypeptides, fusion proteins of the polypeptides,
 CC antibodies raised against the polypeptides (or antigenic epitopes
 CC derived from them) and antigen-presenting cells expressing the
 CC polypeptides. The antibodies are useful for detecting the presence of
 CC cancer, especially prostate cancer. The polypeptides, polynucleotides and
 CC the antigen-presenting cells are useful for stimulating and/or expanding
 CC T cells specific for a tumour protein, and for inhibiting the development
 CC of cancer especially prostate cancer. Compositions comprising the
 CC polynucleotide and/or polypeptide are useful for stimulating an immune
 CC response, and for treating cancer. The oligonucleotide is useful for
 CC detecting cancer. The present sequence is a prostate specific
 CC polynucleotide of the invention.
 CC
 SQ Sequence 1853 BP; 521 A; 381 C; 492 G; 431 T; 28 other;

Query Match 12.6%; Score 252; DB 22; Length 1853;
 Best Local Similarity 99.7%; Pred. NO. 2.4e-86;
 Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAGCCATTGGTCTCAGAGCAAGATGGGCAAGTGGTCCGCTTGC 93
 DB 256 TCTTCTGTGAAGAGCCATTGGTCTCAGAGCAAGATGGGCAAGTGGTCCGCTTGC 315

QY 94 TTCCCTGCTGCAGAGGAGCGGCAAGCAACGTGGGCACTTCTGGAGACCAGCAGAC 153
 DB 316 TTCCCTGCTGCAGAGGAGCGGCAAGCAACGTGGGCACTTCTGGAGACCAGCAGAC 375

QY 154 TCTGCTATGGAAGACACCTCAGAGGAGCAAGATGGGCAAGTGGGCACTTCTCCCTGC 213
 DB 376 TCTGCTATGGAAGACACCTCAGAGGAGCAAGATGGGCAAGTGGGCACTTCTCCCTGC 435

QY 214 TGCAGGGGAGTGCGCAAGCAACGTGGGCACTTCTGGAGACCAGCAGCAGTGTATG 273
 DB 436 TGCAGGGGAGTGCGCAAGCAACGTGGGCACTTCTGGAGACCAGCAGCAGTGTATG 495

QY 274 AAGACTCTAGGAACAAGATGGGCAAGTGGTGTCTGCACCTGCTTCCCTGTCAGAGGGG 333

DB 496 AAGACTCTAGGAACAAGATGGGCAAGTGGTGTCTGCACCTGCTTCCCTGTCAGAGGGG 555
 QY 334 AGC 336
 DB 556 AGC 558

RESULT 44
 AAH93710
 ID AAH93710 standard; cDNA; 1853 BP.
 XX
 AC AAH93710;
 XX
 DT 04-OCT-2001 (first entry)
 XX
 DE Human prostate-specific cDNA sequence B305D splice variant #4.
 XX
 KM Human; prostate cancer; prostate-specific; diagnosis; vaccine;
 KM cytostatic; gene therapy; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200151633-A2.
 XX
 PD 19-JUL-2001.
 XX
 PF 16-JAN-2001; 2001MO-US01574.
 XX
 PR 14-JAN-2000; 2000US-0483672.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
 PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skelky YAM;
 PI Wang A, Meagher MJ;
 XX
 DR WPI; 2001-425873/45.
 XX
 PT New polynucleotide encoding a prostate-specific protein, for
 PT diagnosing, monitoring and treating prostate cancer in a patient and
 PT for use in vaccines -
 PS Claim 1; Page 344-345; 543pp; English.
 XX
 CC The present invention describes polynucleotide sequences (I) which encode
 CC prostate-specific proteins (II), (I) and (II) have cytostatic activity,
 CC and can be used in vaccine production and gene therapy. (I), (II),
 CC antibodies to (II), fusion proteins comprising (II), and isolated
 CC T cells prepared using (I) or (II) are used treat cancer in a patient.
 CC (I) and the antibodies are also used in the detection of cancer in a
 CC patient. The cancer that is diagnosed or treated is particularly
 CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
 CC (I) can be used for monitoring the progression of cancer in a patient.
 CC (I) and (II) can also be used to improve diagnostic and therapeutic
 CC methods for prostate cancer. They can indicate the level of metastasis
 CC as well as the prostate volume. AAH93357 to AAH93944 and AAH01115 to
 CC AAH01318 represent polynucleotide and amino acid sequences used in the
 CC exemplification of the present invention.
 CC
 SQ Sequence 1853 BP; 521 A; 381 C; 492 G; 431 T; 28 other;

Query Match 12.6%; Score 252; DB 22; Length 1853;
 Best Local Similarity 99.7%; Pred. NO. 2.4e-86;
 Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAGCCATTGGTCTCAGAGCAAGATGGGCAAGTGGTCCGCTTGC 93
 DB 256 TCTTCTGTGAAGAGCCATTGGTCTCAGAGCAAGATGGGCAAGTGGTCCGCTTGC 315

QY 94 TTCCCTGCTGCAGAGGAGCGGCAAGCAACGTGGGCACTTCTGGAGACCAGCAGAC 153
 DB 316 TTCCCTGCTGCAGAGGAGCGGCAAGCAACGTGGGCACTTCTGGAGACCAGCAGAC 375

QY 154 TCTGATGAGACACTGAGAGCAAGATGGGCAAGTGGTGGCGCCACTGTTCCCTGC 213
DB 376 TCTGCTATGAAGACACTGAGAGCAAGATGGGCAAGTGGTGGCGCCACTGTTCCCTGC 435
QY 214 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGACACAGCACTCTGTATG 273
DB 436 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGACACAGCACTCTGTATG 495
QY 274 AAGACACTGAGAGCAAGATGGGCAAGTGGTGGCGCTTCTGAGACACAGCACTCTGTATG 333
DB 496 AAGACACTGAGAGCAAGATGGGCAAGTGGTGGCGCTTCTGAGACACAGCACTCTGTATG 555
QY 334 AGC 336
DB 556 AGC 558

RESULT 45
AAH85024
ID AAH85024 standard; cDNA; 1853 BP.
AC AAH85024;
DT 25-SEP-2001 (first entry)
XX
DE Human prostate-specific cDNA sequence B305D splice variant #4.
XX
KW Human; prostate cancer; therapy; diagnosis; cat eye syndrome;
KW chromosome 22q11.2; prostate-specific protein; chromosome 1;
XX prostate specific antigen; PSA; ss.
OS Homo sapiens.
XX
PN W0200134802-A2.
PD 17-MAY-2001.
XX
PF 09-NOV-2000; 2000MO-US30904.
XX
PR 12-NOV-1999; 99US-0439313.
PR 18-NOV-1999; 99US-0443686.
XX
PA (CORI-) CORIXA CORP.
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG,
PI Kalos MD, Reltter MW, Stolk JA, Day CH, Skelky YAW, Wang A;
XX
DR WPI; 2001-308785/32.
XX
PT Isolated polypeptide comprising at least an immunogenic portion of a
PT prostate-specific protein, useful in the diagnosis and therapy of
XX prostate cancer -
PS Claim 31; Page 244; 325pp; English.
XX
CC The present invention describes an isolated polypeptide (P1) comprising
CC at least an immunogenic portion of a prostate-specific protein, or its
CC variant. Also described are polynucleotides (N1) encoding (P1). (P1) and
CC (N1) have cytostatic activity and can be used in vaccine production.
CC The polypeptides, nucleic acids and antibodies from the present
CC invention are useful in the diagnosis and therapy of prostate cancer.
CC Prostate specific genes P704P, P712P, P774P, P775P and B305D are located
CC in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome
CC region. Prostate specific antigen (PSA) P501S was located on
CC chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent
CC polynucleotide and polypeptide sequences used in the exemplification
CC of the present invention.
XX
SQ Sequence 1853 BP; 521 A; 381 C; 492 G; 431 T; 28 other;

Query Match 12.6%; Score 252; DB 22; Length 1853;
Best Local Similarity 99.7%; Pred. No. 2.4e-86;

Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 34 TCTTCTGTAAGAAGCATTTTGGTCTCAGAGACAGATGGGCAAGTGGTGGCGCTTGC 93
DB 256 TCTTCTGTAAGAAGCATTTTGGTCTCAGAGACAGATGGGCAAGTGGTGGCGCTTGC 315
QY 94 TTCCCTGCTGCAGGAGAGCGGCAAGAGCAAGTGGGCACTTCTGAGACACAGCAGC 153
DB 316 TTCCCTGCTGCAGGAGAGCGGCAAGAGCAAGTGGGCACTTCTGAGACACAGCAGC 375
QY 154 TCTGCTATGAAGACACTGAGAGCAAGATGGGCAAGTGGTGGCGCCACTGTTCCCTGC 213
DB 376 TCTGCTATGAAGACACTGAGAGCAAGATGGGCAAGTGGTGGCGCCACTGTTCCCTGC 435
QY 214 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGACACAGCACTCTGTATG 273
DB 436 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGACACAGCACTCTGTATG 495
QY 274 AAGACACTGAGAGCAAGATGGGCAAGTGGTGGCGCTTCTGAGACACAGCACTCTGTATG 333
DB 496 AAGACACTGAGAGCAAGATGGGCAAGTGGTGGCGCTTCTGAGACACAGCACTCTGTATG 555
QY 334 AGC 336
DB 556 AGC 558

Search completed: November 8, 2002, 09:20:02
Job time : 393.277 secs

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Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 8, 2002, 08:45:54 ; Search time 2565.15 Seconds
(Without alignments)
12879.875 Million cell updates/sec

Title: US-09-924-400-303
Perfect score: 2040
Sequence: 1 atgtgtgtgtgaggtgtgtatc.....aaaaaaaaaaaaaaaaaaaaa 2040

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size: 15

Total number of hits satisfying chosen parameters: 1430706

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlun:*
5: em_estlov:*
6: em_estlpl:*
7: em_estlro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_tod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	184	9.0	521	17	AQ204617 HS_3229_B
2	141	6.9	865	12	BF676987 602084215
3	140	6.9	451	9	AI804733 tu42b03.x
4	137	6.7	289	9	AA533501 nJ96a04.s
5	129	6.3	531	17	AQ615477 HS_5144_B
6	117	5.7	621	14	BM763942 K-EST0045

7	117	5.7	633	14	BM763453 K-EST0044
8	117	5.7	817	14	BO441373 AGENCOURT
9	89	4.4	400	17	AO124119 HS_3122_A
10	87	4.3	399	17	AO030111 RPT111-39
11	87	4.3	544	9	AL703938 DKF2686E
12	79	3.9	279	13	BI461255 603206584
13	73	3.6	385	17	AQ063365 CIR-HSP-2
14	59	2.9	707	17	AG045796 Pan trogl
15	57	2.8	607	17	B48260 RPT111-6K4
16	52	2.5	380	12	BF328652 RCG-BN027
17	50	2.5	592	17	AQ372700 RPT111-14
18	49	2.4	495	17	AQ469831 CIRBI-E1-
19	49	2.4	557	17	AQ469663 CIRBI-E1-
20	49	2.4	667	17	AG156382 Pan trogl
21	49	2.4	697	17	AQ030113 RPT111-39
22	47	2.3	187	10	BE069869 CML-BT039
23	47	2.3	476	17	AQ392059 CIRBI-E1-
24	46	2.3	400	17	AQ057106 CIR-HSP-2
25	45	2.2	894	12	BF675049 602136643
26	44	2.2	460	17	AQ360298 HS_5035_A
27	41	2.0	710	17	AG165908 Pan trogl
28	40	2.0	503	17	B55862 CTT-HSP-200
29	39	1.9	1011	17	AQ9000910 HS_-2055_B
30	38	1.9	458	17	AQ247090 HS_-2055_B
31	37	1.8	424	17	AO763344 HS_3162_A
32	37	1.8	694	12	BG720647 602692528
33	36	1.8	652	17	AG054405 Pan trogl
34	35	1.7	156	9	AI349163 ta73C06.x
35	35	1.7	157	9	AI251211 qv38H06.x
36	35	1.7	160	9	AI305627 qw72F03.x
37	35	1.7	166	9	AI343314 tb93912.x
38	35	1.7	184	10	AW302924 xrb6907.x
39	35	1.7	199	10	AW302925 xrb6908.x
40	35	1.7	224	9	AI344928 tb01A04.x
41	35	1.7	232	9	AI336592 ta94d12.x
42	35	1.7	239	9	AI344933 tb01a11.x
43	35	1.7	239	9	AI344936 tb01b03.x
44	35	1.7	250	9	AI335449 tb79F03.x
45	35	1.7	360	9	AI494279 qy98C11.x

ALIGNMENTS

RESULT 1
LOCUS AQ204617 521 bp DNA linear GSS 17-SEP-1998
DEFINITION HS_3229_B1_G12_T7 CTT Approved Human Genomic Sperm Library D Homo
Sapiens genomic clone Plate=3229 COL=23 Row=N, DNA sequence.
ACCESSION AQ204617
VERSION AQ204617.1 GI:3615187
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3229 row: N column: 23

Class: BAC ends
High quality sequence stop: 521.
Location/Qualifiers
1. 521

FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate-3229 Col=23 Row=N"
/clone_lib="CIR Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 161 a 94 c 99 g 161 t 6 others

ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-35;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1595 AGCTAGAAATTTTATGCTATCGAAGAAATGAAGACGAGAGTACTGTCGGAT 1654
|||||
Db 231 AGCTAGAAATTTTATGCTATCGAAGAAATGAAGACGAGAGTACTGTCGGAT 290
|||||
QY 1655 TCCCAAGAAACCTGACTAATGTCGCACTGTCGCAATGCTGATGATTAATTCCTC 1714
|||||
Db 291 TCCCAAGAAACCTGACTAATGTCGCACTGTCGCAATGCTGATGATTAATTCCTC 350
|||||
QY 1715 CAAGAAGAGCAGACACCTGAAGCCAGCAATTCCTGACACTGAGATGAAGATATC 1774
|||||
Db 351 CAAGAAGAGCAGACACCTGAAGCCAGCAATTCCTGACACTGAGATGAAGATATC 410
|||||
QY 1775 ACAG 1778
|||||
Db 411 ACAG 414

RESULT 2
BF676987 865 bp mRNA linear EST 21-DEC-2000
LOCUS 602084215F1 NIH_MGC_83 Homo sapiens CDNA clone IMAGE:4248746 5',
DEFINITION mRNA sequence.
ACCESSION BF676987
VERSION BF676987.1 GI:11950882
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 865)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHCN1067 row: m column: 03
High quality sequence stop: 642.
Location/Qualifiers

FEATURES
source
1. 865
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4248746"
/clone_lib="NIH_MGC_83"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site.1: SfiI (ggccgcctggcc); Site.2: SfiI (ggccattatggcc
); 5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGACC-3' and 3' adaptor

sequence: 5'-ATTCTAGAGCCGCGCGCCGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

BASE COUNT 297 a 140 c 211 g 217 t

ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 2e-25;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 919 ACTGCTCTCACTACTGCTGATGTTGGATCAGCAAGTATGACCTTCTACTTGGAG 978
|||||
Db 353 ACTGCTCTCACTACTGCTGATGTTGGATCAGCAAGTATGACCTTCTACTTGGAG 412
|||||
QY 979 CAAATATTTGATGTATCTTCTCAAGATCTATCTGACAGCGCCAGAGATGCTGTT 1038
|||||
Db 413 CAAATATTTGATGTATCTTCTCAAGATCTATCTGACAGCGCCAGAGATGCTGTT 472
|||||
QY 1039 TCTAGTCATCATCATGTAATT 1059
|||||
Db 473 TCTAGTCATCATCATGTAATT 493
|||||

RESULT 3
A1804733 451 bp mRNA linear EST 07-MAR-2000
LOCUS tu42b03.x1 NCI_CGAP_Pr28 Homo sapiens CDNA clone IMAGE:2253677 3',
DEFINITION mRNA sequence.
ACCESSION A1804733
VERSION A1804733.1 GI:5370205
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 451)
NCI-CGAP http://www.nci.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 543 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers

FEATURES
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1. 451
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2253677"
/clone_lib="NCI_CGAP_Pr28"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: prostate; Vector: pT73D-Pac (pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (clonoids
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT	128 a	79 c	91 g	153 t
ORIGIN				
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Best Local Similarity	100.0%; Pred. No. 6.2e-25;			
Matches 140; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
QY	916	AGGACTGCTCTCATRACCTGCTGATGTTGTGGATCAGCAAGATATAGTACGCTTACTT	975	
DB	47	AGGACTGCTCTCATRACCTGCTGATGTTGTGGATCAGCAAGATATAGTACGCTTACTT	106	
QY	976	GAGCAAAATATGATGATATCTTCACAGATCATATGACAGCGCCAGAGATGCT	1035	
DB	107	GAGCAAAATATGATGATATCTTCACAGATCATATGACAGCGCCAGAGATGCT	166	
QY	1036	GTTTCTACTCATCATCATGT	1055	
DB	167	GTTTCTACTCATCATCATGT	186	
RESULT 4				
LOCUS	AA533501	289 bp	mRNA	linear
DEFINITION	U936a04.s1 NCI-CGAP_Prl1 Homo sapiens CDNA clone IMAGE:1000302,			
VERSION	AA533501			
KEYWORDS	AA533501.1	GI:2277597		
SOURCE	EST.			
ORGANISM	human.			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.			
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
COMMENT	Tumor Gene Index			
	Unpublished (1997)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgaps-remail.nih.gov			
	Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Rodrigo F.			
	Changul, M.D., Michael R. Emmert-Buck, M.D., Ph.D.			
	CDNA Library Preparation: David B. Krizman, Ph.D.			
	CDNA Library Arrayed by: Greg Lennon, Ph.D.			
	DNA Sequencing by: Washington University Genome Sequencing Center			
	clone distribution: NCI-CGAP clone distribution information can be			
	found through the I.M.A.G.E. Consortium/ILMIL at:			
	www-bio.llnl.gov/bdrrp/image/image.html			
	Insert length: 217 Std Error: 0.00			
	Seq primer: -40ml3 fwd. RT from Amersham.			
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SOURCE	Location/Qualifiers			
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	/db_xref="taxon:9606"			
	/clone="IMAGE:1000302"			
	/clone_id="NCI-CGAP_Prl1"			
	/sex="male"			
	/tissue_type="normal prostatic epithelial cells"			
	/lab_host="DH10B"			
	/note="Organ: prostate; Vector: pAMP10; mRNA made from			
	normal prostatic epithelial cells, cDNA made by oligo-dT			
	priming. Non-directionally cloned. Size-selected on			
	agarose gel, average insert size 600 bp. Library made by			
	D. Krizman, NIH."			
BASE COUNT	121 a	36 c	66 g	66 t
ORIGIN				
Query Match	6.7%; Score 137; DB 9; Length 289;			
Best Local Similarity	100.0%; Pred. No. 4.9e-24;			
Matches 137; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
QY	1788	AAATGATCTCAGAGCAATTTTGAGAGCAACAGAACTGGAATATACGATGACAT	1847	
DB	9	AAATGATCTCAGAGCAATTTTGAGAGCAACAGAACTGGAATATACGATGACAT	68	

QY	1848	TCGATTCATGTAAGAAAGACGATGTGAAGTGGTGAAGAAATGATTCGTGACTTCT	1907
DB	69	TTCTGATTCATGTAAGAAAGACGATGTGAAGTGGTGAAGAAATGATTCGTGACTTCT	128
QY	1908	TAGTGTGAAGAAAGAA 1924	
DB	129	TAGTGTGAAGAAAGAA 145	
RESULT 5			
LOCUS	A0615477	531 bp	DNA
DEFINITION	HS.5144_B1.G01.T7A.RPCT-11 Human Male BAC Library Homo sapiens		linear GSS 15-JUN-1999
ACCESSION	A0615477		
VERSION	A0615477.1	GI:5076753	
KEYWORDS	GSS.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 531) Kellera, G.G., Wallace, J.C., Smith, R., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.		
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)		
MEDLINE	99380589		
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones are derived from the human BAC library RPCT-11. For BAC library availability, please contact Pieter de Jong (pieter@ed.jong.med.buffalo.edu). Clones may be purchased from BACpac Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 720 row: N column: 1 Seg primer: 77 Class: BAC ends High quality sequence stop: 531. Location/Qualifiers 1..531 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="plate=720 Col-1 Row=N" /clone_id="RPCT-11 Human Male BAC Library" /sex="male" /note="Vector: pBACe3.6, Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRII. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"		
FEATURES	source		
BASE COUNT	167 a 92 c 92 g 169 t	11 others	
ORIGIN			
Query Match	6.3%	Score 129	DB 17
Best Local Similarity	100.0%	Prod. No. 2.5e-22	
Matches 129	Conservative 0	Mismatches 0	Indels 0
		Gaps 0	
QY	682	CATGCGACTGATCCAAATATTCACAGATGAGTGAATATACACATCTGCACATACGCTATC	741
DB	117	CATGCGACTGATCCAAATATTCACAGATGAGTGAATATACACATCTGCACATACGCTATC	176
QY	742	TATATGGAAGATTAATTAATGCGCAACACATGCTTATATAGTGCGTATTCGAATCA	801
DB	177	TATATGGAAGATTAATTAATGCGCAACACATGCTTATATAGTGCGTATTCGAATCA	236

OY 802 AAAAAGAG 810
|||||
Db 237 AAAAAGAG 245

RESULT 6
BM763942 621 bp mRNA linear EST 04-MAR-2002
LOCUS K-EST0045367 S13KMS5 Homo sapiens cDNA clone S13KMS5-25-A11 5',
DEFINITION mRNA sequence.
ACCESSION BM763942
VERSION BM763942.1 GI:19093557
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 621)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 25 row: A column: 11
High quality sequence stop: 621.
Location/Qualifiers
1. 621
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_11b="S13KMS5-25-A11"
/clone_11b="S13KMS5"
/tissue_type="myeloma"
/cell_line="KMS-5"
/lab_host="Top10F"
/note="Vector: PCNS; Site.1: EcoRI; Site.2: NotI; The poly
(A)+ RNA was dephosphorylated with bacterial alkaline
phosphatase (BAP) and then decapped with tobacco acid
pyrophosphatase (TAP). The decapped intact mRNA was
ligated with DNA-RNA linker including EcoR I site by
treatment of T4 RNA ligase and the first strand cDNA was
synthesized from oligo dt-selected mRNA by priming with
dt-tailed vector. The dt-tailed vector was adjusted to
have about 60nt. The cDNA vector was circularized with E.
coli DNA ligase after digestion of EcoRI which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained cDNA vectors
were used for transformation of competent cells E. coli
Top10F by electroporation method. The cDNA libraries
constructed by this method are full-length enriched cDNA
library."

BASE COUNT 216 a 123 c 127 g 155 t
ORIGIN

Query Match 5.7%; Score 117; DB 14; Length 621;
Best Local Similarity 99.1%; Pred. No. 1.7e-19;
Matches 217; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 510 CAAGCAAAAGAGAGCTGTCTACATCTGGCCTTGCATGGGAATTCACAGTAGTAA 569
|||||
Db 1 CAAGCAAAAGAGAGCTGTCTACATCTGGCCTTGCATGGGAATTCACAGTAGTAA 60

OY 570 ACTCGTGTGAGACAGAGATGTCACTTAATGCTTGCACAAAAAGAGGACAGCTCT 629
|||||
Db 61 ACTCGTGTGAGACAGAGATGTCACTTAATGCTTGCACAAAAAGAGGACAGCTCT 120

OY 630 GATTAAGCCCGCTACATGCCAGGAAGATGATGCTTAATGCTGTGACATGCGAC 669
|||||
Db 121 GACAAAGCCGCTAACATGCCAGGAAGATGATGCTTAATGCTGTGACATGCGAC 180

OY 690 TGATCCAAATATTCAGATGATGGAATACCACTCT 728
|||||
Db 181 TGATCCAAATATTCAGATGATGGAATACCACTCT 219

RESULT 7
BM763453 633 bp mRNA linear EST 04-MAR-2002
LOCUS K-EST0044791 S13KMS5 Homo sapiens cDNA clone S13KMS5-16-A11 5',
DEFINITION mRNA sequence.
ACCESSION BM763453
VERSION BM763453.1 GI:19093068
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 633)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 16 row: A column: 11
High quality sequence stop: 633.
Location/Qualifiers
1. 633
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_11b="S13KMS5-16-A11"
/clone_11b="S13KMS5"
/tissue_type="myeloma"
/cell_line="KMS-5"
/lab_host="Top10F"
/note="Vector: PCNS; Site.1: EcoRI; Site.2: NotI; The poly
(A)+ RNA was dephosphorylated with bacterial alkaline
phosphatase (BAP) and then decapped with tobacco acid
pyrophosphatase (TAP). The decapped intact mRNA was
ligated with DNA-RNA linker including EcoR I site by
treatment of T4 RNA ligase and the first strand cDNA was
synthesized from oligo dt-selected mRNA by priming with
dt-tailed vector. The dt-tailed vector was adjusted to
have about 60nt. The cDNA vector was circularized with E.
coli DNA ligase after digestion of EcoRI which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained cDNA vectors
were used for transformation of competent cells E. coli
Top10F by electroporation method. The cDNA libraries
constructed by this method are full-length enriched cDNA
library."

BASE COUNT 221 a 125 c 129 g 157 t 1 others
ORIGIN

Query Match 5.7%; Score 117; DB 14; Length 633;
Best Local Similarity 99.1%; Pred. No. 1.7e-19;
Matches 217; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 510 CAAGCAAAAGAGAGCTGTCTACATCTGGCCTTGCATGGGAATTCACAGTAGTAA 569
|||||
Db 1 CAAGCAAAAGAGAGCTGTCTACATCTGGCCTTGCATGGGAATTCACAGTAGTAA 60

OY 570 ACTCGTGTGAGACAGAGATGTCACTTAATGCTTGCACAAAAAGAGGACAGCTCT 629


```

Db 61 ACTCTGCTGGACACACGCTGTCACCTATCTCTGCAACAAAGAGACAGCTCT 120
Oy 630 GATAAGGCGCCGACATGCGAGAGATGATGCGTAAAGTGGCTGAGACATGGCAC 689
Db 121 GACAAAGCGCCGACATGCGAGAGATGATGCGTAAAGTGGCTGAGACATGGCAC 180
Oy 690 TGATCCAAATATTCAGATGATGATGAAATACCACTCT 728
Db 181 TGATCCAAATATTCAGATGATGATGAAATACCACTCT 219

RESULT 8
LOCUS BQ441373
DEFINITION BQ441373 817 bp mRNA linear EST 24-MAY-2002
AGENCOURT_7907577 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6103855
5', mRNA sequence.
ACCESSION BQ441373
VERSION BQ441373.1 GI:21180449
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 817)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation (LLN)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLN at:
http://image.llnl.gov
Plate: L10M2340 row: m column: 08
High quality sequence stop: 516.
Location/Qualifiers
1. 817
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6103855"
/clone_lib="NIH_MGC_82"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgccctcgcc); Site_2: SfiI (ggcgccctcgcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGCGCATATGAGC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGAGCGCGCGCATATG-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."
```

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AO124119
LOCUS AO124119 400 bp DNA linear GSS 22-SEP-1998
DEFINITION HS_3122 AL C07 MR C17 Approved Human Genomic Sperm Library D Homo
sapiens genomic clone plate=3122 Col-13 Row=E, DNA sequence.
ACCESSION AO124119
VERSION AO124119.1 GI:3501285
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 400)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
JOURNAL 99380589
MEDLINE
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3122 Row: E Column: 13
Class: BAC ends
High quality sequence stop: 400.
Location/Qualifiers
1. 400
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=3122 Col=13 Row=E"
/clone_lib="C17 Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
E-Coli DH10B"
BASE COUNT 131 a 67 c 88 g 114 t
ORIGIN
Query Match 4.4%; Score 89; DB 17; Length 400;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 635 AGCCGCTACATGCCAGAGATGATGCGTTAATGTTGCTGGAACATGCATGATC 694
Db 237 AGCCGCTACATGCCAGAGATGATGCGTTAATGTTGCTGGAACATGCATGATC 296
Oy 695 CAAATATTCAGATGATGATGAAATACC 723
Db 297 CAAATATTCAGATGATGATGAAATACC 325

RESULT 10
LOCUS AO030111/c 399 bp DNA linear GSS 14-APR-1999
DEFINITION RPII11-39K18.TP RPII-11 Homo sapiens genomic clone RPII-11-39K18,
DNA sequence.
ACCESSION AO030111
VERSION AO030111.1 GI:3274075
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 399)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Baas,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
Venter,J.C.
TITLE Use of BAC End Sequences for Sequence-Ready Map Building (1998)
JOURNAL Unpublished (1998)
```

COMMENT Other_GSSS: RPCI11-39K18.TV
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@long.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.

FEATURES
source location/Qualifiers
1..399
/organism="Homo sapiens"
/db_xref="GDB:7514849"
/db_xref="taxon:9606"
/clone="RPCI-11-39K18"
/clone_1lb="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"

BASE COUNT 110 a 78 c 73 g 138 t

ORIGIN

Query Match 4.3%; Score 87; DB 17; Length 399;
Best Local Similarity 100.0%; Pred. No. 4.5e-12;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1777 AGTGACGACAAATGCTACTCAGACGAATTTGTGAGACGACGACGAAATTTA 1836
|||||
Db 102 AGTGACGACAAATGCTACTCAGACGAATTTGTGAGACGACGACGAAATTTA 43
|||||

QY 1837 CAGCATGAGATTCTGATTCATGAAGAA 1863
|||||
Db 42 CAGCATGAGATTCTGATTCATGAAGAA 16
|||||

RESULT 11
AL703938 544 bp mRNA linear EST 22-MAR-2002
LOCUS DKFZp686E1728.f1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DEFINITION DKFZp686E1728.5', mRNA sequence.
ACCESSION AL703938
VERSION AL703938.1 GI:19687293
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 544)
Ottenswaelder,B., Obermaier,B., Mewes,W., Mewes,H.W., Well,B. and
Wiemann,S.
EST (Ottenswaelder,B., Obermaier,B., Mewes,H.W., Well,B. and
Wiemann,S.)
Unpublished (2001)
Contact: Ottenswaelder B

JOURNAL
MIPS
Am Kioferplatz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Medigenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No sl sequence
available.
This clone (DKFZp686E1728) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source location/Qualifiers
1..544
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZp686E1728"
/clone_1lb="686 (synonym: hlcc3)"
/issue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

BASE COUNT 192 a 94 c 110 g 148 t

ORIGIN

Query Match 4.3%; Score 87; DB 9; Length 544;
Best Local Similarity 100.0%; Pred. No. 3.5e-12;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGAAGAACGCAATCCAGAACAGCTTAAAG 1140
|||||
Db 432 AAAGAAAAACAGATGCTAAAAATCTCTTGAAGAACGCAATCCAGAACAGCTTAAAG 491
|||||

QY 1141 CTGACATCAGAGCAAGACTCACAAGG 1167
|||||
Db 492 CTGACATCAGAGCAAGACTCACAAGG 518
|||||

RESULT 12
B1461255/c 279 bp mRNA linear EST 21-AUG-2001
LOCUS 603206584F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5272364 5',
DEFINITION mRNA sequence.
ACCESSION B1461255
VERSION B1461255.1 GI:15251911
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 279)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L14M1687 row: g column: 21
High quality sequence stop: 236.
location/Qualifiers
1..279
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5272364"
/clone_1lb="NIH_MGC_97"
/lab_host="DH10B"
/note="Organ: testis; Vector: pBluescript (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVA-3',
size-selected for average insert size 2.2 kb and
normalized to R0T 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 87 a 87 c 60 g 45 t

ORIGIN

Query Match 3.9%; Score 79; DB 13; Length 279;
 Best Local Similarity 100.0%; Pred. No. 5.4e-10;
 Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGCTGTTGAGTTGATTCATCGCGCTCTCTTGTGAAGAACCATTTGCTC 60
 Db ATGCTGTTGAGTTGATTCATCGCGCTCTCTTGTGAAGAACCATTTGCTC 25
 OY 61 AGGAGCAAGATGGCAGT 79
 Db AGGAGCAAGATGGCAGT 6

RESULT 13
 LOCUS A0063365 385 bp DNA linear GSS 31-JUL-1998
 DEFINITION CIT-HSP-2348P17.TR CIT-HSP Homo sapiens genomic clone 2348P17, DNA
 ACCESSION A0063365
 VERSION A0063365.1 GI:3361196
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 385)
 Golden, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K.,
 Simon, M., and Venter, J.C.
 Building (1998)
 Use of a random BAC End Sequence Database for Sequence-Ready Map
 Unpublished (1998)
 Other GSSs: CIT-HSP-2348P17.TF
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdadams@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13 Reverse
 Class: BAC ends

FEATURES
 source Location/Qualifiers
 1..385
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="2348P17"
 /clone_1bp="CIT-HSP"
 /sex="Male"
 /cell_type="Sperm"
 /note="Vector: pBelOBAC11; site_1: HindIII; site_2:
 HindIII"

BASE COUNT 118 a 53 c 79 g 135 t
 ORIGIN

Query Match 3.6%; Score 73; DB 17; Length 385;
 Best Local Similarity 100.0%; Pred. No. 1.1e-08;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1408 AGAATTTGGCATGATTCGACTACAAAGAAAACGATGCCAAATACTCTTCTGAA 1467
 Db AGAATTTGGCATGATTCGACTACAAAGAAAACGATGCCAAATACTCTTCTGAA 248
 OY 1468 AACAGCAACCCAG 1480
 Db 249 AACAGCAACCCAG 261

RESULT 14

AG045796/c 707 bp DNA linear GSS 02-NOV-2001
 LOCUS AG045796 Pan troglodytes DNA, clone: PTB-024N04.R, genomic survey sequence.
 DEFINITION AG045796
 ACCESSION AG045796.1 GI:16582688
 VERSION GSS.
 KEYWORDS Pan troglodytes male lymphoblast DNA, clone_1bp:PTB Chimpanzee Male
 BAC library clone:PTB-024N04.R.
 SOURCE Pan troglodytes
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.

REFERENCE 1
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
 Totoki, Y., Watanabe, H. and Sakaki, Y.
 BAC end sequences of library PTB
 Unpublished
 2 (bases 1 to 707)
 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
 Totoki, Y., Watanabe, H. and Sakaki, Y.
 Direct Submission
 Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
 1-7-22 Suenho-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
 Tel:81-45-503-9111, Fax:81-45-503-9170)
 Clones are derived from the chimpanzee BAC library PTB This BAC end
 was generated during the Rad process and may have higher chance of
 clone tracking errors.
 PRIMERS

COMMENT

Sequencing: M13Rev
 LIBRARY
 Vector : pKS145
 R.Site 1 : SacI
 R.Site 2 : SacI.
 Location/Qualifiers
 1..707
 /organism="Pan troglodytes"
 /db_xref="taxon:9598"
 /clone="PTB-024N04.R"
 /sex="male"
 /cell_type="lymphoblast"
 /clone_1bp="PTB Chimpanzee Male BAC library"
 145 c 85 g 237 t 7 others

BASE COUNT 233 a 145 c 85 g 237 t
 ORIGIN

Query Match 2.9%; Score 59; DB 17; Length 707;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1956 GGAAGAAATGGCATGCTAGACCTGAGCTAGACAAATGGAACATGAGCCAGCTTA 2014
 Db 226 GGAAGAAATGGCATGCTAGACCTGAGCTAGACAAATGGAACATGAGCCAGCTTA 168

RESULT 15
 LOCUS B48260/c 607 bp DNA linear GSS 08-APR-1999
 DEFINITION R0C111-6K4.TV R0C11-11 Homo sapiens genomic clone R0C11-6K4, DNA
 sequence.
 ACCESSION B48260
 VERSION B48260.1 GI:2600497
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 607)
 Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden
 , K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter
 , J.C.
 Use of BAC End Sequences for Sequence-Ready Map Building
 Unpublished (1997)
 Contact: Mark Adams

TITLE
 JOURNAL
 COMMENT

Query Match 2.5%; Score 50; DB 17; Length 592;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 745 AATGAAGATAAATTAATGGCAAGACGCTCTTATATGTCGATAT 794
 |||||||
 DB 153 AATGAAGATAAATTAATGGCAAGACGCTCTTATATGTCGATAT 202

RESULT 18
 AQA69831/C 495 bp DNA linear GSS 23-APR-1999
 LOCUS CITBI-El-2588F5.TF CITBI-El Homo sapiens genomic clone 2588F5, DNA
 DEFINITION sequence.
 ACCESSION AQA69831 GI:4653485
 VERSION AQA69831
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 495)
 Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
 Venter,J.C.
 Title Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
 Map Building
 Unpublished (1997)
 Other-GSS: CITBI-El-2588F5.TF
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbe@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
 http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html.
 Seq primer: M13-21
 Class: BAC ends.

FEATURES
 source
 1..495
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="2588F5"
 /clone_11b="CITBI-El"
 /sex="male"
 /cell_type="sperm"
 /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
 Caltech Human BAC Library P"

BASE COUNT 179 a 75 c 67 g 174 t

ORIGIN

Query Match 2.4%; Score 49; DB 17; Length 495;
 Best Local Similarity 100.0%; Pred. No. 0.0058;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1196 AGAAAATGCTCAAGAACCAAGAAATTAATGAGATGATAGAGAGT 1244
 |||||||
 DB 194 AGAAAATGCTCAAGAACCAAGAAATTAATGAGATGATAGAGAGT 146

RESULT 19
 AQA69663 557 bp DNA linear GSS 23-APR-1999
 LOCUS CITBI-El-2588M24.TF CITBI-El Homo sapiens genomic clone 2588M24,
 DEFINITION DNA sequence.
 ACCESSION AQA69663
 VERSION AQA69663.1 GI:4653317
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 557)
 Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
 Venter,J.C.
 Title Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
 Map Building
 Unpublished (1997)
 Other-GSS: CITBI-El-2588M24.TF
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbe@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
 http://www.tigr.org/tldb/hungen/bac_end_search/bac_end_search.html.
 Seq primer: M13-21
 Class: BAC ends.

FEATURES
 source
 1..557
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="2588M24"
 /clone_11b="CITBI-El"
 /sex="male"
 /cell_type="sperm"
 /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
 Caltech Human BAC Library P"

BASE COUNT 201 a 83 c 74 g 199 t

ORIGIN

Query Match 2.4%; Score 49; DB 17; Length 557;
 Best Local Similarity 100.0%; Pred. No. 0.0052;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1196 AGAAAATGCTCAAGAACCAAGAAATTAATGAGATGATAGAGAGT 1244
 |||||||
 DB 194 AGAAAATGCTCAAGAACCAAGAAATTAATGAGATGATAGAGAGT 146

RESULT 20
 AG156382 667 bp DNA linear GSS 09-JAN-2002
 LOCUS pan troglodytes DNA, clone: RP43-020P19.TU, genomic survey
 DEFINITION sequence.
 ACCESSION AG156382
 VERSION AG156382.1 GI:16686060
 KEYWORDS GSS.
 SOURCE Pan troglodytes male lymphocytes DNA, clone_11b:RP43 Chimpanzee
 Male BAC Library clone:RP43-020P19.TU.
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 1
 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
 Totoki,Y., Watanabe,H. and Sakaki,Y.
 Title BAC end sequences of library RPCI-43
 Unpublished
 2 (bases 1 to 667)
 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
 Totoki,Y., Watanabe,H. and Sakaki,Y.
 Title Direct Submission
 Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
 1-7-22 Suenho-chou, Tsukuba, Ibaraki, Japan
 (E-mail:chimpesegsc.riken.go.jp, URL:http://hnp.gsc.riken.go.jp/
 Tel:81-45-503-9111, Fax:81-45-503-9170)
 Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
 end was generated during the Red process and may have higher chance
 of clone tracking errors.

PRIMERS
Sequencing: TJ
LIBRARY
Vector : pBAC3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI
Location/Qualifiers
1. .667
/organism="Pan troglodytes"
/db_xref="taxon:9588"
/clone="RP43-020P19.TJ"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
BASE COUNT 235 a 110 c 98 g 224 t
ORIGIN

Query Match 2.4%; Score 49; DB 17; Length 667;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1196 AGAAATGCTCAAGAACCAATAATAGATGCTGATAGAGAGCT 1244
|||||
Db 212 AGAAATGCTCAAGAACCAATAATAGATGCTGATAGAGAGCT 164

RESULT 21
LOCUS A0030113 697 bp DNA linear GSS 14-APR-1999
DEFINITION RPCI11-39K18.TV RPCI-11 Homo sapiens genomic clone RPCI-11-39K18,
DNA sequence.
ACCESSION A0030113
VERSION A0030113.1 GI:3274077
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 697)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.F., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
Venter,T.C.
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
Unpublished (1998)
Other GSSs: RPCI11-39K18.TP
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pierre@jeong.med.bufileo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.bufileo.edu/ordering>) or from
Research Genetics (inforesgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. .697
/organism="Homo sapiens"
/db_xref="GDB:751484"
/db_xref="taxon:9606"
/clone="RPCI-11-39K18"
/clone_lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site.1: EcoRI; Site.2: EcoRI;
RPCI11 Human Male BAC Library"
BASE COUNT 253 a 120 c 101 g 222 t 1 others
ORIGIN

Query Match 2.4%; Score 49; DB 17; Length 697;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1196 AGAAATGCTCAAGAACCAATAATAGATGCTGATAGAGAGCT 1244
|||||
Db 167 AGAAATGCTCAAGAACCAATAATAGATGCTGATAGAGAGCT 119

RESULT 22
LOCUS BE069869 187 bp mRNA linear EST 09-JUN-2000
DEFINITION CM1-BT0397-201299-073-a11 BT0397 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE069869
VERSION BE069869.1 GI:8414519
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 187)
Dias,Neto,E., Garcia,Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=CM1-BT0397-201>)
299-073-a11ct3-199-12-20ct4-1)
Seq primer: puc 18 forward
High quality sequence start: 82
High quality sequence stop: 141.
Location/Qualifiers
1. .187
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT0397"
/dev_stage="adult"
/note="Organ: breast; Vector: puc18; Site.1: SmaI; Site.2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 66 a 45 c 34 g 42 t
ORIGIN

Query Match 2.3%; Score 47; DB 10; Length 187;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 790 GATATCGATCAAAAACAGCATGGCTCACCACCTGTTACTTGG 836
|||||
Db 91 GATATCGATCAAAAACAGCATGGCTCACCACCTGTTACTTGG 137

RESULT 23

A0392059/c 476 bp DNA linear GSS 06-MAR-1999
 LOCUS CITBI-EI-2555J3.TR CITBI-EI Homo sapiens genomic clone 2555J3, DNA
 DEFINITION sequence.
 ACCESSION A0392059
 VERSION A0392059.1 GI:4363082
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 476)
 AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
 TITLE Use of BAC End sequences from Caltech libraries for Sequence-Ready Map Building
 JOURNAL Unpublished (1997)
 COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hwe@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13 Reverse
 Class: BAC ends.

FEATURES
 source Location/Qualifiers
 1..476
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="2555J3"
 /clone_1lb="CITBI-EI"
 /sex="male"
 /cell_type="sperm"
 /note="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;
 Caltech Human BAC Library D"
 BASE COUNT 170 a 75 c 65 g 166 t
 ORIGIN

Query Match 2.3%; Score 47; DB 17; Length 476;
 Best Local Similarity 100.0%; Pred. No. 0.018;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1550 AGAAAAGATCTCAGACACAGAAATAAATAGAGTGTGATAGACAG 1596
 ||||||||||||||||||||||||||||||||||||||||||||||||
 Db 209 AGAAAAGATCTCAGACACAGAAATAAATAGAGTGTGATAGACAG 163

RESULT 24
 A0057106 400 bp DNA linear GSS 30-JUL-1998
 LOCUS CIT-HSP-2335J19.TF CIT-HSP Homo sapiens genomic clone 2335J19, DNA
 DEFINITION sequence.
 ACCESSION A0057106
 VERSION A0057106.1 GI:3353632
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 400)
 AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., White,C., Shizuya,H., Simon,M. and Venter,J.C.
 TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
 JOURNAL Unpublished (1998)
 COMMENT Other_GSSs: CIT-HSP-2335J19.TR
 Contact: Mark Adams
 Department of Eukaryotic Genomics

The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: madams@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13-21
 Class: BAC ends.

FEATURES
 source Location/Qualifiers
 1..400
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="2335J19"
 /clone_1lb="CIT-HSP"
 /sex="Male"
 /cell_type="Sperm"
 /note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
 HindIII"
 BASE COUNT 124 a 61 c 83 g 132 t
 ORIGIN

Query Match 2.3%; Score 46; DB 17; Length 400;
 Best Local Similarity 100.0%; Pred. No. 0.037;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1056 AATTGGCCAGTACTTCTGACTACAAAGAAAACAGATCTAATA 1101
 ||||||||||||||||||||||||||||||||||||||||||||||||
 Db 219 AATTGGCCAGTACTTCTGACTACAAAGAAAACAGATCTAATA 264

RESULT 25
 BF675049 894 bp mRNA linear EST 21-DEC-2000
 LOCUS 602136643P1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273139 5',
 DEFINITION mRNA sequence.
 ACCESSION BF675049
 VERSION BF675049.1 GI:11948944
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 894)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strussberg, Ph.D.
 Email: cgep@b-remail.nih.gov
 Tissue Procurement: CLONETECH Laboratories, Inc.
 cDNA Library Preparation: CLONETECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: L108 row: e column: 12
 High quality sequence start: 6
 High quality sequence stop: 576.
 Location/Qualifiers
 1..894
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4273139"
 /clone_1lb="NIH_MGC_83"
 /lab_host="DH10B (TI phage-resistant)"
 /note="Organ: prostate; Vector: pBNR-LIB (Clontech);
 Site_1: SfiI (ggccgctggcc); Site_2: SfiI (ggccatattggc)
); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGACCCGAGCGCGCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average

Insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

BASE COUNT 239 a 186 c 208 g 261 t

Query Match 2.2%; Score 45; DB 12; Length 894;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 651 GGAAGATGATGCGTATATTTGCTGGAACATGCGACATGCC 695

Db 46 GGAAGATGATGCGTATATTTGCTGGAACATGCGACATGCC 90

RESULT 26
LOCUS AO360298 460 bp DNA linear GSS 06-MAR-1999

DEFINITION HS.5035.A2.C08_SPEE RPC111 Human Male BAC Library Homo sapiens genomic clone Plate-611 COL-16 Row-E, DNA sequence.

ACCESSION AO360298

VERSION AO360298.1 GI:4209174

KEYWORDS GSS.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 460)

MAHAIAS, G.G., WALLACE, J.C., SMITH, K., SWARTZELL, S., HOLZMAN, T., KELLER, A., SHAKER, R., FURLONG, J., YOUNG, J., ZHAO, S., ADAMS, M.D. and HOOD, L.

Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

JOURNAL MEDLINE 99380589

CONTACT: Mahaias GG, Wallace JC, Hood L

High Throughput Sequencing Center

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu

Plate: 611 row: E column: 16

Seq primer: SP6

Class: BAC ends

High quality sequence stop: 460.

Location/Qualifiers

1. 460

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="Plate-611 COL-16 Row-E"

/clone_lib="RPC111 Human Male BAC Library"

/sex="Male"

/cell_type="Lymphocytes"

/note="Vector: pBAC3.6; RPC111 Human Male BAC Library"

BASE COUNT 144 a 79 c 95 g 141 t 1 others

Query Match 2.2%; Score 44; DB 17; Length 460;

Best Local Similarity 100.0%; Pred. No. 0.1;

Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1717 AGGAAGAGCAGACCTGAAAGCCAGCAATTTCTGACACTGA 1760

Db 335 AGGAAGAGCAGACCTGAAAGCCAGCAATTTCTGACACTGA 378

RESULT 27

LOCUS AG165908 710 bp DNA linear GSS 09-JAN-2002

DEFINITION Pan troglodytes DNA, clone: RP43-033106.TU, genomic survey sequence.

ACCESSION AG165908

VERSION AG165908.1 GI:16695586

KEYWORDS GSS.

SOURCE Pan troglodytes male lymphocytes DNA, clone: lib:RPC1-43 Chimpanzee Male BAC Library clone:RP43-033106.TU.

ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.

REFERENCE 1

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

BAC end sequences of library RPC1-43

Unpublished

2 (bases 1 to 710)

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

(E-mail: chimpanzee@sc.riken.go.jp, URL: http://hnp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)

Clones are derived from the chimpanzee BAC library RPC1-43 This BAC end was generated during the Red process and may have higher chance of clone tracking errors.

PRIMERS

Sequencing: TU

LIBRARY

Vector : pBAC3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI

Location/Qualifiers

1. 710

/organism="Pan troglodytes"

/db_xref="taxon:9598"

/clone="RP43-033106.TU"

/sex="male"

/cell_type="Lymphocytes"

/clone_lib="RPC1-43 Chimpanzee Male BAC Library"

BASE COUNT 218 a 121 c 111 g 258 t 2 others

Query Match 2.0%; Score 41; DB 17; Length 710;

Best Local Similarity 100.0%; Pred. No. 0.36;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 754 AAATTAATGGCCAAAGCAGCTGCTTATATATGTCGATAT 794

Db 221 AAATTAATGGCCAAAGCAGCTGCTTATATATGTCGATAT 261

RESULT 28

LOCUS B55862 503 bp DNA linear GSS 20-JUN-1998

DEFINITION CIT-HSP-2005F16.TR CIT-HSP Homo sapiens genomic clone 2005F16, DNA sequence.

ACCESSION B55862

VERSION B55862.1 GI:2610196

Query Match 2.2%; Score 44; DB 17; Length 460;

Best Local Similarity 100.0%; Pred. No. 0.1;

Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1717 AGGAAGAGCAGACCTGAAAGCCAGCAATTTCTGACACTGA 1760

Db 335 AGGAAGAGCAGACCTGAAAGCCAGCAATTTCTGACACTGA 378

RESULT 27

LOCUS AG165908 710 bp DNA linear GSS 09-JAN-2002

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdamas@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21
Class: BAC ends.

FEATURES

source

1. .503
/organism="Homo sapiens"
/db_xref="GDB:7039242"
/db_xref="taxon:9606"
/clone_id="2005F16"
/clone_id="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelBAC11; Site_1: HindIII; Site_2:
HindIII"
BASE COUNT 152 a 116 c 87 g 148 t
ORIGIN

Query Match 2.0%; Score 40; DB 17; Length 503;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1087 AACAGATGCTAAATAATCTCTTCTGAAACAGCATCCAG 1126
|||||
Db 502 AACAGATGCTAAATAATCTCTTCTGAAACAGCATCCAG 463

RESULT 29
AQ900910 1011 bp DNA linear GSS 10-NOV-1999
LOCUS HS.2055_B1.B05.T7C CIT Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone Plate=2055 Col=9 Row=D, DNA sequence.
ACCESSION AQ900910
VERSION AQ900910.1 GI:6357012
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

CONTACT: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2055 row: D column: 9
Seq primer: T7
Class: BAC ends
High quality sequence stop: 1011.

FEATURES

source

1. .1011
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=2055 Col=9 Row=D"

/clone_id="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
E-Coli DH10B"
BASE COUNT 216 a 214 c 143 g 438 t
ORIGIN

Query Match 1.9%; Score 39; DB 17; Length 1011;
Best Local Similarity 100.0%; Pred. No. 0.81;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1054 GTAATTGGCAGTACTTCTTGACTACAAAGAAAAACAG 1092
|||||
Db 207 GTAATTGGCAGTACTTCTTGACTACAAAGAAAAACAG 245

RESULT 30
AQ247090 458 bp DNA linear GSS 06-OCT-1998
LOCUS HS.2055_B1.B04.T7 CIT Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone Plate=2055 Col=7 Row=D, DNA sequence.
ACCESSION AQ247090
VERSION AQ247090.1 GI:3697272
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

CONTACT: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

Sequence Tagged Connector
Plate: 2055 row: D column: 7
Class: BAC ends
High quality sequence stop: 458.

FEATURES

source

1. .458
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=2055 Col=7 Row=D"
/clone_id="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
E-Coli DH10B"
BASE COUNT 110 a 122 c 68 g 158 t
ORIGIN

Query Match 1.9%; Score 38; DB 17; Length 458;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1088 AACAGATGCTAAATAATCTTCTGAAACAGCAATCCA 1125
|||||
Db 198 AACAGATGCTAAATAATCTTCTGAAACAGCAATCCA 235

RESULT 31
AQ763344/c 424 bp DNA linear GSS 28-JUL-1999
LOCUS HS.3162_A2.B06.MR CIT Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone Plate=3162 Col=12 Row=C, DNA sequence.

```

ACCESSION      AQ763344
VERSION         AQ763344.1  GI:5641460
KEYWORDS
SOURCE          Homo sapiens
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE       1 (bases 1 to 424)
AUTHORS         Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
                Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                Hood,L.
TITLE           Sequence-tagged connectors: A sequence approach to mapping and
                scanning the human genome
JOURNAL         Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE        99380589
COMMENT         Contact: Mahairas GG, Wallace JC, Hood L
                High Throughput Sequencing Center
                University of Washington
                401 Queen Anne Avenue North, Seattle, WA 98109, USA
                Tel: (206) 616-3618
                Fax: (206) 616-3887
                Email: jwallace@u.washington.edu
                Clones may be purchased from Research Genetics (info@resgen.com).
                BAC end Web Server: http://www.htsc.washington.edu
                Plate: 3162 row: C column: 12
                Seq primer: M13 Reverse
                Class: BAC ends
                High quality sequence stop: 424.
FEATURES
  source        location/Qualifiers
                1..424
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="Plate=3162 Col=12 Row=C"
                /clone.lib="CIR Approved Human Genomic Sperm Library D"
                /sex="male"
                /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in
                E-Coli DH10B"
BASE COUNT      147 a      72 c      56 g      146 t      3 others
ORIGIN
Query Match    1.8%; Score 37; DB 17; Length 424;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1208 AAGAACGACGAATTAATAGATGCTGATGACAGGT 1244
|||||
Db 194 AAGAACGACGAATTAATAGATGCTGATGACAGGT 158

RESULT 32
BG720647      694 bp      mRNA      linear      EST 08-MAY-2001
LOCUS        602692528F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4824630 5',
DEFINITION   mRNA sequence.
ACCESSION    BG720647
VERSION      BG720647.1  GI:13999834
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE     1 (bases 1 to 694)
AUTHORS       NIH-MGC http://mgc.nci.nih.gov/.
                National Institutes of Health, Mammalian Gene Collection (MGC)
                Unpublished (1999)
                Contact: Robert Strausberg, Ph.D.
                Email: cgabbs-r@mail.nih.gov
                Tissue Procurement: Miklos Palovits, M.D., Ph.D.
                cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki
                Toshuyuki and Piero Carninci (RIKEN)
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
                DNA Sequencing by: Incyte Genomics, Inc.
                Clone distribution: MGC clone distribution information can be

```

```

found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM10736 row: h column: 07
High quality sequence stop: 694.
FEATURES
  source        location/Qualifiers
                1..694
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:4824630"
                /clone.lib="NIH_MGC_97"
                /lab_host="DH10B"
                /note="Organ: testis; Vector: pBluescript (modified
                pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
                size-selected for average insert size 2.2 kb and
                normalized to ROT 5. This is a primary library enriched
                for full-length clones and constructed using the
                cap-trapper method (Carninci, in preparation). Library
                constructed by M. Brownstein (NIH/NHGRI, National
                Institutes of Health). Note: this is a NIH-MGC Library."
BASE COUNT      108 a      173 c      228 g      185 t
ORIGIN
Query Match    1.8%; Score 37; DB 12; Length 694;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 159 TATGAGACACTCGAGCAAGATGGCAGTGTGTC 195
|||||
Db 645 TATGAGACACTCGAGCAAGATGGCAGTGTGTC 681

RESULT 33
AG054405      652 bp      DNA      linear      GSS 02-NOV-2001
LOCUS        Pan troglodytes DNA, clone: PTB-040B06.F, genomic survey sequence.
ACCESSION    AG054405
VERSION      AG054405.1  GI:16591848
KEYWORDS     GSS.
SOURCE       Pan troglodytes male lymphoblast DNA, clone.lib:PTB Chimpanzee Male
                BAC library clone:PTB-040B06.F.
ORGANISM     Pan troglodytes
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE     1
AUTHORS       Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
                Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE        BAC end sequences of Library PTB
JOURNAL      Unpublished
AUTHORS       2 (bases 1 to 652)
                Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
                Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE        Direct Submission
JOURNAL      Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
                and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
                1-7-22 Suenhiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                (E-mail:chimpbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
                tel:81-45-503-9111, fax:81-45-503-9170)
                Clones are derived from the chimpanzee BAC library PTB This BAC end
                was generated during the R&D process and may have higher chance of
                clone tracking errors.
COMMENT       PRIMERS
                Sequencing: -21M13
                LIBRARY
                Vector : pKS145
                R.Site 1 : SacI
                R.Site 2 : SacI.
                location/Qualifiers
                1..652
                /organism="Pan troglodytes"
                /db_xref="taxon:9598"
                /clone="PTB-040B06.F"
                /sex="male"

```

BASE COUNT 189 a 101 c 152 g 210 t

ORIGIN

Query Match 1.8%; Score 36; DB 17; Length 652;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 820 ACACCACGTCTGCTGCTACATGACGCAAAACAG 855
|||||
Db 398 ACACCACGTCTGCTGCTACATGACGCAAAACAG 433

RESULT 34
AI349163 156 bp mRNA linear EST 16-FEB-1999
DEFINITION la73c06.x2 NCI_CGAP_HSC2 Homo sapiens CDNA clone IMAGE:2049706 3',
AI349163
ACCESSION AI349163
VERSION AI349163
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Herbert Morse, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 243 Std Error: 0.00
Seq primer: -40UP from Glbco.

FEATURES
source Location/Qualifiers
1..156
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:2049706"
/clone_lib="NCI_CGAP_HSC2"
/tissue_type="stem cell 34+/38+"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: bone marrow; Vector: pAMP1; mRNA made from
bone marrow, stem cells 34+/38+, CDNA made by oligo-dT
priming. Directionally cloned. Size-selected on agarose
gel, average insert size 400 bp. Primary library,
non-amplified."

BASE COUNT 56 a 37 c 36 g 27 t

ORIGIN

Query Match 1.7%; Score 35; DB 9; Length 156;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2006 GCCAGCTAAAAA 2040
|||||
Db 111 GCCAGCTAAAAA 145

RESULT 35
AI251211 157 bp mRNA linear EST 03-FEB-1999
LOCUS AI251211
DEFINITION qv38h06.x1 NCI_CGAP_Ov31 Homo sapiens CDNA clone IMAGE:1983899 3',

RNA sequence.
AI251211
AI251211.1 GI:3847740
EST.
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Unknown library type
Insert Length: 244 Std Error: 0.00
Seq primer: -40UP from Glbco.

FEATURES
source Location/Qualifiers
1..157
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:1983899"
/clone_lib="NCI_CGAP_Ov31"
/sex="female"
/tissue_type="Papillary serous carcinoma"
/lab_host="DH10B"
/note="Organ: ovary; Vector: pAMP1; mRNA made from ovarian
carcinoma, CDNA made by oligo-dT priming.
Non-directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Non-amplified library."

BASE COUNT 57 a 37 c 36 g 27 t

ORIGIN

Query Match 1.7%; Score 35; DB 9; Length 157;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2006 GCCAGCTAAAAA 2040
|||||
Db 111 GCCAGCTAAAAA 145

RESULT 36
AI305627 160 bp mRNA linear EST 09-DEC-1998
LOCUS AI305627
DEFINITION qv72f03.x1 NCI_CGAP_Ov33 Homo sapiens CDNA clone IMAGE:1996637 3',
AI305627
ACCESSION AI305627
VERSION AI305627
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Glbco.

FEATURES
source Location/Qualifiers
1..160
/organism="Homo sapiens"
/db_xref="taxon:9606"

/clone="IMAGE:1996637"
/clone_1lb="NCI_CGAP_Ov33"
/sex="female"
/tissue_type="borderline ovarian carcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: ovary; Vector: PAMPI; mRNA made from
borderline ovarian carcinoma, cDNA made by oligo-dT
priming. Directionally cloned. Size-selected on agarose
gel, average insert size 500 bp. Primary library,
non-amplified."

BASE COUNT 59 a 38 c 35 g 26 t 2 others

ORIGIN

Query Match 1.7%; Score 35; DB 9; Length 160;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2006 GCCAGCTAAAAAAAAAAAAAAAAAAAAA.2040
Db 111 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 145

RESULT 37
A1343314 166 bp mRNA linear EST 08-APR-1999
LOCUS tb93912.x1 NCI_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2061958 3',
DEFINITION mRNA sequence.
ACCESSION A1343314
VERSION A1343314.1 GI:4080520
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 166)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution Information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbp/image/image.html
Seq primer: -40UP from Gibco.
Location/Qualifiers

FEATURES
source
1.166
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2061958"
/clone_1lb="NCI_CGAP_Lu25"
/tissue_type="bronchioalveolar carcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: lung; Vector: PAMPI; mRNA made from lung
carcinoma tissue, cDNA made by oligo-dT priming.
Directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."

BASE COUNT 57 a 40 c 39 g 30 t

ORIGIN

Query Match 1.7%; Score 35; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2006 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 2040
Db 122 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 156

JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.

RESULT 38
AM302924 184 bp mRNA linear EST 18-JAN-2000
LOCUS xr86g08.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2767068 3',
DEFINITION mRNA sequence.
ACCESSION AM302924
VERSION AM302924.1 GI:6712604
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 184)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution Information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbp/image/image.html
Seq primer: -40UP from Gibco.
High quality sequence stop: 136.
Location/Qualifiers

FEATURES
source
1.184
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2767068"
/clone_1lb="NCI_CGAP_Lu26"
/tissue_type="invasive adenocarcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: lung; Vector: PAMPI; mRNA made from lung
adenocarcinoma tissue, cDNA made by oligo-dT priming.
Directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."

BASE COUNT 92 a 35 c 33 g 24 t

ORIGIN

Query Match 1.7%; Score 35; DB 10; Length 184;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2006 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 2040
Db 111 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 145

RESULT 39
AM302925 199 bp mRNA linear EST 18-JAN-2000
LOCUS xr86g08.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2767070 3',
DEFINITION mRNA sequence.
ACCESSION AM302925
VERSION AM302925.1 GI:6712605
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 199)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.E. Consortium, LNLN.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution Information can be
found through the I.M.A.G.E. Consortium/LNLN at:
www-bio.lnl.gov/bdrp/image/image.html
Seq primer: -40UP from GIBCO.

FEATURES

source

1.199

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_image="2767070"

/clone_id="NCI-CGAP_Lu26"

/tissue_type="Invasive adenocarcinoma"

/dev_stage="adult"

/lab_host="DH10B"

/note="Organ: Lung; Vector: PAMPI; mRNA made from lung
adenocarcinoma tissue, CDNA made by oligo-dT priming.
Directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."

BASE COUNT

93 a 38 c 40 g 28 t

ORIGIN

Query Match 1.7%; Score 35; DB 10; Length 199;
Best Local Similarity 100.0%; Pred. No. 32;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2006 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 2040

Db 111 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 145

RESULT 40

LOCUS

AI344928

DEFINITION t01a04.x1 NCI-CGAP_Lu26 Homo sapiens CDNA clone IMAGE:2052270 3',

mRNA sequence.

ACCESSION AI344928.1 GI:4082134

VERSION

KEYWORDS

SOURCE

ORGANISM

human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 224)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov

CDNA Library Preparation: David B. Krizman, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LNLN at:

www-bio.lnl.gov/bdrp/image/image.html

Seq primer: -40UP from GIBCO.

FEATURES

source

1.224

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_image="2052270"

/clone_id="NCI-CGAP_Lu26"

/tissue_type="Invasive adenocarcinoma"

/dev_stage="adult"

/lab_host="DH10B"

/note="Organ: Lung; Vector: PAMPI; mRNA made from lung
adenocarcinoma tissue, CDNA made by oligo-dT priming.
Directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,

BASE COUNT 119 a 40 c 36 g 29 t

ORIGIN

non-amplified."

Query Match 1.7%; Score 35; DB 9; Length 224;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2006 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 2040

Db 128 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 162

RESULT 41

LOCUS

AI336592

DEFINITION t044d12.x1 NCI-CGAP_Lu26 Homo sapiens CDNA clone IMAGE:2051735 3',

mRNA sequence.

ACCESSION AI336592.1 GI:4073519

VERSION

KEYWORDS

SOURCE

ORGANISM

human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 232)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov

CDNA Library Preparation: David B. Krizman, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LNLN at:

www-bio.lnl.gov/bdrp/image/image.html

Insert length: 302 Std Error: 0.00

Seq primer: -40UP from GIBCO

High quality sequence stop: 225.

Location/Qualifiers

1.232

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_image="2051735"

/clone_id="NCI-CGAP_Lu26"

/tissue_type="Invasive adenocarcinoma"

/dev_stage="adult"

/lab_host="DH10B"

/note="Organ: Lung; Vector: PAMPI; mRNA made from lung
adenocarcinoma tissue, CDNA made by oligo-dT priming.
Directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."

BASE COUNT 119 a 44 c 40 g 29 t

ORIGIN

Query Match 1.7%; Score 35; DB 9; Length 232;
Best Local Similarity 100.0%; Pred. No. 28;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2006 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 2040

Db 134 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 168

RESULT 42

LOCUS

AI344933

DEFINITION t01a11.x1 NCI-CGAP_Lu26 Homo sapiens CDNA clone IMAGE:2052284 3',

mRNA sequence.

ACCESSION

AI344933

VERSION AI344933.1 GI:4082139
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 239)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.gov/bbrp/image/image.html
Insert length: 291 Std Error: 0.00
Seq primer: -40UP from Gibco.

FEATURES
source
1..239
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2052284"
/clone_lib="NCI-CGAP_Lu26"
/tissue_type="invasive adenocarcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: lung; Vector: PAMPI; mRNA made from lung
adenocarcinoma tissue; cDNA made by oligo-dT priming.
Directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."
BASE COUNT 119 a 48 c 40 g 32 t
ORIGIN

Query Match 1.7%; Score 35; DB 9; Length 239;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2006 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 2040
|||||
Db 146 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 180

RESULT 43
AI344936 239 bp mRNA linear EST 30-DEC-1998
LOCUS tb01b03.x1 NCI_CGAP_Lu26 Homo sapiens CDNA clone IMAGE:2052269 3',
DEFINITION mRNA sequence.
ACCESSION AI344936
VERSION AI344936.1 GI:4082142
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 239)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco.

FEATURES
source
1..239
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2052269"
/clone_lib="NCI-CGAP_Lu26"
/tissue_type="invasive adenocarcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: lung; Vector: PAMPI; mRNA made from lung
adenocarcinoma tissue; cDNA made by oligo-dT priming.
Directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."
BASE COUNT 119 a 48 c 40 g 32 t
ORIGIN

Query Match 1.7%; Score 35; DB 9; Length 239;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2006 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 2040
|||||
Db 146 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 180

RESULT 44
AI335449 250 bp mRNA linear EST 29-DEC-1998
LOCUS tb79f03.x1 NCI_CGAP_Lu26 Homo sapiens CDNA clone IMAGE:2060573 3',
DEFINITION mRNA sequence.
ACCESSION AI335449
VERSION AI335449.1 GI:4072376
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 250)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 240.

FEATURES
source
1..250
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2060573"
/clone_lib="NCI-CGAP_Lu26"
/tissue_type="invasive adenocarcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: lung; Vector: PAMPI; mRNA made from lung
adenocarcinoma tissue; cDNA made by oligo-dT priming.
Directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."
BASE COUNT 136 a 43 c 41 g 30 t
ORIGIN

Query Match 1.7%; Score 35; DB 9; Length 250;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2006 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 2040
 |||
 Db 134 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 168

RESULT 45

A1494279/c

360 bp mRNA linear EST 17-MAR-1999
 qy98c11.x1 NCI-CGAP Brn25 Homo sapiens cDNA clone IMAGE:2020052 3'

Similar to WP:B0432.3 CE07741 ;, mRNA sequence.

ACCESSION

A1494279

VERSION

A1494279.1 GI:4395282

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS

1 (bases 1 to 360)
 NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute / National Institute of Neurological
 Disorders and Stroke, Brain Tumor Genome Anatomy Project
 (CGAP/BRGAP), Tumor Gene Index

JOURNAL

Unpublished (1998)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
 Ph.D.

CDNA

Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.

CDNA

Library Arrayed by: Greg Lennon, Ph.D.

DNA

Sequencing by: Washington University Genome Sequencing Center

Clone

distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
www-bio.livl.gov/bdtp/image/image.html

Insert

Length: 645 Std Error: 0.00

Seq

Primer: -40UP from G1bco

High

quality sequence stop: 318.

FEATURES

Location/Qualifiers

Source

1..360

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2020052"

/clone_lib="NCI CGAP Brn25"

/tissue_type="anaplastic oligodendroglioma"

/lab_host="DH10B"

/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTACCAATCTGAAGTGGGAGCGCGCCATAGCTTTTCTTTTCTTTTCTTTT
 T 3']; double-stranded cDNA was ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of the modified pT73 vector.
 Library is normalized, and was constructed by Bento
 Soares and M. Fatima Bonaldo."

BASE COUNT

69 a 84 c 97 g 110 t

ORIGIN

Query Match 1.7%; Score 35; DB 9; Length 360;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2006

GCCAGCTAAAAAAAAAAAAAAAAAAAAA 2040

Db 41

GCCAGCTAAAAAAAAAAAAAAAAAAAAA 7

Search completed: November 8, 2002, 13:33:11
 Job time : 2591.15 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 8, 2002, 08:45:54 : Search time 2514.85 Seconds
(without alignments) 12879.875 Million cell updates/sec

Title: US-09-924-400-302

Perfect score: 2000
Sequence: 1 atgtgtgtgtgtgtgtgtgtc.....aaaaaaaaaaaaaaaaaaaa 2000

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 15

Total number of hits satisfying chosen parameters: 1430567

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthu:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_luv:*
20: em_gss_pin:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	184	9.2	521	17	AQ204617 HS_3229-B
2	141	7.0	865	12	BF676987 602084215
3	140	7.0	451	9	AI804733 t442D03.x
4	137	6.9	289	9	AA533501 n96804.s
5	129	6.5	531	17	AO615477 HS_5144-B
6	117	5.9	621	14	BM763942 K-EST0045

1413

7	117	5.9	633	14	BM763453	BM763453 K-EST0044
8	117	5.9	817	17	BO441373	BO441373 AGENCOURT
9	87	4.5	400	17	AO124119	AO124119 HS_3122-A
10	87	4.3	399	17	AO303011	AO303011 RPTC11-39
11	87	4.3	544	9	AL703938	AL703938 DKF2686E
12	79	4.0	279	13	BI461255	BI461255 603206584
13	73	3.6	385	17	AO063365	AO063365 CIT-HSP-2
14	59	2.9	707	17	AG045796	AG045796 Pan treg1
15	57	2.9	607	17	BA8260	BA8260 RPTC11-6K4
16	52	2.6	380	12	BF329652	BF329652 RC6-BN027
17	50	2.5	592	17	AO372700	AO372700 RPTC11-14
18	49	2.5	495	17	AO469831	AO469831 CITBI-E1-
19	49	2.5	557	17	AO469663	AO469663 CITBI-E1-
20	49	2.5	667	17	AG156382	AG156382 Pan treg1
21	49	2.5	697	17	AO030113	AO030113 RPTC11-39
22	47	2.4	187	10	BE069869	BE069869 CMT-BT039
23	46	2.3	400	17	AO057106	AO057106 CIT-HSP-2
24	45	2.2	894	12	BF675049	BF675049 602136643
25	44	2.2	460	17	AO360298	AO360298 HS_5035-A
26	41	2.1	476	17	AO392059	AO392059 CITBI-E1-
27	41	2.1	710	17	AG165908	AG165908 Pan treg1
28	40	2.0	184	10	AM302824	AM302824 xr86g07.x
29	40	2.0	199	10	AM302925	AM302925 xr86g08.x
30	40	2.0	224	9	AI344928	AI344928 tb01a04.x
31	40	2.0	232	9	AI336592	AI336592 ta94d12.x
32	40	2.0	239	9	AI344933	AI344933 tb01a11.x
33	40	2.0	239	9	AI344936	AI344936 tb01b03.x
34	40	2.0	250	9	AI335449	AI335449 tb79f03.x
35	40	2.0	360	9	AI494279	AI494279 qy98c11.x
36	40	2.0	367	9	AA766864	AA766864 oc87g12.x
37	40	2.0	421	14	BO230307	BO230307 AGENCOURT
38	40	2.0	442	14	BO127207	BO127207 1157b07.Y
39	40	2.0	503	17	BS5862	BS5862 CIT-HSP-200
40	40	2.0	560	12	BF968779	BF968779 602270486
41	40	2.0	616	12	BG491207	BG491207 602535247
42	40	2.0	831	13	BI915244	BI915244 603184781
43	40	2.0	1018	13	BI826592	BI826592 603036027
44	40	2.0	1024	14	BM919526	BM919526 AGENCOURT
45	39	1.9	160	9	AI305627	AI305627 qw72f03.x

ALIGNMENTS

RESULT 1
AQ204617
LOCUS
DEFINITION
HS_3229_B1.G12.T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3229 COL=23 Row=N, DNA sequence.

ACCESSION
AQ204617
VERSION
AQ204617.1
KEYWORDS
GSS.
SOURCE
human.
ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 521)
Mammalia: Eutheria; Primates: Catarrhini; Hominoidea: Homo.
Mehatras, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, V., Young, V., Zhao, S., Adams, M.D. and Hood, L.

TITLE
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
COMMENT
Contact: Mehatras GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3229 Row: N Column: 23

BASE COUNT 128 a 79 c 91 g 153 t
ORIGIN

Query Match 7.0%; Score 140; DB 9; Length 451;
Best Local Similarity 100.0%; Pred. No. 2.2e-26;

Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 916 AGGACTGCTCTACTACTGCTGTATGTTGTGATCGACAGATATAGTCACTTCTACTT 975
|||||

DB 47 AGGACGCTCATACTCTCTGTATGTTGTGATCGACAGATATAGTCACTTCTACTT 106
|||||

QY 976 GAGCAAAATTTGATGATCTTCTCAAGATCTATCTGACAGCGCCAGAGATATGCT 1035
|||||

DB 107 GAGCAAAATTTGATGATCTTCTCAAGATCTATCTGACAGCGCCAGAGATATGCT 166
|||||

QY 1036 GTTTCATCATCATCATGCT 1055
|||||

DB 1467 GTTTCATCATCATCATGCT 186
|||||

RESULT 4
AA533501 289 bp mRNA linear EST 21-AUG-1997
LOCUS n36a04.s1 NCI-CCAP_Prl1 Homo sapiens cDNA clone IMAGE:1000302,
DEFINITION mRNA sequence.

ACCESSION AA533501
VERSION AA533501
KEYWORDS EST
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 289)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)

JOURNAL Contact: Robert Strausberg, Ph.D.
Email: cga@bcr-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Rodrigo F.
Chaquig, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CNA Library Preparation: David B. Kitzman, Ph.D.
CNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ULNL at:
www-bio.lnl.gov/dbp/image/image.html
Insert Length: 217 Std Error: 0.00
Seq primer: -40m13 fwd. RT from Amersham.

FEATURES
source
1..289
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1000302"
/clone_id="NCI-CCAP_Prl1"
/sex="male"
/tissue_type="normal prostatic epithelial cells"
/lab_host="DH10B"
/note="Organ: prostate; Vector: pAMP10; mRNA made from
normal prostatic epithelial cells, cDNA made by oligo-dT
priming. Non-directionally cloned. Size selected on
agarose gel, average insert size 600 bp. Library made by
D. Kitzman, NIH."

BASE COUNT 121 a 36 c 66 g 66 t
ORIGIN

Query Match 6.9%; Score 137; DB 9; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.9e-25;

Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1743 AAATGATCTCGAAGCAATTTTGTGAAGACAGAACTGGAATATTTACAGATGAGAT 1802
|||||

DB 9 AAATGATCTCGAAGCAATTTTGTGAAGACAGAACTGGAATATTTACAGATGAGAT 68
|||||

QY 1803 TCTGATTCAGAAAGAAACAGATAGAGTGTGAAAAATGATTTCTGACCTTCTCT 1862
|||||

DB 69 TCTGATTCAGAAAGAAACAGATAGAGTGTGAAAAATGATTTCTGACCTTCTCT 128
|||||

QY 1863 TAGTGTGAAGAAAGAA 1879
|||||

DB 129 TAGTGTGAAGAAAGAA 145
|||||

RESULT 5
A0615477 531 bp DNA linear GSS 15-JUN-1999
LOCUS HS_5144.B1.G01.77A.RPCI-11 Human Male BAC library Homo sapiens
DEFINITION genomic clone Plate=720 Col=1 Row=N, DNA sequence.

ACCESSION A0615477
VERSION A0615477.1 GI:5076753
KEYWORDS GSS.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 531)
Mahatras G.G., Wallace J.C., Smith K., Swartzell S., Holzman T.,
Keller A., Shaker R., Furlong J., Young J., Zhao S., Adams M.D. and
Hood L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

JOURNAL Contact: Mahatras G.G., Wallace J.C., Hood L.
MEDLINE 99380589
COMMENT High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieterdejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.hsc.washington.edu
Plate: 720 row: N column: 1
Seq primer: 47
Class: BAC ends
High quality sequence stop: 531.

FEATURES
source
1..531
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=720 Col=1 Row=N"
/clone_id="RPCI-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBACe3.6; Site.1: EcoRI; Site.2: EcoRI;
Male blood DNA was isolated with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"
BASE COUNT 167 a 92 c 92 g 169 t 11 others
ORIGIN

Query Match 6.5%; Score 129; DB 17; Length 531;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;

Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 682 CATGCGACATGATCAAAATATTCACATGATGATGAAATATTCATGACATACCTATC 741
|||||

DB 117 CATGCGACATGATCAAAATATTCACATGATGATGAAATATTCATGACATACCTATC 176
|||||

QY 742 TATAATGAAGTAATTAATGAGCCAAAGCATGCTCTTATATGTCGTGATATGCAATCA 801
|||||

DB 177 TATAATGAAGTAATTAATGAGCCAAAGCATGCTCTTATATGTCGTGATATGCAATCA 236
|||||

DB 61 ACTCGGTGGAGACAGCATGTCACACTTATGTCCTTGACACAAAAGAGCAGCTCT 120
 QY 630 GATTAAGGCCGTACATGCGCAGGAAGATGATGCTTAAATGTTGCTGGAACATGCGAC 689
 DB 121 GACAAAGGCCGTACATGCGCAGGAAGATGATGCTTAAATGTTGCTGGAACATGCGAC 180
 QY 690 TGATCCAAATATTCAGATGATGATGGAATACCACTCT 728
 DB 181 TGATCCAAATATTCAGATGATGATGGAATACCACTCT 219

RESULT 8
 LOCUS BQ441373 817 bp mRNA linear EST 24-MAY-2002
 DEFINITION AGENCOURT_7907577 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:5103855
 5', mRNA sequence.
 ACCESSION BQ441373
 VERSION BQ441373.1 GI:21180449
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 817)
 NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 AUTHORS Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: csapbs@remail.nih.gov
 Tissue Procurement: CLONTECH
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (NLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L1CM2340 row: m column: 08
 High quality sequence stop: 516.
 Location/Qualifiers
 1. 817
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5103855"
 /clone_1lb="NIH_MGC_82"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
 SfiI (ggcgccctcgcc); Site_2: SfiI (ggcgccctcgcc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CAGCGCATTTATGCGC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCCGAGCGCCGACATG-dT(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size
 1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained
 inserts by PCR. This library was enriched for full-length
 clones and was constructed by Clontech Laboratories (Palo
 Alto, CA)."

BASE COUNT 274 a 183 c 189 g 170 t 1 others
 ORIGIN
 Query Match 5.9%; Score 117; DB 14; Length 817;
 Best Local Similarity 100.0%; Pred. No. 8.8e-21;
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1408 AGAATTGGCAATGATTCTGACTACAAAGAAAACAGATGCCAAATCTCTTGAA 1467
 DB 319 AGAATTGGCAATGATTCTGACTACAAAGAAAACAGATGCCAAATCTCTTGAA 378
 QY 1468 AACAGCAACCCAGAACAACTTAAGCTGACATGAGAGAGAGCTCAAGAGCTT 1524
 DB 379 AACAGCAACCCAGAACAACTTAAGCTGACATGAGAGAGAGCTCAAGAGCTT 435

RESULT 9

LOCUS A0124119 400 bp DNA linear GSS 22-SEP-1998
 DEFINITION HS_3122_A1_C07_MR CIT Approved Human Genomic Sperm Library D Homo
 sapiens genomic clone Plate=3122 Col=13 Row=E, DNA sequence.
 ACCESSION A0124119
 VERSION A0124119.1 GI:3501285
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 400)
 Mahairs, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
 Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
 Hood, L.
 Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 TITLE High Throughput Sequencing Center
 JOURNAL 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 MEDLINE Tel: (206) 616-3618
 CONTACT: Mahairs GC, Wallace JC, Hood L
 99380589 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Sequence Tagged Connector
 Plate: 3122 row: E column: 13
 Class: BAC ends
 High quality sequence stop: 400.
 Location/Qualifiers
 1. 400
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="Plate=3122 Col=13 Row=E"
 /clone_1lb="CIT Approved Human Genomic Sperm Library D"
 /sex="male"
 /note="Organ: sperm; Vector: pBel0BAC11; BAC Clones in
 E-Coli DH10B"

BASE COUNT 131 a 67 c 88 g 114 t
 ORIGIN
 Query Match 4.5%; Score 89; DB 17; Length 400;
 Best Local Similarity 100.0%; Pred. No. 2e-13;
 Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 635 AGGCCGTACAAATGCCAGAAATGATGCGCTTATGTTGCTGGAACATGCGACATGATC 694
 DB 237 AGGCCGTACAAATGCCAGAAATGATGCGCTTATGTTGCTGGAACATGCGACATGATC 296
 QY 695 CAAATATTCAGATGATGGAATATACC 723
 DB 297 CAAATATTCAGATGATGGAATATACC 325

RESULT 10
 LOCUS A0030111 399 bp DNA linear GSS 14-APR-1999
 DEFINITION RPC111-39K18.TP RPC1-11 Homo sapiens genomic clone RPC1-11-39K18,
 DNA sequence.
 ACCESSION A0030111
 VERSION A0030111.1 GI:3274075
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 399)
 Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K.,
 Golden, K., Berry, K., Granger, D., Suh, E., White, C., de Jong, P. and
 Venter, J.C.
 Use of BAC End Sequences for Sequence-Ready Map Building (1998)
 TITLE Unpublished (1998)
 JOURNAL

COMMENT Other_GSSS: RPII1-39K18.TV
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPII-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.bufileo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.bufileo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.

FEATURES
Source Location/Qualifiers
1..399
/organism="Homo sapiens"
/db_xref="GDB:7514849"
/db_xref="taxon:9606"
/clone="RPII-11-39K18"
/clone_1lb="RPII-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPII1 Human Male BAC Library"

BASE COUNT 110 a 78 c 73 g 138 t

ORIGIN
Query Match 4.3%; Score 87; DB 17; Length 399;
Best Local Similarity 100.0%; Pred. No. 6.4e-13;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1732 AGTGAACCAACAAATGCTACTCAGACCAATTTGTGCAAGACGACACTGCAATATTA 1791
|||||
Db 102 AGTGAACCAACAAATGCTACTCAGACCAATTTGTGCAAGACGACACTGCAATATTA 43
|||||

QY 1792 CACGATGAGATTCGATTCATGAGAA 1818
|||||
Db 42 CACGATGAGATTCGATTCATGAGAA 16
|||||

RESULT 11
AL703938 544 bp mRNA linear EST 22-MAR-2002
LOCUS DKEZp686E1728_r1 686 (synonym: hlc3) Homo sapiens cDNA clone
DEFINITION DKEZp686E1728 5', mRNA sequence.
ACCESSION AL703938
VERSION AL703938.1 GI:19687293
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 544)
Ottenswaelder, B., Obermaier, B., Mewes, W., Mewes, H.W., Well, B. and Wiemann, S.
EST (Ottenswaelder, B., Obermaier, B., Mewes, H.W., Well, B. and Wiemann, S.)
Unpublished (2001)
Contact: Ottenswaelder B

JOURNAL
COMMENT
MIPS
Am Kiofepitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Medigenomix (Martinsried/Germany) within the CDNA sequencing consortium of the German Genome Project. No sl sequence available.
This clone (DKFZp686E1728) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.

FEATURES
Source Location/Qualifiers
1..544
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKEZp686E1728"
/clone_1lb="686 (synonym: hlc3)"
/issue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH108"
/note="Vector: pTriplex2; Site_1: SfiI; Site_2: SfiI; cDNA-collection"

BASE COUNT 192 a 94 c 110 g 148 t

ORIGIN
Query Match 4.3%; Score 87; DB 9; Length 544;
Best Local Similarity 100.0%; Pred. No. 4.9e-13;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1081 AAGCAAAAGAGATGCTAAATCTCTTGAAGACGACATCCGAAAGACTTAAG 1140
|||||
Db 432 AAGCAAAAGAGATGCTAAATCTCTTGAAGACGACATCCGAAAGACTTAAG 491
|||||

QY 1141 CTGACATCAGAGAGAGAGTCAAGG 1167
|||||
Db 492 CTGACATCAGAGAGAGAGTCAAGG 518
|||||

RESULT 12
BI461255/c 279 bp mRNA linear EST 21-AUG-2001
LOCUS 603206584F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5272364 5',
DEFINITION mRNA sequence.
ACCESSION BI461255
VERSION BI461255.1 GI:15251911
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 279)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Miklos Palovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshinuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M1687 row: g column: 21
High quality sequence, stop: 236.
Location/Qualifiers
1..279
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5272364"
/clone_1lb="NIH_MGC_97"
/lab_host="DH108"
/note="Organ: testis; Vector: pBluescript (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI; XhoI (gtcggag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTN-3', size-selected for average insert size 2.2 kb and normalized to ROP 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NHGRI/NHGRI, National Institutes of Health). Note: this is a NIH-MGC Library."

BASE COUNT 87 a 87 c 60 g 45 t

ORIGIN

Query Match 4.0%; Score 79; DB 13; Length 279;
 Best Local Similarity 100.0%; Pred. No. 9.2e-11;
 Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGCTTGGAGTTCATTCATCCGCGCTCCTTCCTGTAAGAAGCCATTGGTCTC 60
 |||||||
 DB 84 ATGCTGCTTGGAGTTCATTCATCCGCGCTCCTTCCTGTAAGAAGCCATTGGTCTC 25
 |||||||
 QY 61 AGGAGCAAGATGGCAAGT 79
 |||||||
 DB 24 AGGAGCAAGATGGCAAGT 6

RESULT 13
 LOCUS A0063365 385 bp DNA linear GSS 31-JUL-1998
 DEFINITION C1T-HSP-2348P17.TR C1T-HSP Homo sapiens genomic clone 2348P17, DNA
 sequence.

ACCESSION A0063365
 VERSION A0063365
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
 Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuza,H.,
 Simon,M. and Venter,J.C.
 1 (bases 1 to 385)
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

TITLE
 JOURNAL Unpublished (1998)
 COMMENT Use of a random BAC End Sequence Database for Sequence-Ready Map
 Building (1998)
 Other-GSS: C1T-HSP-2348P17.TF
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdamas@tigr.org
 Clones are available from Research Genetics (Info@resgen.com). BAC
 end search page:
 http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13 Reverse
 Class: BAC ends.

FEATURES
 source
 Location/Qualifiers
 1..385
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_11b="C1T-HSP"
 /sex="Male"
 /cell_type="Sperm"
 /note="Vector: pBelBAC11; Site_1: HindIII; Site_2:
 HindIII"

BASE COUNT 118 a 53 c 79 g 135 t
 ORIGIN

Query Match 3.6%; Score 73; DB 17; Length 385;
 Best Local Similarity 100.0%; Pred. No. 2.3e-09;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1408 AGAATTGGCAATTAATTTCTGCTACAAAGAAAACAGATGCCAAATACCTTCTGAA 1467
 |||||||
 DB 189 AGAATTGGCAATTAATTTCTGCTACAAAGAAAACAGATGCCAAATACCTTCTGAA 248
 |||||||
 QY 1468 AACAGCAACCAG 1480
 |||||||
 DB 249 AACAGCAACCAG 261

RESULT 14

AG045796/c
 LOCUS AG045796 707 bp DNA linear GSS 02-NOV-2001
 DEFINITION Pan troglodytes DNA, clone: PTB-024N04.R, genomic survey sequence.
 ACCESSION AG045796
 VERSION AG045796.1 GI:16582688
 KEYWORDS GSS.

SOURCE
 ORGANISM Pan troglodytes male lymphoblast DNA, clone_11b:PTB Chimpanzee Male
 BAC library clone:PTB-024N04.R.
 Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.

REFERENCE
 AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
 1
 Totoki,Y., Watanabe,H. and Sakaki,Y.

TITLE
 JOURNAL BAC end sequences of library PTB
 UNPUBLISHED
 2 (bases 1 to 707)
 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
 Totoki,Y., Watanabe,H. and Sakaki,Y.

TITLE
 JOURNAL Submitted (02-NOV-2001) Asao Fujiyama, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Japan
 1-7-22 Suenho-cho,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:chimbases@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/
 Tel:81-45-503-9111, Fax:81-45-503-9110)
 Clones are derived from the chimpanzee BAC library PTB r115 BAC end
 was generated during the Rad process and may have higher chance of
 clone tracking errors.
 PRIMERS
 Sequencing: M13rev

LIBRARY
 Vector : pKS145
 R.Site 1 : SacI
 R.Site 2 : SacI.
 Location/Qualifiers
 1..707
 /organism="Pan troglodytes"
 /db_xref="taxon:9598"
 /clone="PTB-024N04.R"
 /sex="male"
 /cell_type="lymphoblast"
 /clone_11b="PTB Chimpanzee Male BAC library"

BASE COUNT 233 a 145 c 85 g 237 t
 ORIGIN

Query Match 2.9%; Score 59; DB 17; Length 707;
 Best Local Similarity 100.0%; Pred. No. 4.8e-06;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1911 GGAAGAAATTCATGCTAAGACTGAGCTAGACACAAATGAACATCAGACGCTAA 1969
 |||||||
 DB 226 GGAAGAAATTCATGCTAAGACTGAGCTAGACACAAATGAACATCAGACGCTAA 168
 |||||||

RESULT 15
 LOCUS B48260/c 607 bp DNA linear GSS 08-APR-1999
 DEFINITION RPII11-6K4.TV RPII-11 Homo sapiens genomic clone RPII-11-6K4, DNA
 sequence.

ACCESSION B48260
 VERSION B48260.1 GI:2600497
 KEYWORDS GSS.

SOURCE
 ORGANISM human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
 AUTHORS Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Golden
 1 (bases 1 to 607)
 'J.C., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter
 Use of BAC End Sequences for Sequence-Ready Map Building
 Unpublished (1997)
 Contact: Mark Adams

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC ends.

FEATURES
source
1..607
/organism="Homo sapiens"
/db_xref="GDB:7502163"
/db_xref="taxon:9606"
/clone="RPCI-11-6K4"
/clone_id="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"

BASE COUNT
186 a 131 c 109 g 181 t

ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 575 TGCTGACAGACGATGTCACCTATGCTTGCACACAAAGAGACAGCTCTGA 631
|||||
Db 148 TGCTGACAGACGATGTCACCTATGCTTGCACACAAAGAGACAGCTCTGA 92

RESULT 16
BF329652 380 bp mRNA linear EST 22-NOV-2000
LOCUS RC6-BN0276-160600-011-F12 BN0276 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION BF329652
VERSION BF329652.1 GI:11300400
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 380)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6&ct2=RC6-BN0276-160600-011-F12&ts=2000-06-16&tt=1>
Seq primer: puc 18 forward
High quality sequence start: 99

High quality sequence stop: 379.
FEATURES
source
1..380
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="BN0276"
/dev_stage="Adult"
/note="Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT
80 a 106 c 109 g 85 t

ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 296 GCAAGTGTGCTGCACGCTTCCCTGCTGACAGGGAGCGGACAGACAA 347
|||||
Db 202 GCAAGTGTGCTGCACGCTTCCCTGCTGACAGGGAGCGGACAGACAA 151

RESULT 17
AQ372700 592 bp DNA linear GSS 20-MAY-1999
LOCUS RPCI11-14712-TV RPCI-11 Homo sapiens genomic clone RPCI-11-14712,
DEFINITION
DNA sequence.
ACCESSION AQ372700
VERSION AQ372700.1 GI:4343723
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 592)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
Unpublished (1997)
Other GSSs: RPCI11-14712-TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeet@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.

FEATURES
source
1..592
/organism="Homo sapiens"
/db_xref="GDB:7556257"
/db_xref="taxon:9606"
/clone="RPCI-11-14712"
/clone_id="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"

BASE COUNT
199 a 87 c 99 g 207 t

ORIGIN

Query Match 2.5%; Score 50; DB 17; Length 592;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 745 AATGAAGATTAATTAATGCGCAAGACACTGCTTATATATGTCGTGATAT 794
 |||||||
 Db 153 AATGAAGATTAATTAATGCGCAAGACACTGCTTATATGTCGTGATAT 202

RESULT 18
 A0469831/ 495 bp DNA linear GSS 23-APR-1999
 LOCUS A0469831.1
 DEFINITION CITBI-EI-2588F5.TF CITBI-EI Homo sapiens genomic clone 2588F5, DNA sequence.
 ACCESSION A0469831.1 GI:4653485
 VERSION A0469831.1
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 495)
 Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
 TITLE Use of BAC End Sequences from Caltech Libraries for Sequence-Ready Map Building
 JOURNAL Unpublished (1997)
 COMMENT Other-GSS: CITBI-EI-2588F5.TF
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbeetlgr.org
 Clones are available from Research Genetics (Info@resgen.com). BAC end search page:
 http://www.tlgr.org/tldb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13-21
 Class: BAC ends.

FEATURES
 Location/Qualifiers
 1..495
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="2588F5"
 /clone_1lb="CITBI-EI"
 /sex="male"
 /cell_type="sperm"
 /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
 Caltech Human BAC Library D"
 BASE COUNT 179 a 75 c 67 g 174 t
 ORIGIN

Query Match 2.5%; Score 49; DB 17; Length 495;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1196 AGAAATGCTCTCAGAACCGAAGTAATTAAGATGCTGATAGAGAGT 1244
 |||||||
 Db 194 AGAAATGCTCTCAGAACCGAAGTAATTAAGATGCTGATAGAGAGT 146

RESULT 19
 A0469663/ 557 bp DNA linear GSS 23-APR-1999
 LOCUS A0469663.1
 DEFINITION CITBI-EI-2588M24.TF CITBI-EI Homo sapiens genomic clone 2588M24,
 DNA sequence.
 ACCESSION A0469663.1 GI:4653317
 VERSION A0469663.1
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 557)
 Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.
 TITLE Use of BAC End Sequences from Caltech Libraries for Sequence-Ready Map Building
 JOURNAL Unpublished (1997)
 COMMENT Other-GSS: CITBI-EI-2588M24.TF
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbeetlgr.org
 Clones are available from Research Genetics (Info@resgen.com). BAC end search page:
 http://www.tlgr.org/tldb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13-21
 Class: BAC ends.

FEATURES
 Location/Qualifiers
 1..557
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="2588M24"
 /clone_1lb="CITBI-EI"
 /sex="male"
 /cell_type="sperm"
 /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
 Caltech Human BAC Library D"
 BASE COUNT 201 a 83 c 74 g 199 t
 ORIGIN

Query Match 2.5%; Score 49; DB 17; Length 557;
 Best Local Similarity 100.0%; Pred. No. 0.002;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1196 AGAAATGCTCTCAGAACCGAAGTAATTAAGATGCTGATAGAGAGT 1244
 |||||||
 Db 194 AGAAATGCTCTCAGAACCGAAGTAATTAAGATGCTGATAGAGAGT 146

RESULT 20
 AG156382/ 667 bp DNA linear GSS 09-JAN-2002
 LOCUS AG156382
 DEFINITION Pan troglodytes DNA, clone: RP43-020P19.TJ, genomic survey sequence.
 ACCESSION AG156382
 VERSION AG156382.1 GI:16686060
 KEYWORDS GSS.
 SOURCE Pan troglodytes male lymphocytes DNA, clone_1lb:RPCI-43 Chimpanzee Male BAC Library clone:RP43-020P19.TJ.
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
 1
 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
 TITLE BAC end sequences of library RPCI-43
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 667)
 AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
 DIRECT SUBMISSION Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-cho,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpesgsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
 Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the Rad process and may have higher chance of clone tracking errors.

PRIMERS
Sequencing: TJ
LIBRARY
Vector : PBAC3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI
Location/Qualifiers
1.667
/organism="Pan troglodytes"
/db_xref="taxon:9588"
/clone="RP43-020P19.TJ"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
BASE COUNT 235 a 110 c 98 g 224 t
ORIGIN

Query Match 2.5%; Score 49; DB 17; Length 667;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1196 AGAAATGCTCAAGAACCAATAATAAGATGCTAGTACAGAGCT 1244
Db 212 AGAAATGCTCAAGAACCAATAATAAGATGCTAGTACAGAGCT 164
|||||

RESULT 21
A0030113/C 697 bp DNA linear GSS 14-APR-1999
DEFINITION RPCI11-39K18.TV RPCI-11 Homo sapiens genomic clone RPCI-11-39K18,
DNA sequence.
ACCESSION A0030113
VERSION A0030113.1 GI:3274077
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (Bases 1 to 697)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.F., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
Venter,U.C.
USE OF BAC End Sequences for Sequence-Ready Map Building (1998)
JOURNAL
COMMENT
Other-GSS: RPCI11-39K18.TP
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@ejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from
Research Genetics (inforesgen.com). BAC end search page:
http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1.697
/organism="Homo sapiens"
/db_xref="GDB:751484"
/db_xref="taxon:9606"
/clone="RPCI-11-39K18"
/clone_lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: PBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
BASE COUNT 253 a 120 c 101 g 222 t 1 others
ORIGIN

Query Match 2.5%; Score 49; DB 17; Length 697;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1196 AGAAATGCTCAAGAACCAATAATAAGATGCTAGTACAGAGCT 1244
Db 167 AGAAATGCTCAAGAACCAATAATAAGATGCTAGTACAGAGCT 119
|||||

RESULT 22
BE069869 187 bp mRNA linear EST 09-JUN-2000
LOCUS CML-BT0397-201299-073-a1 BT0397 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION BE069869
VERSION BE069869.1 GI:8414519
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (Bases 1 to 187)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.R., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
JOURNAL
MEDLINE
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et=CML-BT0397-201299-073-a1&tl=1999-12-20&tl=1>)
Seq primer: puc 18 forward
High quality sequence start: 82
High quality sequence stop: 141.
Location/Qualifiers
1.187
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT0397"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 66 a 45 c 34 g 42 t
ORIGIN

Query Match 2.4%; Score 47; DB 10; Length 187;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 790 GATATCGATCAAAAACCAACATGCGCTCACACACTGTACTTGG 836
Db 91 GATATCGATCAAAAACCAACATGCGCTCACACACTGTACTTGG 137
|||||

RESULT 23

A0057106 400 bp DNA linear GSS 30-JUL-1998
 LOCUS CIT-HSP-2335J19.TF CIT-HSP Homo sapiens genomic clone 2335J19, DNA
 DEFINITION sequence.
 ACCESSION A0057106
 VERSION A0057106.1 GI:3353632
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 400)
 Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Baas,S., Linher,K.,
 Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
 Simon,M. and Venter,J.C.
 Use of a random BAC End Sequence Database for Sequence-Ready Map
 Building (1998)
 TITLE Unpublished (1998)
 JOURNAL Other_GSSs: CIT-HSP-2335J19.TF
 COMMENT Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdamas@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
 http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
 Seq primer: M13-21
 Class: BAC ends.

FEATURES
 source
 1..400
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="2335J19"
 /clone_1lb="CIT-HSP"
 /sex="Male"
 /cell_type="Sperm"
 /note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
 HindIII"

BASE COUNT 124 a 61 c 83 g 132 t
 ORIGIN

Query Match 2.3%; Score 46; DB 17; Length 400;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1056 AATTGCCAGTACTTCTGACTACAAAGAAAACAGATGCTAAAA 1101
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 219 AATTGCCAGTACTTCTGACTACAAAGAAAACAGATGCTAAAA 264

RESULT 24
 BF675049 894 bp mRNA linear EST 21-DEC-2000
 LOCUS 602136643P1 NIH_MGC_83 Homo sapiens CDNA clone IMAGE:4273139 5',
 DEFINITION mRNA sequence.
 ACCESSION BF675049
 VERSION BF675049.1 GI:11948944
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 894)
 NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CLONETECH Laboratories, Inc.
 CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM1088 row: e column: 12
 High quality sequence start: 6
 High quality sequence stop: 576.

FEATURES
 source
 1..894
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4273139"
 /clone_1lb="NIH_MGC_83"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
 Site_1: SfiI (ggcgccctcgcc); Site_2: SfiI (ggccatctggcc
); 5' and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor
 sequence: 5'-ATCTAGAGCGCGCGCGCCGACATG-dT(30)BN-3'
 (where B = A, C, or G and N = A, C, G, or T). Average
 insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA)."

BASE COUNT 239 a 186 c 208 g 261 t
 ORIGIN

Query Match 2.2%; Score 45; DB 12; Length 894;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 651 GGAAGATGATGCGCTTATGTTGCTGGAACATGCACATGATCC 695
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 46 GGAAGATGATGCGCTTATGTTGCTGGAACATGCACATGATCC 90

RESULT 25
 A0360298 460 bp DNA linear GSS 06-MAR-1999
 LOCUS HS_5035_A2_C08_SPEE RPC111 Human Male BAC Library Homo sapiens
 DEFINITION genomic clone Plate-611 Col-16 Row-E, DNA sequence.
 ACCESSION A0360298
 VERSION A0360298.1 GI:4209174
 KEYWORDS GSS.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 460)
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
 Hood,L.
 Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 TITLE High Throughput Sequencing Center
 JOURNAL University of Washington
 MEDLINE 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 COMMENT Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: http://www.htsc.washington.edu
 Plate: 611 row: E column: 16
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 460.

FEATURES
 source
 1..460
 /organism="Homo sapiens"

```

/db_xref="taxon:9606"
/clone="Plate-611 Col-16 Row-E"
/clone_lib="RPC11 Human Male BAC Library"
/sex="male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; RPC11 Human Male BAC Library"
BASE COUNT      144 a      79 c      95 g      141 t      1 others
ORIGIN

Query Match      2.1%; Score 41; DB 17; Length 460;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1672 AGAAGAGACAGACACCTGAAAGCCAGCAATTCCTGACACTGA 1715
|||||
Db 335 AGAAGAGACAGACACCTGAAAGCCAGCAATTCCTGACACTGA 378

RESULT 26
AQ392059/c      476 bp      DNA      linear      GSS 06-MAR-1999
LOCUS
DEFINITION      CITR1-E1.2555J3.TR CITR1-E1 Homo sapiens genomic clone 2555J3, DNA
sequence.
ACCESSION      AQ392059
VERSION      AQ392059.1 GI:4363082
KEYWORDS      GSS.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 476)
AUTHORS      Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.
TITLE      Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
Map Building
JOURNAL      Unpublished (1997)
COMMENT      Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
FEATURES
source
1..476
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2555J3"
/clone_lib="CITR1-E1"
/sex="male"
/cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"
BASE COUNT      170 a      75 c      65 g      166 t
ORIGIN

Query Match      2.1%; Score 41; DB 17; Length 476;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1204 TTCGACAGACAGAAATTAATAGCATGTCATAGAGAGGT 1244
|||||
Db 201 TTCGACAGACAGAAATTAATAGCATGTCATAGAGAGGT 161

RESULT 27
AG165908
LOCUS      AG165908      710 bp      DNA      linear      GSS 09-JAN-2002

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```

DEFINITION      Pan troglodytes DNA, clone: RP43-033106.TJ, genomic survey
sequence.
ACCESSION      AG165908
VERSION      AG165908.1 GI:16695586
KEYWORDS      GSS.
SOURCE      Pan troglodytes male lymphocytes DNA, clone_lib:RPC1-43 Chimpanzee
Male BAC Library clone:RP43-033106.TJ.
ORGANISM      Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE      1
AUTHORS      Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totochi,Y., Watanabe,H. and Sakaki,Y.
TITLE      BAC end sequences of library RPC1-43
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 710)
AUTHORS      Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totochi,Y., Watanabe,H. and Sakaki,Y.
TITLE      Direct Submission
JOURNAL      Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-cho,Tsukumi-Ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT      Clones are derived from the chimpanzee BAC library RPC1-43 This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: TJ
LIBRARY
Vector : pBAC3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
FEATURES
source
1..710
location/Qualifiers
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-033106.TJ"
/sex="male"
/cell_type="Lymphocytes"
/clone_lib="RPC1-43 Chimpanzee Male BAC Library"
BASE COUNT      218 a      121 c      111 g      258 t      2 others
ORIGIN

Query Match      2.1%; Score 41; DB 17; Length 710;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 754 AAATTATGCCAAGACACCTCTTATATGTCGTGATAT 794
|||||
Db 221 AAATTATGCCAAGACACCTCTTATATGTCGTGATAT 261

RESULT 28
AM302924      184 bp      mRNA      linear      EST 18-JAN-2000
LOCUS      x186907.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2767068 3',
DEFINITION      mRNA sequence.
ACCESSION      AM302924
VERSION      AM302924.1 GI:6712604
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 184)
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL      Unpublished (1997)
COMMENT      Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
cDNA Library Preparation: David B. Kitzman, Ph.D.

```

cDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: -400p from Gibco
High quality sequence stop: 136.

FEATURES

Location/Qualifiers

1..184

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2767068"

/clone_lib="NCI-CGAP_Lu26"

/tissue_type="invasive adenocarcinoma"

/dev_stage="adult"

/lab_host="DH10B"

/note="Organ: lung; Vector: PAMPI; mRNA made from lung
adenocarcinoma tissue, cDNA made by oligo-dT priming.
directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."

BASE COUNT 92 a 35 c 33 g 24 t

ORIGIN

Query Match

2.0%; Score 40; DB 10; Length 184;

Best Local Similarity 100.0%; Pred. No. 0.98;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1961 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 2000

Db 111 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 150

RESULT 29
AM302925 199 bp mRNA linear EST 18-JAN-2000
LOCUS xrb6g08.x1 NCI-CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2767070 3',
DEFINITION mRNA sequence.
ACCESSION AM302925
VERSION AM302925.1 GI:6712605
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 199)
NCI-CGAP http://www.ncbi.nlm.nih.gov/nclogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: -400p from Gibco.

FEATURES

Location/Qualifiers

1..199

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2767070"

/clone_lib="NCI-CGAP_Lu26"

/tissue_type="invasive adenocarcinoma"

/dev_stage="adult"

/lab_host="DH10B"

/note="Organ: lung; Vector: PAMPI; mRNA made from lung
adenocarcinoma tissue, cDNA made by oligo-dT priming.
directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."

FEATURES

Location/Qualifiers

1..199

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2767070"

/clone_lib="NCI-CGAP_Lu26"

/tissue_type="invasive adenocarcinoma"

/dev_stage="adult"

/note="Organ: lung; Vector: PAMPI; mRNA made from lung
adenocarcinoma tissue, cDNA made by oligo-dT priming.
directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."

BASE COUNT 93 a 38 c 40 g 28 t

ORIGIN

Query Match

2.0%; Score 40; DB 10; Length 199;

Best Local Similarity 100.0%; Pred. No. 0.92;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1961 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 2000

Db 111 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 150

RESULT 30
AI344928 224 bp mRNA linear EST 30-DEC-1998
LOCUS tb01a04.x1 NCI-CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2052270 3',
DEFINITION mRNA sequence.
ACCESSION AI344928
VERSION AI344928.1 GI:4082134
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 224)
NCI-CGAP http://www.ncbi.nlm.nih.gov/nclogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: -400p from Gibco.

FEATURES

Location/Qualifiers

1..224

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2052270"

/clone_lib="NCI-CGAP_Lu26"

/tissue_type="invasive adenocarcinoma"

/dev_stage="adult"

/lab_host="DH10B"

/note="Organ: lung; Vector: PAMPI; mRNA made from lung
adenocarcinoma tissue, cDNA made by oligo-dT priming.
directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."

BASE COUNT 119 a 40 c 36 g 29 t

ORIGIN

Query Match

2.0%; Score 40; DB 9; Length 224;

Best Local Similarity 100.0%; Pred. No. 0.83;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1961 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 2000

Db 128 GCCAGCTAAAAAAAAAAAAAAAAAAAAA 167

RESULT 31
AI336592 232 bp mRNA linear EST 16-FEB-1999
LOCUS ta94d12.x1 NCI-CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2051735 3',
DEFINITION mRNA sequence.
ACCESSION AI336592
VERSION AI336592.1 GI:4073519
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 232)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.E. Consortium, LNL
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.gov/bdrp/image/image.html
Insert length: 302 Std Error: 0.00
Seq primer: -40UP from GIBCO
High quality sequence stop: 225.
Location/Qualifiers
1. .232
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2051735"
/clone_id="NCI_CGAP_Lu26"
/tissue_type="invasive adenocarcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: Lung; Vector: pAMP1; mRNA made from lung
adenocarcinoma tissue, CDNA made by oligo-dT priming.
Directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."

BASE COUNT 119 a 44 c 40 g 29 t
ORIGIN

Query Match 2.0%; Score 40; DB 9; Length 232;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1961 GCCAGCTAAAAA 2000
|||||
Db 134 GCCAGCTAAAAA 173

RESULT 32
AI344933 239 bp mRNA linear EST 16-FEB-1999
LOCUS t010a11.x1 NCI_CGAP_Lu26 Homo sapiens CDNA clone IMAGE:2052284 3',
DEFINITION mRNA sequence.
ACCESSION AI344933
VERSION AI344933.1 GI:4082139
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 239)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.E. Consortium, LNL
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.gov/bdrp/image/image.html
Insert length: 291 Std Error: 0.00
Seq primer: -40UP from GIBCO.
Location/Qualifiers

FEATURES

source
1. .239
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2052284"
/clone_id="NCI_CGAP_Lu26"
/tissue_type="invasive adenocarcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: Lung; Vector: pAMP1; mRNA made from lung
adenocarcinoma tissue, CDNA made by oligo-dT priming.
Directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."

BASE COUNT 119 a 48 c 40 g 32 t
ORIGIN

Query Match 2.0%; Score 40; DB 9; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1961 GCCAGCTAAAAA 2000
|||||
Db 146 GCCAGCTAAAAA 185

RESULT 33
AI344936 239 bp mRNA linear EST 30-DEC-1998
LOCUS t010b03.x1 NCI_CGAP_Lu26 Homo sapiens CDNA clone IMAGE:2052269 3',
DEFINITION mRNA sequence.
ACCESSION AI344936
VERSION AI344936.1 GI:4082142
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 239)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: I.M.A.G.E. Consortium, LNL
DNA Sequencing by: Washington University Genome Sequencing Center
clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.gov/bdrp/image/image.html
Seq primer: -40UP from GIBCO.
Location/Qualifiers
1. .239
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2052269"
/clone_id="NCI_CGAP_Lu26"
/tissue_type="invasive adenocarcinoma"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: Lung; Vector: pAMP1; mRNA made from lung
adenocarcinoma tissue, CDNA made by oligo-dT priming.
Directionally cloned. Size-selected on agarose gel,
average insert size 500 bp. Primary library,
non-amplified."

BASE COUNT 119 a 48 c 40 g 32 t
ORIGIN

Query Match 2.0%; Score 40; DB 9; Length 239;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1961 GCCAGCTAAAAA 2000

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Db      146  GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 185
RESULT 34
LOCUS   A1335449          250 bp  mRNA  linear  EST 29-DEC-1998
DEFINITION  lb9f03.x1 NCI_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2060573 3',
            mRNA sequence.
ACCESSION A1335449
VERSION   A1335449.1  GI:4072376
KEYWORDS
SOURCE    human.
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 250)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
JOURNAL   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            CDNA Library Preparation: David B. Krizman, Ph.D.
            CDNA Library Arrayed by: I.M.A.G.E. Consortium, LNL.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            www.bio.lnl.gov/bbrp/image/image.html
            Seq primer: -400P from Gibco
            High quality sequence stop: 240.
FEATURES
source    Location/Qualifiers
            1..250
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:2060573"
            /clone_1lb="NCI_CGAP_Lu26"
            /tissue_type="invasive adenocarcinoma"
            /dev_stage="adult"
            /lab_host="DH10B"
            /note="Organ: Lung; Vector: PAMPI; mRNA made from lung
            adenocarcinoma tissue; CDNA made by oligo-dr priming.
            Directionally cloned. Size-selected on agarose gel,
            average insert size 500 bp. Primary library,
            non-amplified."
BASE COUNT 136 a 43 c 41 g 30 t
ORIGIN
Query Match      2.0%; Score 40; DB 9; Length 250;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1961 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 134 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 173
RESULT 35
LOCUS   A1494279          360 bp  mRNA  linear  EST 17-MAR-1999
DEFINITION  qy98c11.x1 NCI_CGAP_Brn25 Homo sapiens CDNA clone IMAGE:2020052 3',
            similar to WP:B0432.3 CE07741 ;, mRNA sequence.
ACCESSION A1494279
VERSION   A1494279.1  GI:4395282
KEYWORDS
SOURCE    human.
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 360)
AUTHORS   NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project

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JOURNAL   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
            Ph.D.
            CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            CDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            www.bio.lnl.gov/bbrp/image/image.html
            Insert length: 645  Std Error: 0.00
            Seq primer: -400P from Gibco
            High quality sequence stop: 318.
FEATURES
source    Location/Qualifiers
            1..360
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:2020052"
            /clone_1lb="NCI_CGAP_Brn25"
            /tissue_type="anaplastic oligodendroglioma"
            /lab_host="DH10B"
            /note="Organ: brain; Vector: pRT73D-Pac (Pharmacia) with a
            modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
            strand CDNA was primed with a Not I - oligo(dT) primer (5'
            TGTATACCAATCTGAAGTGGAGCGCCGACCAAGCTTTTCTTTTCTTTT
            T 3'); double-stranded CDNA was ligated to Eco RI
            adaptors (Pharmacia), digested with Not I and cloned into
            the Not I and Eco RI sites of the modified pRT73 vector.
            Library is normalized, and was constructed by Bento
            Soares and M.Fatima Bonaldo."
BASE COUNT 69 a 84 c 97 g 110 t
ORIGIN
Query Match      2.0%; Score 40; DB 9; Length 360;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1961 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 41 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2
RESULT 36
LOCUS   AA766864          367 bp  mRNA  linear  EST 18-MAR-1998
DEFINITION  oc87g12.s1 NCI_CGAP_GCB1 Homo sapiens CDNA clone IMAGE:1356742 3',
            similar to TR:P90993 P90993 CODED FOR BY C. ELEGANS CDNA YK187H7.5.
            ;, mRNA sequence.
ACCESSION AA766864
VERSION   AA766864.1  GI:2818102
KEYWORDS
SOURCE    human.
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 367)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
JOURNAL   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
            Ph.D., Gerald Marti, M.D.
            CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            CDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:

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www.bio.lnl.gov/brp/image/image.html
 Insert Length: 626 Std Error: 0.00
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 218.
 Location/Qualifiers

FEATURES

Source

1.367

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1356742"
 /clone_1lb="NCI CGAP GCBI"
 /tissue_type="germinal center B cell"
 /lab_host="DH10B"
 /note="Vector: pRT3D-Pac (Pharmacia) with a modified
 polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
 was prepared from human tonsillar cells enriched for
 germinal center B cells by flow sorting (CD20+, 19D-),
 provided by Dr. Gerald Marti (CBER). cDNA synthesis was
 primed with a Not I - Oligo(dT) primer
 [5'-TGTTCACATCTGAAGTGGAGCGCGCCCTCATTTTTTTTTTTT-3',
]. Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pRT3 vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonafido."

BASE COUNT

61 a 88 c 106 g 111 t
 1 others

Query Match 2.0%; Score 40; DB 9; Length 367;
 Best Local Similarity 100.0%; Pred. No. 0.54;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1961 GCCAGCTAAAAA
 Db 51 GCCAGCTAAAAA
 12

RESULT 37
 BQ230307
 LOCUS
 DEFINITION
 AGENCOUNT_7567202 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6060433
 5', mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 human.
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC http://mgs.nci.nih.gov/
 1 (bases 1 to 421)
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: DCTD/DTF/Gazdar
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LLM13138 row: 1 column: 02
 High quality sequence stop: 420.
 Location/Qualifiers

FEATURES

Source

1.421

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6060433"
 /clone_1lb="NIH MGC 68"
 /tissue_type="large cell carcinoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: lung; Vector: PCMV-SPORT6; site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.8 kb. Library constructed by Life
 Technologies.
 BASE COUNT 155 a 106 c 99 g 61 t
 ORIGIN

Query Match 2.0%; Score 40; DB 14; Length 421;
 Best Local Similarity 100.0%; Pred. No. 0.48;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1961 GCCAGCTAAAAA
 Db 323 GCCAGCTAAAAA
 362

RESULT 38
 BQ127207
 LOCUS
 DEFINITION
 BQ127207 442 bp mRNA linear EST 19-APR-2002
 1157607.y1 Melton Normalized Mixed Mouse Pancreas 1 NI-MSI Mus
 musculus cDNA clone IMAGE:5945796 5' similar to TR:088306 O88306
 DJ-1.; mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus
 house mouse.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 442)
 Melton, D., Brown, J., Kenty, G., Pernutt, A., Lee, C., Kaestner, K.,
 Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
 Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Bilstain, A.,
 Schmitt, A., Theising, B., Rittler, E., Ronko, I., Bennett, J., Cardenas
 M., Gibbons, M., McCann, R., Cole, R., Tsagaris, V., Williams, T.,
 Jackson, Y., and Bowers, Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohpc.harvard.edu
 Library was constructed by Dr. Douglas Melton DNA sequencing by:
 Washington University Genome Sequencing Center This clone is
 available royalty-free through LNL. Please contact the IMAGE
 Consortium (info@image.lnl.gov) for further information
 Putative full length read
 vector to vector length is 443
 Seq primer: -40RP from Gibco.
 Location/Qualifiers

FEATURES

Source

1.442

/organism="Mus musculus"
 /strain="ICR"
 /db_xref="taxon:10090"
 /clone="IMAGE:5945796"
 /clone_1lb="Melton Normalized Mixed Mouse Pancreas 1
 NI-MSI"
 /sex="Both for embryonic & newborn, male for adult and
 adult islet"
 /dev_stage="Embryonic day 10.5, E12.5, E16.5, newborn,
 adult, mixed"
 /lab_host="DH10B"
 /note="Vector: pSPORT1. Site_1: Not I; Site_2: Sal I. Five
 libraries representing E10.5/12.5 pancreatic bud, E16.5
 pancreas, newborn pancreas, adult pancreas, and adult
 islets of langerhans were separately constructed using
 Superscript Plasmid library kit (Life Technologies). cDNA
 was made by oligo-dT priming and size-selected by column
 fractionation. Libraries were amplified once on solid
 support and plasmid DNA from each library was prepared

and mixed in equal amounts. The mixed library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded mixed library plasmid DNA was mixed with 5 micrograms PCR product representing mixed library inserts and hybridized to an Ecot of 6. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."

BASE COUNT 137 a 113 c 115 g 77 t

Query Match 2.0%; Score 40; DB 14; Length 442;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1961 GCCAGCTAAAAA
DB 402 GCCAGCTAAAAA

RESULT 39
LOCUS B55862 503 bp DNA linear GSS 20-JUN-1998
DEFINITION CIT-HSP-2005F16.TF CIT-HSP Homo sapiens genomic clone 2005F16, DNA sequence.
ACCESSION B55862
VERSION B55862.1 GI:2610196
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 503)
AUTHORS Adams M.D., Rounsley S.D., Field C.E., Bass S., Linher K., Golden K., Berry K., Granger D., Sun E., Wible C., Shizuya H., Simon M. and Venter J.C.
TITLE Use of a random BAC End Sequence Database for sequence-Ready Map Building
JOURNAL Unpublished (1997)
COMMENT Other-GSS: CIT-HSP-2005F16.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdamad@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21
Class: BAC ends.

FEATURES
source Location/Qualifiers
1..503
/organism="Homo sapiens"
/db_xref="GDB:7039242"
/db_xref="taxon:9606"
/clone="2005F16"
/clone_11b="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelobAC11; Site_1: HindIII; Site_2: HindIII"

BASE COUNT 152 a 116 c 87 g 148 t

Query Match 2.0%; Score 40; DB 17; Length 503;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1087 AACGAGATGCTAAATCTCTTCTGAAACAGCAATCCAG 1126
DB 502 AACGAGATGCTAAATCTCTTCTGAAACAGCAATCCAG 463

RESULT 40
LOCUS BF968779 560 bp mRNA linear EST 22-JAN-2001
DEFINITION 602270486F1 NIH-MGC_84 Homo sapiens cDNA clone IMAGE:4358564 5', mRNA sequence.
ACCESSION BF968779
VERSION BF968779.1 GI:12335994
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 560)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rcmail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM9996 row 1 column: 21
High quality sequence stop: 155.

FEATURES
source Location/Qualifiers
1..560
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4358564"
/clone_11b="NIH-MGC_84"
/tissue_type="adrenal cortex carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo dT primed. Average insert size 1.229 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH-MGC Library."

BASE COUNT 261 a 64 c 112 g 123 t

Query Match 2.0%; Score 40; DB 12; Length 560;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 40; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1961 GCCAGCTAAAAA
DB 57 GCCAGCTAAAAA

RESULT 41
LOCUS BG491207 616 bp mRNA linear EST 27-MAR-2001
DEFINITION 60235247F1 NIH-MGC_41 Homo sapiens cDNA clone IMAGE:4654258 5', mRNA sequence.
ACCESSION BG491207
VERSION BG491207.1 GI:13452719
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 616)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rcmail.nih.gov
Tissue Procurement: DCTD/DRP

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINTL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINTL at:
<http://image.llnl.gov>
Plate: L10M1441 row: m column: 11
High quality sequence size: 587.

BASE COUNT	142 a	175 c	206 g	93 t
ORIGIN				

Query Match	2.0%;	Score 40;	DB 12;	Length 616;
Best Local Similarity	100.0%;	Pred. No. 0.35;		
Matches 40;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Qy 1961 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
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Db 537 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 576
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RESULT 42					
BI915244					
LOCUS	BI915244	831 bp	mRNA	linear	EST 16-OCT-2001
DEFINITION	603184781P1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5248436 5', mRNA sequence.				

FEATURES	Location/Qualifiers
source	1. .831

and male age 26 weeks. Library is ϕ 109-8T primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note this is a NIH-MGC Library.*

245 c	245 g	94 t
-------	-------	------

BASE COUNT	247	a	245	c	245	g	94	t
ORIGIN								
Query Match	2.0%;		Score 40;	DB 13;	Length 831;			
Best Local Similarity	100.0%;		Pred. No. 0.27;					
Matches	40;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps 0.
Oy	1961	GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA						2000
Dd	485	GCCACGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA						524
<hr/>								
RESULT 43								
BIR22692	BIR22692		1018 bp		mRNA	linear		EST 04-OCT-2001
LOCUS	603036027P1 NIH_MGC_115		Homo sapiens		cdna clone IMAGE:5177071	5',		
DEFINITION	mRNA sequence.							
ACCESSION	BIR22692							
VERSION	BIR22692.1		GI:15934242					

REFERENCE 1 (bases 1 to 1018)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Ge

Email: c9apb3-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: L14M11441 row: e column: 08
High quality sequence stop: 603.

BASE COUNT	361 a	242 c	286 g	129 t
ORIGIN				

[illegible]

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Qy 1961 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
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Db 542 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 581

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RESULT 44
BM919526      1024 bp      mRNA      linear      EST 12-MAR-2002
LOCUS         AGENCOURT.6761896 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5748822
DEFINITION    5', mRNA sequence.
ACCESSION     BM919526
VERSION       BM919526.1 GI:19369905
KEYWORDS      EST.
SOURCE        human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 1024)
AUTHORS       NIH-MGC http://mgc.nci.nih.gov/.
TITLE         National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished (1999)
COMMENT       Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               Tissue Procurement: Life Technologies, Inc.
               cDNA Library Preparation: Life Technologies, Inc.
               cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Agencourt Bioscience Corporation
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
               Plate: LLAM12777 row: d column: 07
               High quality sequence stop: 606.
               Location/Qualifiers
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                   /clone_image="5748822"
                   /clone_lib="NIH_MGC_120"
                   /lab_host="DH10B"
                   /note="Organ: pooled pancreas and spleen; Vector:
                   PCMV-SPORT6; Site_1: Not; Site_2: EcoRV (destroyed); RNA
                   source anonymous pool of spleen and pancreas from 28 yo
                   male. Library is oligo-dT primed and directionally cloned
                   (EcoRV site is destroyed upon cloning). Average insert
                   size 1.5 kb, insert size range 1-2.5 kb. Library is
                   normalized and enriched for full-length clones and was
                   constructed by C. Gruber (Invitrogen). Research Genetics
                   tracking code 025. Note: this is a NIH_MGC Library."
BASE COUNT    290 a      262 c      305 g      161 t      6 others
ORIGIN
Query Match      2.0%; Score 40; DB 14; Length 1024;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1961 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 577 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 616

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JOURNAL        Unpublished (1997)
COMMENT        Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               cDNA Library Preparation: David B. Kitzman, Ph.D.
               cDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL
               DNA Sequencing by: Washington University Genome Sequencing Center
               Clone distribution: NCI-CGAP clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               www-bio.llnl.gov/dbp/image/image.html
               Seq primer: 40up from Gibco.
FEATURES
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    1..160
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      /db_xref="taxon:9606"
      /clone_image="1996637"
      /clone_lib="NCI-CGAP_Ov33"
      /sex="female"
      /tissue_type="borderline ovarian carcinoma"
      /dev_stage="adult"
      /lab_host="DH10B"
      /note="Organ: ovary; Vector: pAMP1; mRNA made from
      borderline ovarian carcinoma, cDNA made by oligo-dT
      priming. Directionally cloned. Size-selected on agarose
      gel, average insert size 500 bp. Primary library,
      non-amplified."
BASE COUNT      59 a      38 c      35 g      26 t      2 others
ORIGIN
Query Match      1.9%; Score 39; DB 9; Length 160;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1961 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1999
Db 111 GCCAGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 149

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Search completed: November 8, 2002, 13:32:45
 Job time : 2546.85 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2002, 13:01:09 ; Search time 88.8713 Seconds
(without alignments)
8143.939 Million cell updates/sec

Title: US-09-924-400-303
Perfect score: 2040
Sequence: 1 atgtgtgttgatgttgc.....aaaaaaaaaaaaaaaaa 2040

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 320260 seqs, 177392727 residues

Word size: 15

Total number of hits satisfying chosen parameters: 20466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

Published Applications_NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCr_NEM_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEM_PUB.seq:*
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- 11: /cgn2_6/ptodata/1/pubpna/US10_NEM_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEM_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2040	100.0	2040	10	US-09-825-301-7
2	2040	100.0	2040	10	US-09-759-143-375
3	2040	100.0	2040	10	US-09-780-669-375
4	2040	100.0	2040	10	US-09-810-936-303
5	2040	100.0	2040	10	US-09-822-827-375
6	2040	100.0	2040	10	US-09-429-755-303
7	1551	76.0	2000	10	US-09-825-301-6
8	1551	76.0	2000	10	US-09-759-143-374
9	1551	76.0	2000	10	US-09-780-669-374
10	1551	76.0	2000	10	US-09-810-936-302
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13	1128	55.3	1155	10	US-09-825-301-5
14	1128	55.3	1155	10	US-09-759-143-373
15	1128	55.3	1155	10	US-09-780-669-373
16	1128	55.3	1155	10	US-09-810-936-301
17	1128	55.3	1155	10	US-09-822-827-373
18	1128	55.3	1155	10	US-09-429-755-301
19	1044	51.2	1590	10	US-09-810-936-323

20	975	47.8	1155	10	US-09-810-936-328	Sequence 328, App
21	491	24.1	1512	10	US-09-759-143-368	Sequence 368, App
22	491	24.1	1512	10	US-09-780-669-368	Sequence 368, App
23	491	24.1	1512	10	US-09-810-936-294	Sequence 294, App
24	491	24.1	1512	10	US-09-822-827-368	Sequence 368, App
25	491	24.1	1512	10	US-09-429-755-294	Sequence 294, App
26	491	24.1	1512	10	US-09-759-143-369	Sequence 369, App
27	252	12.4	1853	10	US-09-780-669-369	Sequence 369, App
28	252	12.4	1853	10	US-09-810-936-295	Sequence 295, App
29	252	12.4	1853	10	US-09-822-827-369	Sequence 369, App
30	252	12.4	1853	10	US-09-429-755-295	Sequence 295, App
31	120	5.9	879	10	US-09-759-143-531	Sequence 531, App
32	120	5.9	879	10	US-09-780-669-531	Sequence 531, App
33	120	5.9	879	10	US-09-810-936-531	Sequence 531, App
34	120	5.9	879	10	US-09-822-827-531	Sequence 531, App
35	120	5.9	879	10	US-09-429-755-531	Sequence 531, App
36	120	5.9	1059	10	US-09-759-143-372	Sequence 372, App
37	120	5.9	1059	10	US-09-780-669-372	Sequence 372, App
38	120	5.9	1059	10	US-09-810-936-298	Sequence 298, App
39	120	5.9	1059	10	US-09-822-827-372	Sequence 372, App
40	120	5.9	1059	10	US-09-429-755-298	Sequence 298, App
41	120	5.9	1851	10	US-09-825-301-1	Sequence 1, App11
42	120	5.9	1851	10	US-09-759-143-366	Sequence 366, App
43	120	5.9	1851	10	US-09-780-669-366	Sequence 366, App
44	120	5.9	1851	10	US-09-810-936-291	Sequence 291, App
45	120	5.9	1851	10	US-09-810-936-292	Sequence 292, App

ALIGNMENTS

RESULT 1
US-09-825-301-7
Sequence 7, Application US/09825301
Patent No. US2002009738A1
GENERAL INFORMATION:
APPLICANT: Houghton, Raymond L.
APPLICANT: Dillon, David C.
APPLICANT: Molesh, David A.
APPLICANT: Xu, Jiangchun
APPLICANT: Zehentner, Barbara
APPLICANT: Persing, David H.
TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
OF INVENTION: AND MONITORING OF BREAST CANCER
FILE REFERENCE: 210121.513
CURRENT APPLICATION NUMBER: US/09/825,301
CURRENT FILING DATE: 2001-04-02
NUMBER OF SEQ ID NOS: 77
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-825-301-7

Query Match	100.0%	Score 2040:	DB 10:	Length 2040:
Best Local Similarity	100.0%	Pred. No. 0:		
Matches 2040:	Conservative	0:	Mismatches	0:
			Indels	0:
			Gaps	0:

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DB 1 ATGTGTGTGAGTGTGATTCATGCGGCTGCTTCTGTGAAGACCATTTGCTC 60
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DB 61 AGGACCAAGATGGCAAGTGTGCTGCGTTCCTCCCTGCTGCAAGGAGCGCAAG 120
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DB 121 AGCAACGTGGGACCTTGTGAGACCAACGACTGTGATGAACACTGAGGACAA 180
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OY 181 ATGGCAAGTGTGCGGCACTGCTTCCCTCAGAGGAGTGGCAAGCAAGCTG 240
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Db 181 ATGGGCAAGTGTGCGCCACCTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACGTG 240
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Db 241 GGGCTTCTTGAGAGCAGCAGACTGCTGATGAGACACTCAGAAACAAGATGGGCAAG 300
QY 301 TGGTGTGCTGCTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGTGGCGCTTGG 360
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Db 361 GGGAGCTAGATGACAGTGTCTCATGAGGCCAGGTACAGCTCCGTGGAGAGAGATCTG 420
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Db 421 GACAGCTCCACAGAGCTGCTGCTGGGTAAAGTCCCGAGAAAGATCTCATGCTATG 480
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Db 481 CTCAGGAGACACTGAGCTGAACAAAGAGACCAAAAGAGACTGCTTACATCTGGCC 540
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Db 541 TCTGCCAATGGGAATTCAGAGTAGTAAACCTGCTGAGACAGAGATGCTCAACTTAAT 600
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QY 721 AACACCTGACAGCTGATCTATATGAGATGAAATTAATGAGCAAGAGACGCTCTTA 780
Db 721 AACACCTGACAGCTGATCTATATGAGATGAAATTAATGAGCAAGAGACGCTCTTA 780
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Db 1621 GAATGAGAGAGCAGGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
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Db 1741 CAGCAATTTCTGACACTGAGATGAGAGATATCACAGTACCAACAAATGATACTCAG 1800
QY 1801 AAGCAATTTTGTAGAGAACGAGACACTGGAATTTACAGATGAGATTTGATTCATGAA 1860
Db 1801 AAGCAATTTTGTAGAGAACGAGACACTGGAATTTACAGATGAGATTTGATTCATGAA 1860
QY 1861 GAAAGCAGATGAGAGTGTGAAAAATGATTTGAGCTTCTCTTACTTGTAAAGAA 1920
Db 1861 GAAAGCAGATGAGAGTGTGAAAAATGATTTGAGCTTCTCTTACTTGTAAAGAA 1920
QY 1921 GAAAAAGCAATCTTGCATGAAAAATGATGATGATGATGATGATGATGATGATGATG 1980
Db 1921 GAAAAAGCAATCTTGCATGAAAAATGATGATGATGATGATGATGATGATGATGATG 1980
QY 1981 GAGCTAGACACATGAAACATCAGAGCAGCTTAAAAATGATGATGATGATGATGATG 2040
Db 1981 GAGCTAGACACATGAAACATCAGAGCAGCTTAAAAATGATGATGATGATGATGATG 2040

RESULT 2
US-09-759-143-375
; Sequence 375, Application US/09759143
; Patent No. US20020222481
; GENERAL INFORMATION:
; APPLICANT: Xu, JIANGCHUN
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, YUQU
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, CRAIG H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

;; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
;; FILE REFERENCE: 210121.427C23
;; CURRENT APPLICATION NUMBER: US/09/759,143
;; NUMBER OF SEQ ID NOS: 934
;; SOFTWARE: FASTSEQ for Windows Version 3.0
;; SEQ ID NO: 375
;; LENGTH: 2040
;; TYPE: DNA
;; ORGANISM: Homo sapien
US-09-759-143-375

Query Match 100.0%; Score 2040; DB 10; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGGTGATTCATGCCGGCTGCTTCTGTGAAGAGCCATTGGTCTC 60
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DB 61 AGGAGCAAGATGGGCAAGTGGTGGCGGCTTCCCTGCTGCAAGAGCGGCAAG 120
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DB 121 AGCAACGTGGGCACTTCTGGAGACACGACGACTGCTATGAAGACACTCAGAGCAAG 180
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QY 361 GGAGACTACGATGACAGTGGCTTCTGATGAGAGCCAGGATACAGTCCGCTGGAGAGATCTG 420
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RESULT 3

US-09-780-669-375
; Sequence 375, Application US/09780669
; Patent No. US20020051977A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqun
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780, 669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-780-669-375

Query Match 100.0%; Score 2040; DB 10; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGTGTTGAGTTGATTCATGCCGCTGCTCTTCTGTGAAGAACCATTTGTCTC 60
Db 1 ATGGGTGTTGAGTTGATTCATGCCGCTGCTCTTCTGTGAAGAACCATTTGTCTC 60
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Db	1501	TCAGAGGAAAGTCACAAAGGCTTGAAGGCGAGTGAATATGCGCAGCCAGAGAAAAAGATCT	15600
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Db	1621	GAATATGAAGAGCAGCGAAGTACTCATGTGCGATTTCCAGAAACCTGACTATATGTCGCC	16800
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Db	1661	ACTGCTGGCAATGGTATATGATATGATTAATTTCTCCAGAGAGAGCAGAACACCTGAAAGC	17400
Qy	1741	CAGCAATTCCTGCACTGAGATGAAGAGATCACAGTGAAGCAACAAATGATATCTCAG	18000
Db	1741	CAGCAATTCCTGCACTGAGATGAAGAGATCACAGTGAAGCAACAAATGATATCTCAG	18000
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Db	1861	GAAGAAGATAGAAGGCTGTGAAAAAATGAAATCTGACCTTTCCTTAGTTGTAAGAA	19200
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      RESULT 4
      US-09-810-936-303
      ; Sequence 303, Application US/09810936
      ; Patent No. US20020068285A1
      ; GENERAL INFORMATION:
      ; APPLICANT: Fridakis, Tony N.
      ; APPLICANT: Reed, Steven G.
      ; APPLICANT: Smith, John M.
      ; APPLICANT: Mishner, Linda E.
      ; APPLICANT: Dillon, David C.
      ; APPLICANT: Retter, Marc W.
      ; APPLICANT: Wang, Aljun
      ; APPLICANT: Skelky, Yasir A.W.
      ; APPLICANT: Harlocker, Susan L.
      ; APPLICANT: Day, Craig H.
      ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
      ; FILE REFERENCE: 210121.419C11
      ; CURRENT APPLICATION NUMBER: US/09/810.936
      ; CURRENT FILING DATE: 2001-03-16
      ; NUMBER OF SEQ ID NOS: 334
      ; SOFTWARE: FastSeq for Windows Version 3.0
      ; SEQ ID NO 303
      ; LENGTH: 2040
      ; TYPE: DNA
      ; ORGANISM: Homo sapien
      US-09-810-936-303

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Query Match	100.0%;	Score 2040;	DB 10;	Length 2040;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2040;	Conservative 0;	Mismatches	0;	Indels 0;
				Gaps 0;
QY	1	ATGGCGGTTGAGCTTGATTCATGCCGGCTGCCCTTCTGTGACAGACCAATTGGTCTC	60	

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D	b		61	AGGAGCAAGATGGGCAAGTGGTCTGCTCCGTTGGTTCCCTGCTGCAGGAGGAGCGGCAG	120
O	y		121	AGCAACTGGGCACTTTTGGAGACACAGACGACTGCTGTATGAACACTCAGAGCAG	180
D	b		121	AGCAACCGGGCACTTCTTGAGAGACACAGACGACTGTGTATGAACACTCAGAGCAG	180
O	y		181	ATGGGCAAGTGGTGGCGGCCACTGCTTCCCTGCTGCAGGGGGAGTGGCAAGCAAGTG	240
D	b		181	ATGGGCAAGTGGTGGCGGCCACTGCTTCCCTGCTGCAGGGGGAGTGGCAAGCAAGTG	240
O	y		241	GGCCCTTCTGGAGACACAGACGACTGCTGTATGAACACTCAGGAAACAGATGGGCAG	300
D	b		241	GGCCCTTCTGGAGACACAGACGACTGCTGTATGAACACTCAGGAAACAGATGGGCAG	300
O	y		301	TGGTGTGCCACTGCTTCCCTGCTGCAGGGGAGCGGCAGAGCAGAGTGGGCGCTGG	360
D	b		301	TGGTGTGCCACTGCTTCCCTGCTGCAGGGGAGCGGCAGAGAGATGGGCGCTGG	360
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QY 1921 GAAAGAGAGATCTTGTGAG 1980
Db 1921 GAAAGAGAGATCTTGTGAG 1980
QY 1981 GAGGTAGACAG 2040
Db 1981 GAGGTAGACAG 2040

RESULT 5

US-09-822-827-375
; Sequence 375, Application US/09822827
; Patent No. US2002008180A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822.827

; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-375
Query Match 100.0%; Score 2040; DB 10; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGTTGAGGTGATTCATGCGGCTGCTCTTCTGTGAAGAACCATTTGCTCTC 60
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Db 121 AGCAAGTGGGCACTTCTGAGACACAG 180
QY 181 ATGGGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 181 ATGGGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 241 GGGCTTCTGAGACACAG 300
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QY 301 TGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
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QY 361 GGAGACTAGATGACAG 420
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QY 421 GACAGAGTCCACAG 480
Db 421 GACAGAGTCCACAG 480
QY 481 CTCAGGAG 540
Db 481 CTCAGGAG 540
QY 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCTGCTGAGACAGAGATGCAACTTAAT 600
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QY 601 GTCTTTACACAAACAAAG 660
Db 601 GTCTTTACACAAACAAAG 660
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Db 661 TGTGCGTTAATGTTGCTGGAACATGGACATGATCAATATTCAGATGAGTAAAT 720
QY 721 ACCACTGTGACATGCTATCTATATGAAGATTAATTAATGAGCAAGAGAGAGAGAGAGAGAGAGAG 780
Db 721 ACCACTGTGACATGCTATCTATATGAAGATTAATTAATGAGCAAGAGAGAGAGAGAGAGAGAGAG 780
QY 781 TATGTGCTGATATGCAATCAAAAAACAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
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QY 841 CATGAGCAAAACAGCAAGTGTGTAATTTTAAATCAAGAAAAAGCAATTTTAAATGCA 900
Db 841 CATGAGCAAAACAGCAAGTGTGTAATTTTAAATCAAGAAAAAGCAATTTTAAATGCA 900

QY 901 CTGATAGATATGGAAGAGCTGCTCATACTTGCTGATATGTTGGATCAGCAAGTATA 960
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Db 901 CTGGATAGATATGGAAGAGCTGCTCATACTTGCTGATATGTTGGATCAGCAAGTATA 960
QY 961 GTCAGCCTTCTACTGAGCAAAATATGATGTATCTTCCAGATCTATCTGAGCAGAC 1020
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Db 961 GTCAGCCTTCTACTGAGCAAAATATGATGTATCTTCCAGATCTATCTGAGCAGAC 1020
QY 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTATATTTGCCAGTTACTTCTGACTAC 1080
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Db 1201 ATGCTCAAGAACCAAGAAATAATTAAGATGGTGTAGAGAGTTGAGAAAGAAATGAAG 1260
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Db 1261 AAGCATGAAAGTAAATATATGATGGGATTTACTAGAAAACTGACTAATGCTGCTGCTGSC 1320
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Db 1321 AATGGTGAATATGATATATCTCTCAAGAGAGAGCAACCTGAAATATGCAATTT 1380
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Db 1381 CCTGACAAAGAAAGTGAAGAGTATCAGAAATTTGCGAATTTGTTCTGACTACAAAGAA 1440
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Db 1441 AAACGATGCCAAATTTACTCTTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
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Db 1501 TCAGAGGAAGAGTCACAAAAGGCTTGAGGGCAGTGAATAATGGCCAGCAAGAAAGATCT 1560
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Db 1561 CAAGAACCAGAAATTAATTAAGATGGTGTAGAGAGCTGAGAAATTTTATGCTATCGAA 1620
QY 1621 GAAATGAGAGACGACGGAAGTACTCATGTGCGATTTCCAGAAAACCTGACTAATGCTGCC 1680
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Db 1621 GAAATGAGAGACGACGGAAGTACTCATGTGCGATTTCCAGAAAACCTGACTAATGCTGCC 1680
QY 1681 ACTGCGCAATGGTATGATGATGATTAATTTCTCCAGGAAGAGCAACCTGTAAGAC 1740
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Db 1681 ACTGCGCAATGGTATGATGATGATTAATTTCTCCAGGAAGAGCAACCTGTAAGAC 1740
QY 1741 CAGCAATTTCTGACACTGAGATGAGATATCAGTACAGCAACCAATATGATATCTGAG 1800
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Db 1741 CAGCAATTTCTGACACTGAGATGAGATATCAGTACAGCAACCAATATGATATCTGAG 1800
QY 1801 AAGCAATTTTCTGAGAGACAGAACACTGGAATTTACAGATGAGATTTCTGATTCGTGAA 1860
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Db 1801 AAGCAATTTTCTGAGAGACAGAACACTGGAATTTACAGATGAGATTTCTGATTCGTGAA 1860
QY 1861 GAAAAAGCAGATGAGAGTGTGTAATAAATGAAATTCGACTTCTTGTGTTGTAAGAA 1920
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Db 1861 GAAAAAGCAGATGAGAGTGTGTAATAAATGAAATTCGACTTCTTGTGTTGTAAGAA 1920
QY 1921 GAAAAAGCAGATGAGAGTGTGTAATAAATGTAAGTTGCGGGAAGAAATTTGCCATGTAAGCTG 1980
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Db 1921 GAAAAAGCAGATGAGAGTGTGTAATAAATGTAAGTTGCGGGAAGAAATTTGCCATGTAAGCTG 1980
QY 1981 GAGCTAGACCAATGAAACATCAGAGCCGCTTAATAAAAAAAAAAAAAAAAAAAAAA 2040

Db 1981 GAGCTAGACCAATGAAACATCAGAGCCGCTTAATAAAAAAAAAAAAAAAAAAAAAA 2040
| | | | |
RESULT 6
US-09-429-755-303
; Sequence 303, Application US/09429755A
; Patent No. US2002011467A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, David C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429/755A
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-303
Query Match 100.0%; Score 2040; DB 10; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGATGCTGAGATGATTCATCCATCCGCGCTCTTCTGTAAGAACCATTTGGTCTC 60
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Db 1 ATGATGCTGAGATGATTCATCCATCCGCGCTCTTCTGTAAGAACCATTTGGTCTC 60
QY 61 AGAGACAGATGGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
| | | | |
Db 61 AGAGACAGATGGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 121 ACCAAGCTGGGCACTTCTGAGACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 180
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Db 121 ACCAAGCTGGGCACTTCTGAGACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 180
QY 181 ATGGGCAATGCTGCGCCACTGCTTCCCTCTGAGGGGAGTGGCAAGCAAGCAAGCTG 240
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Db 181 ATGGGCAATGCTGCGCCACTGCTTCCCTCTGAGGGGAGTGGCAAGCAAGCAAGCTG 240
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Db 241 GGCCTTCTGAGACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 300
QY 301 TGGTGTGCTGCTGCTTCCCTGCTGCAAGGGGAGGGGCAAGCAAGCAAGCAAGCAAG 360
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Db 301 TGGTGTGCTGCTGCTTCCCTGCTGCAAGGGGAGGGGCAAGCAAGCAAGCAAGCAAG 360
QY 361 GGAGACTAGATGACAGTCTTCCATGAGAGCCAGGTACACGTCCCTGGAGAAATCTG 420
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Db 361 GGAGACTAGATGACAGTCTTCCATGAGAGCCAGGTACACGTCCCTGGAGAAATCTG 420
QY 421 GACAACTCTCAGAGAGCTGCTGAGTAAAGTCCCAAGAAAGATCTCATCTGATG 480
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Db 421 GACAACTCTCAGAGAGCTGCTGAGTAAAGTCCCAAGAAAGATCTCATCTGATG 480
QY 481 CTCAGGAGACCTGAGCTGAAGCAAGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
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Db 481 CTCAGGAGACCTGAGCTGAAGCAAGAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
QY 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTGCTGAGAGAGATGCAACTTAAT 600
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Db 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTGCTGAGAGAGATGCAACTTAAT 600
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Db 601 GTCTTGACACAAAAAGAGACAGCTGTATAAGCCCTACATCCAGAGAAATGAA 660
QY 661 TGTGCGTTAATGTTGCGAAGATGCGCATGATCCAAATTTCCAGATGATGAAAT 720
Db 661 TGTGCGTTAATGTTGCGAAGATGCGCATGATCCAAATTTCCAGATGATGAAAT 720
QY 721 ACCACTCTGCATACGCTATCTATATGAAGATAAATTAATGGCCAAAGCAGCTCTTA 780
Db 721 ACCACTCTGCATACGCTATCTATATGAAGATAAATTAATGGCCAAAGCAGCTCTTA 780
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QY 841 CATGAGCAAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
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Db 901 CTGGATGATATGGAAGAGACTGCTCATCTTGCTGATGTTGTGATCAGCAAGTATA 960
QY 961 GTGAGCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGACG 1020
Db 961 GTGAGCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGACG 1020
QY 1021 GCCAGAGATGATGCTGTTTGTAGCATCATGATTAATTTGCCAGTACTTCTGACATAC 1080
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QY 1081 AAGAAAAACAGATGCTAAATAATCTCTTCTGAAAAACAGCAATCCAGAACAGCTTAAG 1140
Db 1081 AAGAAAAACAGATGCTAAATAATCTCTTCTGAAAAACAGCAATCCAGAACAGCTTAAG 1140
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Db 1141 CTGACATCAAGAGAGAGTACAAAGTCTAAAGGCGTGAATTAATGACCGACAGAGAA 1200
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Db 1201 ATGCTCAAGAACAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAAGAAATGAG 1260
QY 1261 AAGCATGAAAATGATAATGATGAGGATTAAGAAAACTGACTAATGCTGCTGCTGCG 1320
Db 1261 AAGCATGAAAATGATAATGATGAGGATTAAGAAAACTGACTAATGCTGCTGCTGCG 1320
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Db 1321 AATGCTGATATGATTAATTTCTCAAGAGAGAGAGCAACCTGAAATTCAGCAATTT 1380
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Db 1381 CCTGACAAAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 1441 AAAACAGATGCGCAAAATCTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAGCTGACA 1500
Db 1441 AAAACAGATGCGCAAAATCTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAGCTGACA 1500
QY 1501 TCAGAGGAAGAGTACAAAGAGCTGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1560
Db 1501 TCAGAGGAAGAGTACAAAGAGCTGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1560
QY 1561 CAAGAAGCAAGATTAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
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Db 1621 GAAATGAAGAAGCAGGAAGTACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 1681 ACTGCTGCGCAATGATGATGATTAATTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
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Db 1681 ACTGCTGCGCAATGATGATGATTAATTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
QY 1741 CAGCAATTTCTGACATGAGATGAAGATATACAGTACAGCAAGCAAAATGATTAATCAG 1800
Db 1741 CAGCAATTTCTGACATGAGATGAAGATATACAGTATACAGCAAGCAAAATGATTAATCAG 1800
QY 1801 AAGCAATTTTGTGAAG 1860
Db 1801 AAGCAATTTTGTGAAG 1860
QY 1861 GAAAGAGAGATGAG 1920
Db 1861 GAAAGAGAGATGAG 1920
QY 1921 GAAAAAGACATCTTGCATGAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
Db 1921 GAAAAAGACATCTTGCATGAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1980
QY 1981 GAGCTAGACACAAATGAAATCAG 2040
Db 1981 GAGCTAGACACAAATGAAATCAG 2040

RESULT 7
US-09-825-301-6
; Sequence 6, Application US/09825301
; Patent No. US2002009738A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Dillon, David C.
; APPLICANT: Molesh, David A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Zehentner, Barbara
; APPLICANT: Pershing, David H.
; TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
; FILE REFERENCE: 210121.513
; CURRENT APPLICATION NUMBER: US/09/825, 301
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-825-301-6

Query Match 76.0%; Score 1551; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGTTGAGGTGATTCATGCGGCTGCGCTCTTCTGTAAGAACCATTTGGTCTC 60
Db 1 ATGATGTTGAGGTGATTCATGCGGCTGCGCTCTTCTGTAAGAACCATTTGGTCTC 60
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Db 61 AGGAGCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
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Db 121 AGCAAGTGGGCACTTCTGAGAGACAGAGACTGTCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGGTGGCGCCACTCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGCTG 240
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QY 241 GCGGCTTCTGAGAGACAGAGACTGTCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
Db 241 GCGGCTTCTGAGAGACAGAGACTGTCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
QY 301 TGTGCTGCCACTGCTTCCCTGCTGCAAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
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Db 301 TGTGTCGCCACTGCTCCCTGCTGTCAGGGGAGCGGACAGCAAGGTGGCCCTTGG 360
Qy 361 GGAGACTGACATGACAGTGCCTTCATGAGCCCGAGTACCCAGTCCGCTGGAGAAATCTGG 420
Db 361 GGAGACTGACATGACAGTGCCTTCATGAGCCCGAGTACCCAGTCCGCTGGAGAAATCTGG 420
Qy 421 GACAAAGCTCCACAGAGCTGCTGAGTGGGTTAAAGTCCCGAGAAAGATCTCATCTCATG 480
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Qy 481 CTCAGGGACACTGACGTGACACAGAGGACAAAGAGAGAGCTCTCTACATCTGGCC 540
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Db 661 TGTGCGTAAATGTTGCTGGAACATGACACTGATCCAAATATTCAGATGATGGAAT 720
Qy 721 ACCACTGCACTAGGCTATCTATATGAAAGTAAATTAATGAGCCAAAGCACTGCTT 780
Db 721 ACCACTGCACTAGGCTATCTATATGAAAGTAAATTAATGAGCCAAAGCACTGCTT 780
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Db 781 TATGCTGCTGATATGATCAAAAACAAAGCATGAGCTGACACACTGTTACTTGTGTA 840
Qy 841 CATGAGCAAAAACAGCAAGTGTGTAATTTTATATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGTGTGTAATTTTATATCAAGAAAAAGCAATTTAAATGCA 900
Qy 901 CTGATATATATGAAAGAGCTGCTCATCTGCTGATGTTGGAGTACACAGTATA 960
Db 901 CTGATATATATGAAAGAGCTGCTCATCTGCTGATGTTGGAGTACACAGTATA 960
Qy 961 GTCAAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
Db 961 GTCAAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
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Qy 1141 CTGACATCAGAGAGAGTTCACAAAGTTCAAAGCAGTGAATAGCCAGCAGAGAA 1200
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Qy 1441 AAACAGATGCCAAATATCTTCTGAAAACAGCAACCCAGAACTTAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATATCTTCTGAAAACAGCAACCCAGAACTTAAGCTGACA 1500
Qy 1501 TCAGAGAGAGAGTCAACAAAGGCTTGAAGGAGGAGTGAATAGGCGAGCAGAG 1551
Db 1501 TCAGAGAGAGAGTCAACAAAGGCTTGAAGGAGGAGTGAATAGGCGAGCAGAG 1551

RESULT 8
US-09-759-143-374
; Sequence 374, Application US/09759143
; Patent No. US2002002248A1
GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedyick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-374

Query Match 76.0%; Score 1551; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGCTGAGTGGATTCATGCGCGGCTGCTCTCTGTAAGAACCATTTGGTCTC 60
Db 1 ATGCTGCTGAGTGGATTCATGCGCGGCTGCTCTCTGTAAGAACCATTTGGTCTC 60
Qy 61 AGAGCAAGATGGCAAGTGTGCTGCTGCTTCCCTGTCAGAGAGAGCGCAAG 120
Db 61 AGAGCAAGATGGCAAGTGTGCTGCTGCTTCCCTGTCAGAGAGAGCGCGCAAG 120
Qy 121 AGCAAGTGGGCACTTCTGAGACCAAGCACTGCTATGAAGCACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACCAAGCACTGCTATGAAGCACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGTGCGCGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGTGCGCGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAAGCTG 240
Qy 241 GCGCTTCTGAGACAGACAGTCTGCTATGAAGCACTCAGAACTGAGGCAAG 300
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Qy 301 TGTGCTGCACTGCTTCCCTGCTGAGGGGAGCGCAAGCAAGTGGCGCTTGG 360
Db 301 TGTGCTGCACTGCTTCCCTGCTGAGGGGAGCGCAAGCAAGTGGCGCTTGG 360

QY 361 GGAGACTACGATGACAGTGCCTTCATGAGGCCAGGTACCACTCCGTGGAGAGATCTG 420
DB 361 GGAGACTACGATGACAGTGCCTTCATGAGGCCAGGTACCACTCCGTGGAGAGATCTG 420
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DB 601 GTCTTGACAACAAAAGAGAGAGAGCTCTGATAAAGGCCGTACAAATGCCAGAGATGAA 660
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DB 661 TGTGGTAAATGTTGCTGGAGCATGGCACTGATCCAAATATTCAGATGAGATGGAAT 720
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DB 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAAGCCAAATTTAAATGCA 900
QY 901 CTGGATAGATATGGAAGAGTGCCTCATCTGCTATGTTGGATCAGACAGTATA 960
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QY 961 GTCAAGCCCTTACTTGACCAAAATATGATGATCTCTCAAGATCTATCTGGACAGAG 1020
DB 961 GTCAAGCCCTTACTTGACCAAAATATGATGATCTCTCAAGATCTATCTGGACAGAG 1020
QY 1021 GCCAGAGGTATGCTGTTTCTAGTCATCATGTAATTTGCCAGTACTTTCTGACTAC 1080
DB 1021 GCCAGAGGTATGCTGTTTCTAGTCATCATGTAATTTGCCAGTACTTTCTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTGTAAGAACAGCAATCCAGAACAAAGCTTAAAG 1140
DB 1081 AAAGAAAAACAGATGCTAAAAATCTCTGTAAGAACAGCAATCCAGAACAAAGCTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGTCAACAAGGTTCAAAAGGCACTGTAATAATAGCCAGCAGAGAA 1200
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QY 1201 ATGTCTCAAGAACCAAAAAATATATAGATGCTGATAGAGGTTGAAGAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACCAAAAAATATATAGATGCTGATAGAGGTTGAAGAGAAATGAAG 1260
QY 1261 AAGCATGAAGATATATATGTTGGATTTACTAGAAAACCTGACTAAATAGGTCTGCTGGC 1320
DB 1261 AAGCATGAAGATATATATGTTGGATTTACTAGAAAACCTGACTAAATAGGTCTGCTGGC 1320
QY 1321 AATGCTGATTAATGATTAATTCCTCAAGAGAGAGACAGAACCTGAAATATGCAATTT 1380
DB 1321 AATGCTGATTAATGATTAATTCCTCAAGAGAGAGACAGAACCTGAAATATGCAATTT 1380
QY 1381 CCTGACAACGAAGTGAAGAGATATACAGAAATTTGCGAATTAAGTTTCTGACTACAAAGAA 1440
DB 1381 CCTGACAACGAAGTGAAGAGATATACAGAAATTTGCGAATTAAGTTTCTGACTACAAAGAA 1440

QY 1441 AAACAGATCCCAAAATTAATCTTTCTGAAAAACAGAACCCAGAACAGACTTAAAGCTGACA 1500
DB 1441 AAACAGATCCCAAAATTAATCTTTCTGAAAAACAGAACCCAGAACAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGGAAGAGTCAACAAGGCTTAGAGGCACTGAAATATGGCCAGCCAGAG 1551
DB 1501 TCAGAGGAAGAGTCAACAAGGCTTAGAGGCACTGAAATATGGCCAGCCAGAG 1551

RESULT 10
US-09-810-936-302
; Sequence 302, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Skelky, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-810-936-302

Query Match 76.0%; Score 1551; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGTGAGTGGATGATTCATGCGCGCTGCTCTTCTGTAAGAAAGCAATTTGGTCTC 60
DB 1 ATGGTGTGAGTGGATGATTCATGCGCGCTGCTCTTCTGTAAGAAAGCAATTTGGTCTC 60
QY 61 AGGACCAAGATGGGCAAGTGGTGGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
DB 61 AGGACCAAGATGGGCAAGTGGTGGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTGGGAGACCAAGCAAGCACTGCTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTGGGAGACCAAGCAAGCACTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTCAGAGGGGAGTGGCAAGAACGTG 240
DB 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTCAGAGGGGAGTGGCAAGAACGTG 240
QY 241 GCGGCTTCTGGAGACCAAGCACTCTGCTATGAAGACACTCAGAACAAAGTGGGCAAG 300
DB 241 GCGGCTTCTGGAGACCAAGCACTCTGCTATGAAGACACTCAGAACAAAGTGGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGGAGGCAAGCAAGTGGGCGCTGG 360
DB 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGGAGGCAAGCAAGTGGGCGCTGG 360
QY 361 GGAGACTACAGATGACAGTGCCTTCATGAGGCCAGGTACCACTCCGTGGAGAGATCTG 420
DB 361 GGAGACTACAGATGACAGTGCCTTCATGAGGCCAGGTACCACTCCGTGGAGAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCGAGAAAGATCTCATGCTATG 480
DB 421 GACAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCGAGAAAGATCTCATGCTATG 480

QY	481	CTCAGGGACACTGACGTCGACCAAGGAGCAAGCAAAAGAGACGTCCTCATCTGACC	540
Db	481	CTCAGGGACACTGACGTCGACCAAGGAGCAAGCAAAAGAGACGTCCTCATCTGACC	540
QY	541	TCCTGCACATGGGAATTCAGAAAGTAAAGTAAAGCTCTGCTGGACAGACGATGTCACCTTAAT	600
Db	541	TCCTGCACATGGGAATTCAGAAAGTAAAGTAAAGCTCTGCTGGACAGACGATGTCACCTTAAT	600
QY	601	GTCCTTGACAAACAAAAGAGACAGCTGCGATTAAGAGCCGTCACATGGCCAGGAAGATGAA	660
Db	601	GTCCTTGACAAACAAAAGAGAGACAGCTGCGATTAAGAGCCGTCACATGGCCAGGAAGATGAA	660
QY	661	TGTGCGTTAAATGTTGTGCGAATCGACATGGCAGCTGATCCAAATATTCACAGATGATGGAAT	720
Db	661	TGTGCGTTAAATGTTGTGCGAATCGACATGGCAGCTGATCCAAATATTCACAGATGATGGAAT	720
QY	721	ACCACTCTGCACCTACGCTATCTATTAATGAAGATAAATTAATGCGCAAAAGCACTGCTCTTA	780
Db	721	ACCACTCTGCACCTACGCTATCTATTAATGAAGATAAATTAATGCGCAAAAGCACTGCTCTTA	780
QY	781	TATGTCCTGTATTCGAATCAAAAAACAAGCATGGCGTCACACACCTGTTACTTGGSTGA	840
Db	781	TATGTCCTGTATTCGAATCAAAAAACAAGCATGGCGTCACACACCTGTTACTTGGSTGA	840
QY	841	CATGAGCAAAAACAGCAAGTCGTGAATTTTTAATCAAAAAAAAGCGAATTTAAATGCA	900
Db	841	CATGAGCAAAAACAGCAAGTCGTGAATTTTTAATCAAAAAAAAGCGAATTTAAATGCA	900
QY	901	CTGGATATGATATGGAAGAGACTGCTGTCATACCTGCTGATATGTTGGATCAGCAAGTATA	960
Db	901	CTGGATATGATATGGAAGAGACTGCTGTCATACCTGCTGATATGTTGGATCAGCAAGTATA	960
QY	961	GTCAGCCTTCTACTTGAGCAAAATATTTGATGATATCTTCAAGATCTATCTTGGACAGAG	1020
Db	961	GTCAGCCTTCTACTTGAGCAAAATATTTGATGATATCTTCAAGATCTATCTTGGACAGAG	1020
QY	1021	GCCAGAGATATGCTGTTTCTTAAGTCATCATATGTAATTTGGCACTTCTTGACATAC	1080
Db	1021	GCCAGAGATATGCTGTTTCTTAAGTCATCATATGTAATTTGGCACTTCTTGACATAC	1080
QY	1081	AAACAAAACAGATGCTAAAAATCTCTTGCAAAAACAGCAATCCAGAACAGACTTAAAG	1140
Db	1081	AAACAAAACAGATGCTAAAAATCTCTTGCAAAAACAGCAATCCAGAACAGACTTAAAG	1140
QY	1141	CTGACATCAGAGGAGAGTCACAAAGGTTCAAAAGCAGTGAATAATGCCAGCCAGAGAAA	1200
Db	1141	CTGACATCAGAGGAGAGTCACAAAGGTTCAAAAGCAGTGAATAATGCCAGCCAGAGAAA	1200
QY	1201	ATGTCCTAAAGACACAGAAATTAATTAAGATGGTGATGAGAGAGTTGAAGAAATAATGAG	1260
Db	1201	ATGTCCTAAAGACACAGAAATTAATTAAGATGGTGATGAGAGAGTTGAAGAAATAATGAG	1260
QY	1261	AAGCATGAAAGTAAATATGTGGGATTACTAGAAAACTGACATAATGATGTCTACTGCTGC	1320
Db	1261	AAGCATGAAAGTAAATATGTGGGATTACTAGAAAACTGACATAATGATGTCTACTGCTGC	1320
QY	1321	AATGCTATATATGATTAATTTCTCTCAAGSAGAGCAGAAACCTGGAATAATGCAATTT	1380
Db	1321	AATGCTATATATGATTAATTTCTCTCAAGSAGAGCAGAAACCTGGAATAATGCAATTT	1380
QY	1381	CCTGACACAGAAAGTGAAGTATCACAGAAATTTGGGATTTGTTCTGACTACCAATAA	1440
Db	1381	CCTGACACAGAAAGTGAAGTATCACAGAAATTTGGGATTTGTTCTGACTACCAATAA	1440
QY	1441	AAACAGATGCCAAAATCTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAAATCTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA	1500
QY	1501	TCAGAGAAAGATCACAAGAGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG	1551
Db	1501	TCAGAGAAAGATCACAAGAGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG	1551

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RESULT 11
US-09-822-827-374
; Sequence 374: Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-374

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Query Match	76.0%:	Score 1511:	DB 10:	Length 2000:
Best Local Similarity	100.0%:	Pred. No. 0:		
Matches 1511:	Conservative	0:	Mismatches	0:
			Indels	0:
			Gaps	0:
Oy	1	ATGGTGTGATGAGTTGATTCATGCGCGGCTCTTGTGTGAAGAAGCCATTGGTCTC	60	
Db	1	ATGGTGTGATGAGTTGATTCATGCGCGGCTCTTGTGTGAAGAAGCCATTGGTCTC	60	
Oy	61	AGGAGCAAGATGGGCAAGTGTGTCGCTTGCTTCCCTGCTGCAAGGAGACCGGCAAG	120	
Db	61	AGGAGCAAGATGGGCAAGTGTGTCGCTTGCTTCCCTGCTGCAAGGAGACCGGCAAG	120	
Oy	121	AGCAACGTGGGCACTTCTGTGAGACCCAGCAGACTCTGTATGTAAGACACTCAGAGCAAG	180	
Db	121	AGCAACGTGGGCACTTCTGTGAGACCCAGCAGACTCTGTATGTAAGACACTCAGAGCAAG	180	
Oy	181	ATGGCAAGTGGTGCOCGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGACAACTG	240	
Db	181	ATGGCAAGTGGTGCOCGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGACAACTG	240	
Oy	241	GGCGCTTCTGAGAGACCAGCAGACTCTGCTATGTAAGACACTCAGAAACAATGGGCAAG	300	
Db	241	GGCGCTTCTGAGAGACCAGCAGACTCTGCTATGTAAGACACTCAGAAACAATGGGCAAG	300	
Oy	301	TGGTCTGCGCACTGCTTCCCTGCTGCAAGGGGAGGGGCAAGGAGGAGGCGGCTGG	360	
Db	301	TGGTCTGCGCACTGCTTCCCTGCTGCAAGGGGAGGGGCAAGGAGGAGGCGGCTGG	360	
Oy	361	GGAGACTAGATGACAGTGCCTTCATGAGACCAGCTACCACTCCGTGGAGAAATCTG	420	
Db	361	GGAGACTAGATGACAGTGCCTTCATGAGACCAGCTACCACTCCGTGGAGAAATCTG	420	
Oy	421	GACAAGCTCCAGAGAGCTGCTGTTGAGAGCCAGCTACCACTCCGTGGAGAAATCTG	480	
Db	421	GACAAGCTCCAGAGAGCTGCTGTTGAGAGCCAGCTACCACTCCGTGGAGAAATCTG	480	
Oy	481	CTCAGGGCACTGACGTGAACAAGAACACAAAGAGAGCTGCTTCACTCTGGCC	540	
Db	481	CTCAGGGCACTGACGTGAACAAGAACACAAAGAGAGCTGCTTCACTCTGGCC	540	
Oy	541	TCTGCCAATGGGAATTCAGAAAGTAAATCTCTCTGAGACAGAGATGTCAACTTAAT	600	
Db	541	TCTGCCAATGGGAATTCAGAAAGTAAATCTCTCTGAGACAGAGATGTCAACTTAAT	600	
Oy	601	GTTCCTTGACAAACAAAAGGAGACAGCTGATTAAGCCGTCACAAAGCCAGAAAGTGA	660	
Db	601	GTTCCTTGACAAACAAAAGGAGACAGCTGATTAAGCCGTCACAAAGCCAGAAAGTGA	660	
Oy	661	TGTGGCTTAATGTCTGTGAACATGAGCTGATCCAAATATTCAGATGATGGAAT	720	
Db	661	TGTGGCTTAATGTCTGTGAACATGAGCTGATCCAAATATTCAGATGATGGAAT	720	
Oy	721	ACCACTGTGACACTACGCTATCTATAATGAAGATAAATTAAGGCCAAAGCACTGCTTTA	780	
Db	721	ACCACTGTGACACTACGCTATCTATAATGAAGATAAATTAAGGCCAAAGCACTGCTTTA	780	


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Db 721 ACCACTGTCAGTACGATCTATATATGAGATTAATTAATGCGCAAGCACTGCTCTTA 780
Qy 781 TATGTCGTGATATGATTCATAAAGCAAGCATGGCTCACACCACTGTTACTTGSTGA 840
Db 781 TATGTCGTGATATGATTCATAAAGCAAGCATGGCTCACACCACTGTTACTTGSTGA 840
Qy 841 CATGAGCAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Qy 901 CTGATATATATGAGAGACTGCTCTCATCTCTGATATGTTGGATCAGCAAGTATA 960
Db 901 CTGATATATATGAGAGACTGCTCTCATCTCTGATATGTTGGATCAGCAAGTATA 960
Qy 961 GTCAGACCTTACTGAGCAAAATATGATGATCTTCAGAGATCTATCTGGAGAGAG 1020
Db 961 GTCAGACCTTACTGAGCAAAATATGATGATCTTCAGAGATCTATCTGGAGAGAG 1020
Qy 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGGCACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGGCACTTCTGACTAC 1080
Qy 1081 AAAGAAAAACAGATCTTAAAAATCTCTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
Db 1081 AAAGAAAAACAGATCTTAAAAATCTCTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
Qy 1141 CTGACATAGAGAGAGACTTCACAAAGTTCACAAAGCAGTGAATAATAGCCAGCAAGAAA 1200
Db 1141 CTGACATAGAGAGAGACTTCACAAAGTTCACAAAGCAGTGAATAATAGCCAGCAAGAAA 1200
Qy 1201 ATGTCCTAAGAACAGAAATTAATTAAGATGGTATAGAGAGTTGAAGAAAGATGAAG 1260
Db 1201 ATGTCCTAAGAACAGAAATTAATTAAGATGGTATAGAGAGTTGAAGAAAGATGAAG 1260
Qy 1261 AAGCATGAAAGTAAATTAATGAGGATTAAGTAAAGCTGACTAATGTTGCTGCTGGC 1320
Db 1261 AAGCATGAAAGTAAATTAATGAGGATTAAGTAAAGCTGACTAATGTTGCTGCTGGC 1320
Qy 1321 AATGGTGAATGATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1321 AATGGTGAATGATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Qy 1381 CCTGACAAAGAAAGTGAAGATATCAGAGAAATTTGCAATTAATGTTGCTGACTACAAAGA 1440
Db 1381 CCTGACAAAGAAAGTGAAGATATCAGAGAAATTTGCAATTAATGTTGCTGACTACAAAGA 1440
Qy 1441 AAACGATGCCAAATTAATCTTTCTGAAAAACAGCAACCAAGAAAGACTTAAAGCTGACA 1500
Db 1441 AAACGATGCCAAATTAATCTTTCTGAAAAACAGCAACCAAGAAAGACTTAAAGCTGACA 1500
Qy 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGAGTGAATGGCCAGCCAGAG 1551
Db 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGAGTGAATGGCCAGCCAGAG 1551
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RESULT 12
US-09-429-755-302
; Sequence 302, Application US/09429755A
; Patent No. US2002011467A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.41966
; CURRENT APPLICATION NUMBER: US/09/429,755A
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-302

Query Match      76.0%; Score 1551; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTCGTTGAGCTGATTCATGCGCGCTGCTCTTCTGTAAGAGCAATTTGGTCTC 60
Db 1 ATGTCGTTGAGCTGATTCATGCGCGCTGCTCTTCTGTAAGAGCAATTTGGTCTC 60
Qy 61 AGGACCAAGATGGGAAGGGTGGCTGCGTCCCTGCTGAGGAGAGCGGCAAG 120
Db 61 AGGACCAAGATGGGAAGGGTGGCTGCGTCCCTGCTGAGGAGAGCGGCAAG 120
Qy 121 AGCAAGTGGGACATTCCTGAGACACGACGACTGCTATGAAAGACACTCAGAGCAAG 180
Db 121 AGCAAGTGGGACATTCCTGAGACACGACGACTGCTATGAAAGACACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGGTGGCCGCACTGCTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGGTGGCCGCACTGCTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
Qy 241 GGGCGTTCTGGAGACGACGACGACTCTGTAATGAAGACACTCAGAAACAAGATGGGCAAG 300
Db 241 GGGCGTTCTGGAGACGACGACGACTCTGTAATGAAGACACTCAGAAACAAGATGGGCAAG 300
Qy 301 TGGTCTGCACTGCTCCCTGCTGCAAGGGGAGCGGCAAGAGATGGGCGCTTGG 360
Db 301 TGGTCTGCACTGCTCCCTGCTGCAAGGGGAGCGGCAAGAGATGGGCGCTTGG 360
Qy 361 GGAGACTACGATGACAGTGCCTTCATGAGCCAGGATACCAAGTCCGTTGAGAGATCTG 420
Db 361 GGAGACTACGATGACAGTGCCTTCATGAGCCAGGATACCAAGTCCGTTGAGAGATCTG 420
Qy 421 GACAAAGCTTCACAGAGCTGCTGTTGGGTTAAAGTCCCAAGAAAGATCTCATCTGATG 480
Db 421 GACAAAGCTTCACAGAGCTGCTGTTGGGTTAAAGTCCCAAGAAAGATCTCATCTGATG 480
Qy 481 CTCAGGAGACACTGAGCTGAAACAAGAGACAAAGAGAGAGTCTTACATCTGCGC 540
Db 481 CTCAGGAGACACTGAGCTGAAACAAGAGAGACAAAGAGAGAGTCTTACATCTGCGC 540
Qy 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCTGCTGAGACAGATGTCACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCTGCTGAGACAGATGTCACTTAAT 600
Qy 601 GTCCCTTGACAAACAAAAGAGAGACACTCTGATTAAGGCCGTACATGCCAGAAATGAA 660
Db 601 GTCCCTTGACAAACAAAAGAGAGACACTCTGATTAAGGCCGTACATGCCAGAAATGAA 660
Qy 661 TGTGCTTAATGTTGCTGGAACATGGACACTGATCCAAATATTCAGATGATGATGAAT 720
Db 661 TGTGCTTAATGTTGCTGGAACATGGACACTGATCCAAATATTCAGATGATGATGAAT 720
Qy 721 ACCACTGTGCACTACGATATCTATATGAAGATTAATTAATGAGCAAGCACTGCTTAA 780
Db 721 ACCACTGTGCACTACGATATCTATATGAAGATTAATTAATGAGCAAGCACTGCTTAA 780
Qy 781 TATGTCGTGATATGATTCATAAAGCAAGCATGGCTCACACCACTGTTACTTGSTGA 840
Db 781 TATGTCGTGATATGATTCATAAAGCAAGCATGGCTCACACCACTGTTACTTGSTGA 840
Qy 841 CATGAGCAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Qy 901 CTGATATGATATGAGAGACTGCTCTCATCTCTGATATGTTGGATCAGCAAGTATA 960
Db 901 CTGATATGATATGAGAGACTGCTCTCATCTCTGATATGTTGGATCAGCAAGTATA 960
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Qy	61	GTGACGCTTACTGTGGGCAAAATATGTGATGATCTCCAAAGATCTATCTGAGACAGC	1020
Db	961	GTCAACCTTTACTTGTGACAAATATGTGATGATCTCTCAAGATCTATCTGAGACAGC	1020
Qy	1021	GCCAGAGATGATGCTGTTTCTTACTCATCATGTAATTTGCCATTTACTTTCGACTAC	1080
Db	1021	GCCAGAGATGATGCTGTTTCTTACTCATCATGTAATTTGCCATTTACTTTCGACTAC	1080
Qy	1081	AAAGAAAACACAGTGTCTAAAAATCTTTTGAAAACAGCAATCCAGAACAGACTTAAG	1140
Db	1081	AAAGAAAACACAGTGTCTAAAAATCTTTTGAAAACAGCAATCCAGAACAGACTTAAG	1140
Qy	1141	CTGACATCAGAGGAAGGTGCACAAAGCTTCAAGGCAAGTGAATAATGACACCGAGAAA	1200
Db	1141	CTGACATCAGAGGAAGGTGCACAAAGCTTCAAGGCAAGTGAATAATGACACCGAGAAA	1200
Qy	1201	ATGTCTTCAGAACACAGAAATTAATTAAGATGTGTGATAGAGAGTTGAAGAAATGAG	1260
Db	1201	ATGTCTTCAGAACACAGAAATTAATTAAGATGTGTGATAGAGAGTTGAAGAAATGAG	1260
Qy	1261	AAGCATGAAGTAAATTAATGTGGGATTACTAGAAAACTGACTAATGTGTCACTGTGGC	1320
Db	1261	AAGCATGAAGTAAATTAATGTGGGATTACTAGAAAACTGACTAATGTGTCACTGTGGC	1320
Qy	1321	AATGCTATTAATGATTAATTCCTCAAGGAAGACAGAACCTCGAATAATCACCAATTT	1380
Db	1321	AATGCTATTAATGATTAATTCCTCAAGGAAGACAGAACCTCGAATAATCACCAATTT	1380
Qy	1381	CCTGACACAAAGAGTGAAGATATCACAATAATTTGCAATTGTTCTGACTACAAAGAA	1440
Db	1381	CCTGACACAAAGAGTGAAGATATCACAATAATTTGCAATTGTTCTGACTACAAAGAA	1440
Qy	1441	AAACAGATGCCAAATATCTCTTGTGAAAACAGAACCCAGAACAGACTTAAGCTGACA	1500
Db	1441	AAACAGATGCCAAATATCTCTTGTGAAAACAGAACCCAGAACAGACTTAAGCTGACA	1500
Qy	1501	TCACAGGAAGATGCACAAAGGCTTGAGGGCACTGAAATATGGCCAGCCAGAG	1551
Db	1501	TCACAGGAAGATGCACAAAGGCTTGAGGGCACTGAAATATGGCCAGCCAGAG	1551

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RESULT 13
US-09-825-301-5
; Sequence 5, Application US/09825301
; Patent No. US2002009738A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Molesh, David A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Zehentner, Barbara
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
; OF INVENTION: AND MONITORING OF BREAST CANCER
; FILE REFERENCE: 210121.513
; CURRENT APPLICATION NUMBER: US/09/825,301
; CURRENT FILING DATE: 2001-04-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-825-301-5

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Query Match	55.3%	Score 1128	DB 10	Length 1155
Best Local Similarity	100.0%	Pred. No. 0		
Matches 1128	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	ATGTGTTGAGTTCATGTCATGCGGCGTGCCTCTTCTGTGAAGAGCAATTTGCTTC	60	
		ATGGGTGGTGGAGTTCATTCATGCGCGGTGCCTCTTCTGTGAAGAGCAATTTGCTTC	60	

QY	61	AGGACAGATGGGCAAGTGGTGGCGGCTGGTCCCTGGTGGAGGAGCGGGCAAG	120
Db	61	AGGACAGATGGGCAAGTGGTGGCGGCTGGTCCCTGGTGGAGGAGCGGGCAAG	120
QY	121	AGCAACGTGGGCACTTGTGGAGACCAGCAGCACTGTGTATGAAGACACTCAGAGCAAG	180
Db	121	AGCAACGTGGGCACTTGTGGAGACCAGCAGCACTGTGTATGAAGACACTCAGAGCAAG	180
QY	181	ATGGGCAAGTGGTGGCGGCACTGTCCCTGTCTCAGGGGGAGTGGCAAGCAAGCTG	240
Db	181	ATGGGCAAGTGGTGGCGGCACTGTCCCTGTCTCAGGGGGAGTGGCAAGCAAGCTG	240
QY	241	GGCGCTTCGGAGACGACGACACTCTGTATGAAGACACTAGGAAACAAGTGGGCAAG	300
Db	241	GGCGCTTCGGAGACGACGACACTCTGTATGAAGACACTAGGAAACAAGTGGGCAAG	300
QY	301	TGGTCTGCGCACCTGCTTCCCTGCTGTGCAGGGGGAGCGGCAGAGCTGGGGCTTGG	360
Db	301	TGGTCTGCGCACCTGCTTCCCTGCTGTGCAGGGGGAGCGGCAGAGCTGGGGCTTGG	360
QY	361	GGAGACTAGATGACAGAGCCCTTCAATGGAGCCAGGTACCACTGTCGGTGGAAATCTG	420
Db	361	GGAGACTAGATGACAGAGCCCTTCAATGGAGCCAGGTACCACTGTCGGTGGAAATCTG	420
QY	421	GACAACTCCACAGAGCTCCCTGTTGGGGTAAAGTCCCCAGAAAGATCTCATCTCATG	480
Db	421	GACAACTCCACAGAGCTCCCTGTTGGGGTAAAGTCCCCAGAAAGATCTCATCTCATG	480
QY	481	CTCAGGAGCACTGACAGTGAACAAGAACAGCAAGCAAAAGAGCACTGTACATGTGGCC	540
Db	481	CTCAGGAGCACTGACAGTGAACAAGAACAGCAAGCAAAAGAGCACTGTACATGTGGCC	540
QY	541	TCTGCCAATGGGAATTCAGAAATAGTAAAACTCCTGCTGGAGAGAGATGTCAACTAT	600
Db	541	TCTGCCAATGGGAATTCAGAAATAGTAAAACTCCTGCTGGAGAGAGATGTCAACTAT	600
QY	601	GTCCTTGACACAAAAGAGGACAGCTGTATAAAGCCGTACATGCCAGAGATGAA	660
Db	601	GTCCTTGACACAAAAGAGGACAGCTGTATAAAGCCGTACATGCCAGAGATGAA	660
QY	661	TGTGGGTTAATGTCTGTGAACATGGCACTGTATCCAAATATTCAGATGAGATGGAAT	720
Db	661	TGTGGGTTAATGTCTGTGAACATGGCACTGTATCCAAATATTCAGATGAGATGGAAT	720
QY	721	ACCACCTGTGCACATAGCTATCTATATGAGATTAATTAATGGCCAAAGCACTGCTCTA	780
Db	721	ACCACCTGTGCACATAGCTATCTATATGAGATTAATTAATGGCCAAAGCACTGCTCTA	780
QY	781	TATGTGCTGATATGGAATCAAAAACAAGCATGGCCTCACACCCTGTACTTGGTGT	840
Db	781	TATGTGCTGATATGGAATCAAAAACAAGCATGGCCTCACACCCTGTACTTGGTGT	840
QY	841	CATGAGCAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAATGCA	900
Db	841	CATGAGCAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAATGCA	900
QY	901	CTGGATAGATGAGAGGACTGCTCTCATCTTCTGTATGTTGTGATCAGCAAGTATA	960
Db	901	CTGGATAGATGAGAGGACTGCTCTCATCTTCTGTATGTTGTGATCAGCAAGTATA	960
QY	961	GTCACCTTCTACTTGGAGCAAAATTTGATGTATTTTCTCAAGATCTTCTGAGACAGG	1020
Db	961	GTCACCTTCTACTTGGAGCAAAATTTGATGTATTTTCTCAAGATCTTCTGAGACAGG	1020
QY	1021	GCCAGAGATAGCTGTTTCTAGTATCATCATCTGTAATTTGGCACTTCTGTGACTAC	1080
Db	1021	GCCAGAGATAGCTGTTTCTAGTATCATCATCTGTAATTTGGCACTTCTGTGACTAC	1080
QY	1081	AAAGAAAAACAGATGCTAAAAATCTCTTGTGAAAAACAGCAATCCAGAA	1128
Db	1081	AAAGAAAAACAGATGCTAAAAATCTCTTGTGAAAAACAGCAATCCAGAA	1128

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RESULT 14
US-09-143-373
; Sequence 373, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqul
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-373

Query Match      55.3%; Score 1128; DB 10; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGTGGTTGAGTGTGATTCATGCCGGCTGCTCTTGTGTAAGAGCCATTGGTCTC 60
DB 1 AAGGTGGTTGAGTGTGATTCATGCCGGCTGCTCTTGTGTAAGAGCCATTGGTCTC 60
QY 61 AAGAGCAAGATGGGCAAGTGGTGGTCCGCTGCTCCCTGCGCAGGGAGAGCCGCAAG 120
DB 61 AAGAGCAAGATGGGCAAGTGGTGGTCCGCTGCTCCCTGCGCAGGGAGAGCCGCAAG 120
QY 121 AAGCAAGTGGGCACTTCTGAGACACGACGACTGTCTATGAAGACTCAGAGCAAG 180
DB 121 AAGCAAGTGGGCACTTCTGAGACACGACGACTGTCTATGAAGACTCAGAGCAAG 180
QY 181 AAGGGCAAGTGTGCCGCACTGCTTCCCTGCTGCAAGGGAGAGTGGCAAGCAAGTGG 240
DB 181 AAGGGCAAGTGTGCCGCACTGCTTCCCTGCTGCAAGGGAGAGTGGCAAGCAAGTGG 240
QY 241 GGGGCTTGGAGACACGACGACTGTCTATGAAGACTCAGAGCAAGAGTGGGCAAG 300
DB 241 GGGGCTTGGAGACACGACGACTGTCTATGAAGACTCAGAGCAAGAGTGGGCAAG 300
QY 301 TGGTGGTGGCACTGCTTCCCTGCTGCAAGGGAGAGCGGCAAGAGTGGGCGCTTGG 360
DB 301 TGGTGGTGGCACTGCTTCCCTGCTGCAAGGGAGAGCGGCAAGAGTGGGCGCTTGG 360
QY 361 GGAGACTAGATGACAGTGCCTTCAATGAGCCAGGTACCAAGTCCGCTGGAGAAATCTG 420
DB 361 GGAGACTAGATGACAGTGCCTTCAATGAGCCAGGTACCAAGTCCGCTGGAGAAATCTG 420
QY 421 GACAAGCTCACAAGAGCTGCTGGTGGGTTAAAGTCCCAAGAAAGATCTCATCTGATG 480
DB 421 GACAAGCTCACAAGAGCTGCTGGTGGGTTAAAGTCCCAAGAAAGATCTCATCTGATG 480
QY 481 CTCAGGACACTGACGTGAACAAGAGCAAGCAAGAGAGACTGCTACATCTGGCC 540
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DB 481 CTCAGGACACTGACGTGAACAAGAGCAAGCAAGAGAGACTGCTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCACAAGTAGTAAATCTCTCTGACAGACGATGTCACTTAAT 600
DB 541 TCTGCCAATGGGAATTCACAAGTAGTAAATCTCTCTGACAGAGATGTCACTTAAT 600
QY 601 GTCCCTGACACAAAAGAGAGACAGCTGTGATAAAGCCGTACAAATGCCAGAAATGAA 660
DB 601 GTCCCTGACACAAAAGAGAGACAGCTGTGATAAAGCCGTACAAATGCCAGAAATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATAGTATGAAAT 720
DB 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATAGTATGAAAT 720
QY 721 ACCACTCTGCACTACGCTTCTATATGAAAGATAAATTAATGGCCAAAGACAGTCTTA 780
DB 721 ACCACTCTGCACTACGCTTCTATATGAAAGATAAATTAATGGCCAAAGACAGTCTTA 780
QY 781 TATGGTGTGATATGAAATCAAAAACAGCATGGCTCACACCACTGTACTTGGTGA 840
DB 781 TATGGTGTGATATGAAATCAAAAACAGCATGGCTCACACCACTGTACTTGGTGA 840
QY 841 CATGACCAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAACGAATTTAAATGCA 900
DB 841 CATGACCAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAACGAATTTAAATGCA 900
QY 901 CTGATAGATATGGAAGACAGTCTCTCATCTTCTGATGTTGTGATCAGCAAGTATA 960
DB 901 CTGATAGATATGGAAGACAGTCTCTCATCTTCTGATGTTGTGATCAGCAAGTATA 960
QY 961 GTGAGCTTCTACTTGTAGCAAAATATGATGATCTTCAAGATATATCTGGACAGAG 1020
DB 961 GTGAGCTTCTACTTGTAGCAAAATATGATGATCTTCAAGATATATCTGGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTATGATCATCATGATATTTGGCAGTTACTTGTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTATGATCATCATGATATTTGGCAGTTACTTGTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAATCTCTTCTGAAACAGCAATCCAGAA 1128
DB 1081 AAGAAAAACAGATGCTAAATCTCTTCTGAAACAGCAATCCAGAA 1128

RESULT 15
US-09-780-669-373
; Sequence 373, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqul
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hurlal, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT FILING DATE: 2001-01-12
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;; CURRENT FILING DATE: 2001-02-09
;; NUMBER OF SEQ ID NOS: 943
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 373
;; LENGTH: 1155
;; TYPE: DNA
;; ORGANISM: Homo sapien
US-09-780-669-373

Query Match 55.3%; Score 1128; DB 10; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGTGGTGTAGGTGATGATCCATCCGCGCTCTCTCTGTAAGAACCATTTGGCTC 60
QY 61 AGAGCAAGATGGGCAAGTGGTGGCTGCTCCCTGCTGCAAGGAGGAGCGGCAAG 120
Db 61 AGAGCAAGATGGGCAAGTGGTGGCTGCTCCCTGCTGCAAGGAGGAGCGGCAAG 120
QY 121 AGCAACTGGGCACTTGTGAGACACAGAGACTCTGCTATGAAGACATCAGAGCAAG 180
Db 121 AGCAACTGGGCACTTGTGAGACACAGAGACTCTGCTATGAAGACATCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCCGCACTGCTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGGTGGCCGCACTGCTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGCTG 240
QY 241 GGGCGCTTCTGAGACACAGAGACTCTGCTATGAAGACATCAGAGCAAGATGGGCAAG 300
Db 241 GGGCGCTTCTGAGACACAGAGACTCTGCTATGAAGACATCAGAGCAAGATGGGCAAG 300
QY 301 TGGGCGCCACAGCTGCTCCCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Db 301 TGGGCGCCACAGCTGCTCCCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
QY 361 GGAAGTACATGATGATGCTGCTTCTGAGAGCCAGTACCACTCCCTGAGAGATCTG 420
Db 361 GGAAGTACATGATGATGCTGCTTCTGAGAGCCAGTACCACTCCCTGAGAGATCTG 420
QY 421 GACAAAGTCCACAGAGCTGCTGCTGAGGAGGAGTCCCAAGAAAGATCTCATGCTATG 480
Db 421 GACAAAGTCCACAGAGCTGCTGCTGAGGAGGAGTCCCAAGAAAGATCTCATGCTATG 480
QY 481 CTCAGGCACTGCTGAGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 481 CTCAGGCACTGCTGAGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 TCTGCAATGGAATGAGAAATGTAATAAATCTGCTGAGACAGATGCAACTTAAT 600
Db 541 TCTGCAATGGAATGAGAAATGTAATAAATCTGCTGAGACAGATGCAACTTAAT 600
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Db 601 GTCTTGAACAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 TGTGCGTAAATGTTGTGGAACATGAGCACTGATCCAATATCTCAGATGATGGAAT 720
Db 661 TGTGCGTAAATGTTGTGGAACATGAGCACTGATCCAATATCTCAGATGATGGAAT 720
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Db 721 ACCACTGTGCACTGCTATCTATATGAAGATTAATTAATGAGCAAGCACTGCTCTTA 780
QY 781 TATGCTCTGATATGATGATCAAAAAACAGATGGCTCACACACATGTTACTTGATGA 840
Db 781 TATGCTCTGATATGATGATCAAAAAACAGATGGCTCACACACATGTTACTTGATGA 840
QY 841 CATGAGCAAAAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Db 841 CATGAGCAAAAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
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QY 901 CTGATGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Db 901 CTGATGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTCTCAAGATATATGAGAGAGAG 1020
Db 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTCTCAAGATATATGAGAGAGAG 1020
QY 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATGATTAATTTGCCAGTACTTCTGACTAC 1080
Db 1021 GCCAGAGATGATGCTGTTTCTAGTCATCATGATTAATTTGCCAGTACTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAAAATCTCTTGAAAAACAGCAATCCAGAA 1128
Db 1081 AAGAAAAACAGATGCTAAAAATCTCTTGAAAAACAGCAATCCAGAA 1128
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RESULT 16
US-09-810-936-301
; Sequence 301, Application US/09810936
; Patent No. US2002006825A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, David C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 301
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-936-301

Query Match 55.3%; Score 1128; DB 10; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGTGGTGTAGGTGATGATCCGCGCTCTCTCTGTAAGAACCATTTGGCTC 60
Db 1 ATGTGGTGTAGGTGATGATCCGCGCTCTCTCTGTAAGAACCATTTGGCTC 60
QY 61 AGAGCAAGATGGGCAAGTGGTGGCTGCTCCCTGCTGCAAGGAGGAGCGGCAAG 120
Db 61 AGAGCAAGATGGGCAAGTGGTGGCTGCTCCCTGCTGCAAGGAGGAGCGGCAAG 120
QY 121 AGCAACTGGGCACTTGTGAGACACAGAGACTCTGCTATGAAGACATCAGAGCAAG 180
Db 121 AGCAACTGGGCACTTGTGAGACACAGAGACTCTGCTATGAAGACATCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCCGCACTGCTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGGTGGCCGCACTGCTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGCTG 240
QY 241 GGGCGCTTCTGAGACACAGAGACTCTGCTATGAAGACATCAGAGCAAGATGGGCAAG 300
Db 241 GGGCGCTTCTGAGACACAGAGACTCTGCTATGAAGACATCAGAGCAAGATGGGCAAG 300
QY 301 TGGTGGTGGCACTGCTTCCCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Db 301 TGGTGGTGGCACTGCTTCCCTGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
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QY	361	GGAGCTACAGTATGACAGTGGCTTCATGAGAGCCAGGTACCAGCTCCGTGGAGAACTATG	420
Db	361	GGAGCTACAGTATGACAGTGGCTTCATGAGAGCCAGGTACCAGCTCCGTGGAGAACTATG	420
QY	421	GACAAGCTCCACAGAGCTGGCTGGTGGGGTAAAGTCCCGAGAAAGATCTCATCTCATG	480
Db	421	GACAAGCTCCACAGAGCTGGCTGGTGGGGTAAAGTCCCGAGAAAGATCTCATCTCATG	480
QY	481	CTCAGGACACTGACGTGAACAAGAGACACAGCAAAAGAGAGACTGCTCTACATCTGGCC	540
Db	481	CTCAGGACACTGACGTGAACAAGAGAGACACAGCAAAAGAGAGACTGCTCTACATCTGGCC	540
QY	541	TCTGCCAATGGGAATTCAGAAAGTAAATAAACCTCCCTGACAGACATGTCACTTAAT	600
Db	541	TCTGCCAATGGGAATTCAGAAAGTAAATAAACCTCCCTGACAGACATGTCACTTAAT	600
QY	601	GTCCTTGACAAACAAAAGAGACAGCTCTGATAAAGGCGCTGCAATGCGAGAAATGAA	660
Db	601	GTCCTTGACAAACAAAAGAGACAGCTCTGATAAAGGCGCTGCAATGCGAGAAATGAA	660
QY	661	TGTGCGTTAATGTWCTGTGGAACATGGCACTGATCCAAATATTTCCAGATGATGAAAT	720
Db	661	TGTGCGTTAATGTWCTGTGGAACATGGCACTGATCCAAATATTTCCAGATGATGAAAT	720
QY	721	ACGACCTGACATACGCTATCTATATGAAAGATAAATTAATGCGCAAAAGCACTGCTTA	780
Db	721	ACGACCTGACATACGCTATCTATATGAAAGATAAATTAATGCGCAAAAGCACTGCTTA	780
QY	781	TATAGTCTCATATTCGATTCATAAAACAAAGCATGGCCTCACACCACTGTTACTGGTGA	840
Db	781	TATAGTCTCATATTCGATTCATAAAACAAAGCATGGCCTCACACCACTGTTACTGGTGA	840
QY	841	CATGACCAAAACAGCAAGTCGTGAAATTTTAAATCAGAAAAAAGCGAATTTAAATGCA	900
Db	841	CATGACCAAAACAGCAAGTCGTGAAATTTTAAATCAGAAAAAAGCGAATTTAAATGCA	900
QY	901	CTGATATGATATGGAAGAGATGCTCTCATACCTTGCCTGATGTTGTGGATCAGCAAGTATA	960
Db	901	CTGATATGATATGGAAGAGATGCTCTCATACCTTGCCTGATGTTGTGGATCAGCAAGTATA	960
QY	961	GTCAGCCTTCTACTTGAGCAAAATATTTGATGTATCTTCCAGATCTATCTGGACAGAG	1020
Db	961	GTCAGCCTTCTACTTGAGCAAAATATTTGATGTATCTTCCAGATCTATCTGGACAGAG	1020
QY	1021	GCCAGAGATATGCTGTTTCTAGTCATCATATGATTAATTTGCCAGTTACTTCTGACTAC	1080
Db	1021	GCCAGAGATATGCTGTTTCTAGTCATCATATGATTAATTTGCCAGTTACTTCTGACTAC	1080
QY	1081	AAACAAAACAGATGCTAAAAATCTTCTTGAAACAGCAATCCAGAA	1128
Db	1081	AAACAAAACAGATGCTAAAAATCTTCTTGAAACAGCAATCCAGAA	1128
RESULT 17			
US-09-822-827-373			
Sequence 373, Application US/09822827			
Patent No. US20020081680A1			
GENERAL INFORMATION:			
APPLICANT: Xu, Jiangchun			
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER			
FILE REFERENCE: 210121.534E1			
CURRENT APPLICATION NUMBER: US/09/822,827			
CURRENT FILING DATE: 2001-03-28			
NUMBER OF SEQ. ID NOS: 982			
SOFTWARE: FastSeq for Windows Version 3.0			
SEQ ID NO 373			
LENGTH: 1155			
TYPE: DNA			
ORGANISM: Homo sapien			
US-09-822-827-373			
Query Match	55.3%	Score 1128;	DB 10; Length 1155;

	Best Local Similarity	100.0%	Pred. No. 0:	Mismatches	0:	Indels	0:	Gaps	0:
	Matches 1128:	Conservative	0:	Mismatches	0:	Indels	0:	Gaps	0:
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Db	1	ATGGTGTTGAAGGTGTGATTCATGCCGGCGTCCCTTCTGTGTAAGAAGCCATTGGTCTC	60						
OY	61	AGGACCAAGATGGGCAAGTGGTGGTGCCTTCCCTGCTGCAAGGAGACGGGCAAG	120						
Db	61	AGGACCAAGATGGGCAAGTGGTGGTGCCTTCCCTGCTGCAAGGAGACGGGCAAG	120						
OY	121	AGCAACGTGGGCACTCTTGAGAACCCACGACTCTGTAATAACAACATCCAGAGCAAG	180						
Db	121	AGCAACGTGGGCACTCTTGAGAACCCACGACTCTGTAATAACAACATCCAGAGCAAG	180						
OY	181	ATGGGCAAGTGGTGGCGGCACACTGTCCCTCTCTCAGAGGGGAGTGGCAAGACAACTG	240						
Db	181	ATGGGCAAGTGGTGGCGGCACACTGTCCCTCTCTCAGAGGGGAGTGGCAAGACAACTG	240						
OY	241	GGCGCTTGTGAGACACCAGCACCTCTGCTATGAAGACATCAGGAACAAGATGGGCAAG	300						
Db	241	GGCGCTTGTGAGACACCAGCACCTCTGCTATGAAGACATCAGGAACAAGATGGGCAAG	300						
OY	301	TGTGCTCTGCCACTGCTTCCCCTGCTGCAAGGGGAGACGGCAABAAGCAAGTGGGCGCTGG	360						
Db	301	TGTGCTCTGCCACTGCTTCCCCTGCTGCAAGGGGAGACGGCAABAAGCAAGTGGGCGCTGG	360						
OY	361	GGAGACTACGATGAGACAGTAGTCCCTTCATGTGAGACCCAGGTACACAGTCCGTGGAAAGATCTG	420						
Db	361	GGAGACTACGATGAGACAGTAGTCCCTTCATGTGAGACCCAGGTACACAGTCCGTGGAAAGATCTG	420						
OY	421	GACAACTCCACAGAGCTGCGTGTGGGGTAAAGTCCCCAGAAAGATCTCATCTGATG	480						
Db	421	GACAACTCCACAGAGCTGCGTGTGGGGTAAAGTCCCCAGAAAGATCTCATCTGATG	480						
OY	481	CTCAGGACACTGACAGTGAACAAGAGCAACAGCAAAAGAGACATGCTTACATCTGGCC	540						
Db	481	CTCAGGACACTGACAGTGAACAAGAGCAACAGCAAAAGAGACATGCTTACATCTGGCC	540						
OY	541	TCTGCGCATGGGAATTCAGAAAGTAAATAAACCCTGCTGAGACAGATGTCACACTTAAT	600						
Db	541	TCTGCGCATGGGAATTCAGAAAGTAAATAAACCCTGCTGAGACAGATGTCACACTTAAT	600						
OY	601	GTCCTTGAACAACAAAAGAGGACAGCTCTGATTAAGGCCCTGACAAATGCCAGGAAGATGA	660						
Db	601	GTCCTTGAACAACAAGAGGACAGCTCTGATTAAGGCCCTGACAAATGCCAGGAAGATGA	660						
OY	661	TGTGCGTTAATGTCTGTGGACATGGGCACTGATCCAATATTCACAGATAGATGGAAT	720						
Db	661	TGTGCGTTAATGTCTGTGGACATGGGCACTGATCCAATATTCACAGATAGATGGAAT	720						
OY	721	ACCACCTCTGCACACTATGCTATCTATTAATGAAGTAATTAATGAGCCAAACACTGCTCTTA	780						
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OY	781	TATGCTGCTGATATTCGAATCAAAAAACAAGCATGGGCTCTCACCACTGTTACTTGGTGA	840						
Db	781	TATGCTGCTGATATTCGAATCAAAAAACAAGCATGGGCTCTCACCACTGTTACTTGGTGA	840						
OY	841	CATGAGCAAAAAACAGCAAGTGTGAATTTTTAATCAAGAAAAAGCGAATTTAAATGCA	900						
Db	841	CATGAGCAAAAAACAGCAAGTGTGAATTTTTAATCAAGAAAAAGCGAATTTAAATGCA	900						
OY	901	CTGGATTAATATNGAAGAGACGTCTCACTACTCTGTATGTGTGGATCACCAAGTATA	960						
Db	901	CTGGATTAATATNGAAGAGACGTCTCACTACTCTGTATGTGTGGATCACCAAGTATA	960						
OY	961	GTCAGCCTTCTACTGTAGCAAAATTTATGATGATCTTCTCAAGATCTATCTGACAGACG	1020						
Db	961	GTCAGCCTTCTACTGTAGCAAAATTTATGATGATCTTCTCAAGATCTATCTGACAGACG	1020						
OY	1021	GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTAACTTCTGACTAC	1080						
Db	1021	GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTAACTTCTGACTAC	1080						

Db 1021 GCCAGAGATGCTGCTTTTCAGTCATCATCATGTAATTTGCGAGTCTTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAAAATCTCTTGAAAAACAGCAATCCAGAA 1128
Db 1081 AAGAAAAACAGATGCTAAAAATCTCTTTCTGAAAAACAGCAATCCAGAA 1128

RESULT 18

US-09-429-755-301
; Sequence 301, Application US/09429755A
; Patent No. US20020111467A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 301
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-301

Query Match 55.3%; Score 1128; DB 10; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTGTTGAGTTGATTCATGCGGCTCTCTTCTTGAAAGAACCTTTGCTC 60
Db 1 ATGTTGTTGAGTTGATTCATGCGGCTCTCTTCTTGAAAGAACCTTTGCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGCTTCCCTCTGACAGGAGAGGGCGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGTGCTGCGCTTCCCTCTGACAGGAGAGGGCGCAAG 120
QY 121 AGCAAGCTGGGCACTTCTGAGACACAGACACTCTGCTATGAAGACACTGAGGCAAG 180
Db 121 AGCAAGCTGGGCACTTCTGAGACACAGACACTCTGCTATGAAGACACTGAGGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
QY 241 GGGCCTTCTGAGACACAGACACTTCTGTAAGACACTCAGAAACATGAGGCAAG 300
Db 241 GGGCCTTCTGAGACACAGACACTTCTGTAAGACACTCAGAAACATGAGGCAAG 300
QY 301 TGTGTTGCTCCACTCTTCCCTGCTGCAAGGGGAGCGGCAAGAGTGGCGCTTGG 360
Db 301 TGTGTTGCTCCACTCTTCCCTGCTGCAAGGGGAGCGGCAAGAGTGGCGCTTGG 360
QY 361 GGAAGCTACGATGACAGTCTTCTGAGAGCCAGTACCCAGTCCGCGGAGAAAGTGTG 420
Db 361 GGAAGCTACGATGACAGTCTTCTGAGAGCCAGTACCCAGTCCGCGGAGAAAGTGTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGTTGGGGTAAATCCCAAGAAAGATCTATGCTCATG 480
Db 421 GACAAGCTCCACAGAGCTGCTGTTGGGGTAAATCCCAAGAAAGATCTATGCTCATG 480
QY 481 CTCAGGGAAGCTGACGTGAACAGAGACAAAGAGAGACTGCTCTACATCTGGCC 540
Db 481 CTCAGGGAAGCTGACGTGAACAGAGACAAAGAGAGACTGCTCTACATCTGGCC 540
QY 541 TCTTCCATGGGAATTCAAGATGTAATAACTCTGCTGGACAGACATGTCAACTTAAT 600
Db 541 TCTTCCATGGGAATTCAAGATGTAATAACTCTGCTGGACAGACATGTCAACTTAAT 600

Db 541 TCTTCCATGGGAATTCAAGATGTAATAACTCTGCTGGACAGACATGTCAACTTAAT 600
QY 601 GTCTTGCACACAAAAGAGAGACAGCTGATTAAGGCGCTACATGCGCAGAGATGAA 660
Db 601 GTCTTGCACACAAAAGAGAGACAGCTGATTAAGGCGCTACATGCGCAGAGATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGGCAGCTGATCCAAATATTCAGATGATGAAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGGCAGCTGATCCAAATATTCAGATGATGAAAT 720
QY 721 ACCACTGTCAGCTACGCTATATATGAGATTAATTAATGCGCAAGAGCTGCTCTTA 780
Db 721 ACCACTGTCAGCTACGCTATATATGAGATTAATTAATGCGCAAGAGCTGCTCTTA 780
QY 781 TATGTTGCTGATATGCAATCAAAAACAGAGATGCGCTCACACACAGTTCCTGCTGA 840
Db 781 TATGTTGCTGATATGCAATCAAAAACAGAGATGCGCTCACACACAGTTCCTGCTGA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATAGATATGGAAGAGCTGCTCATCTGCTGATATGTTGATGACAGCAAGTATA 960
Db 901 CTGATAGATATGGAAGAGCTGCTCATCTGCTGATATGTTGATGACAGCAAGTATA 960
QY 961 GTCAAGCTTCTACTGTGAGCAAAATATGATATCTCTCAAGATCTATCTGACAGACG 1020
Db 961 GTCAAGCTTCTACTGTGAGCAAAATATGATATCTCTCTCAAGATCTATCTGACAGACG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAA 1128
Db 1081 AAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAA 1128

RESULT 19

US-09-810-936-323
; Sequence 323, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Lynda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 323
; LENGTH: 1590
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-810-936-323

Query Match 51.2%; Score 1044; DB 10; Length 1590;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1094; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 34 TCTTCTGGAAGAACCTTTTGGTCTCAGAGCAAGTGGCAAGTGGTCTGCCGTTGC 93
Db 34 TCTTCTGGAAGAACCTTTTGGTCTCAGAGCAAGTGGCAAGTGGTCTGCCGTTGC 93

Db 469 TCTCTGTGAAGAGCCATTGGTCTCAGAGACAGATGGGCAAGTGTGCTGCCGTTGC 528
QY 94 TTCCCTGCTGCAGAGAGCGGCAAGAGACAGTGGGCACTTCTGAGACGACGAC 153
Db 529 TTCCCTGCTGCAGAGAGCGGCAAGAGACAGTGGGCACTTCTGAGACGACGAC 568
QY 154 TCTGCTATGAAGACACTCAGAGAGAGATGGGCAAGTGTGCTGCCGCACTGCTTCCCTGC 213
Db 589 TCTGCTATGAAGACACTCAGAGAGAGATGGGCAAGTGTGCTGCCGCACTGCTTCCCTGC 648
QY 214 TCGAGGGGAGTGGGCAAGAGCAAGTGGGCGCTTCTGAGACAGACAGACTTGTCTATG 273
Db 649 TCGAGGGGAGTGGGCAAGAGCAAGTGGGCGCTTCTGAGACAGACAGACTTGTCTATG 708
QY 274 AAGACACTCAGAGAAAGATGGGCAAGTGGGCGCTTCTGAGACAGACAGACTTGTCTATG 333
Db 709 AAGACACTCAGAGAAAGATGGGCAAGTGGGCGCTTCTGAGACAGACAGACTTGTCTATG 768
QY 334 AAGGCGAAGAGCAAGTGGGCGCTTGGGAGAGACTAGACAGTGCCTTCTATGAGGCC 393
Db 769 AAGGCGAAGAGCAAGTGGGCGCTTGGGAGAGACTAGACAGTGCCTTCTATGAGGCC 828
QY 394 AGGTACCACTGCTGCTGAGAAAGTCTGACAGAGCTCCAGAGAGCTGCTGCTGCTAAA 453
Db 829 AGGTACCACTGCTGCTGAGAAAGTCTGACAGAGCTCCAGAGAGCTGCTGCTGCTAAA 888
QY 454 GTCCCGAAGAGGATCTCATGCTCATGCTCAGGAGACAGTGCCTGCAAGAGAGCAAG 513
Db 889 GTCCCGAAGAGGATCTCATGCTCATGCTCAGGAGACAGTGCCTGCAAGAGAGCAAG 948
QY 514 CAAAAGAGAGCTGCTTACATCTGCGCTTGCCTGCAAGTGCCTGCAAGTGCCTGCAAG 573
Db 949 CAAAAGAGAGCTGCTTACATCTGCGCTTGCCTGCAAGTGCCTGCAAGTGCCTGCAAG 1008
QY 574 CTGCTGAGAGAGAGTGTCACTTAATGTCTTGTGACACAAAAAGAGAGAGCTGTGAT 633
Db 1009 CTGCTGAGAGAGAGTGTCACTTAATGTCTTGTGACACAAAAAGAGAGAGCTGTGAT 1068
QY 634 AAGGCGCTCAATGCGAGAGAGTGAATGCGTGAATGCTGCAAGAGAGAGAGAGAGAG 693
Db 1069 AAGGCGCTCAATGCGAGAGAGTGAATGCGTGAATGCTGCAAGAGAGAGAGAGAGAG 1128
QY 694 CCAAAATATTCAGATGATGGAATATACACTCTGCACTAGCCTATCTATATGAGAGAT 753
Db 1129 CCAAAATATTCAGATGATGGAATATACACTCTGCACTAGCCTATCTATATGAGAGAT 1188
QY 754 AAATTAATGCGCAAGAGAGTCTCTTAATATGCTGTGATATGCAATCAAAAAAGAGAT 813
Db 1189 AAATTAATGCGCAAGAGAGTCTCTTAATATGCTGTGATATGCAATCAAAAAAGAGAT 1248
QY 814 GGGCTCACACACTGTTACTTGGTGTACATGAGCAAAAAAGAGAGAGAGAGAGAGAGAT 873
Db 1249 GGGCTCACACACTGTTACTTGGTGTACATGAGCAAAAAAGAGAGAGAGAGAGAGAGAT 1308
QY 874 ATCAAGAAAAAAGCGAATTTAAATGAGAGAGATGATATGAGAGAGAGAGAGAGAGAT 933
Db 1309 ATCAAGAAAAAAGCGAATTTAAATGAGAGAGATGATATGAGAGAGAGAGAGAGAGAT 1368
QY 934 GCTGATGTTGTGAGTACAGCAAGTATAGTACGCTTCTACTTGAAGCAAAATATGATGTA 993
Db 1369 GCTGATGTTGTGAGTACAGCAAGTATAGTACGCTTCTACTTGAAGCAAAATATGATGTA 1428
QY 994 TCTTTCAGAGATCTATCTGAGAGAGAGAGAGAGAGATGCTTCTATGATCTATCTAT 1053
Db 1429 TCTTTCAGAGATCTATCTGAGAGAGAGAGAGAGAGATGCTTCTATGATCTATCTAT 1488
QY 1054 GTAAATTTGCACTTACTTCTGACTCAAAAGAAAAAGAGATGCTTCTATGATCTTCTGAA 1113
Db 1489 GTAAATTTGCACTTACTTCTGACTCAAAAGAAAAAGAGATGCTTCTATGATCTTCTGAA 1548
QY 1114 AACAGCAATCCAGAA 1128
Db 1549 AACAGCAATCCAGAA 1563

RESULT 20
US-09-810-936-328
; Sequence 328, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Al-jun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; THERAPY AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419c11
; CURRENT APPLICATION NUMBER: US/09/810, 936
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 328
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-810-936-328

Query Match 47.8%; Score 975; DB 10; Length 1155;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1125; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGCTGTTGAGGTTGATTCATGCCGCTGCTTCTGTGGAAGAGCCATTGCTTC 60
Db 1 ATGCTGTTGAGGTTGATTCATGCCGCTGCTTCTGTGGAAGAGCCATTGCTTC 60
QY 61 AGAGAGAAATGGGCAAGTGTGCTGCTGCTTCCCTGTCAGAGAGAGAGAGAGAG 120
Db 61 AGAGAGAAATGGGCAAGTGTGCTGCTGCTTCCCTGTCAGAGAGAGAGAGAGAG 120
QY 121 AGCAAGTGGGCACTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Db 121 AGCAAGTGGGCACTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGAGAGAGAGAGAGAGAGAGAG 240
Db 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGAGAGAGAGAGAGAGAGAGAG 240
QY 241 GGGCTTCTGAG 300
Db 241 GGGCTTCTGAG 300
QY 301 TGGTGTGCGACAGTCTCCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 301 TGGTGTGCGACAGTCTCCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 GGAGACTAG 420
Db 361 GGAGACTAG 420
QY 421 GAG 480
Db 421 GAG 480
QY 481 CTGAG 540
Db 481 CTGAG 540
QY 541 TCTGCCAATGGAATTCAGAAAGTAAATCTCTCTGAGAGAGAGAGAGAGAGAT 600
Db 541 TCTGCCAATGGAATTCAGAAAGTAAATCTCTCTGAGAGAGAGAGAGAGAGAT 600

OY	601	GTCTGTGACACAAAAGAGGACAGCTCTGTATAAAGGCGCTACAAATGCCAGGAAGATGGA	660
Db	601	GTCTTGTGACAAAAGAGGACAGCTCTGTATAAAGGCGCTACAAATGCCAGGAAGATGGA	660
OY	661	TGTGCGTTAATGTTCTGTGAACATGAGCAGCTGATCCAAATATTCAGATGAGTATGGAAT	720
Db	661	TGTGCGTTAATGTTCTGTGAACATGAGCAGCTGATCCAAATATTCAGATGAGTATGGAAT	720
OY	721	ACCACTCTGCACCTACGCTATCTATTAATGAAGATTAATTAATGGCCAAAGCATCTGCTCTTA	780
Db	721	ACCACTCTGCACCTACGCTATCTATTAATGAAGATTAATTAATGGCCAAAGCATCTGCTCTTA	780
OY	781	TATGCTGCTGATATTCGAATCAATCAAAAACAACATGAGCGCTCACACACTGTTACTTGGTGTGA	840
Db	781	TATGCTGCTGATATTCGAATCAATCAAAAACAACATGAGCGCTCACACACTGTTACTTGGTGTGA	840
OY	841	CATGACGCAAAAACAGCAAGCTGTGAAATTTTAAATCAAGAAAAAAGCGAATTTAAATGCA	900
Db	841	CATGACGCAAAAACAGCAAGCTGTGAAATTTTAAATCAAGAAAAAAGCGAATTTAAATGCA	900
OY	901	CTGGATAGATATGGAAGAGCTGCTCATPACTGCTGATGCTGTGATGTTGGATCAGCAAGTATA	960
Db	901	CTGGATAGATATGGAAGAGCTGCTCATPACTGCTGATGCTGTGATGTTGGATCAGCAAGTATA	960
OY	961	GTCAGCCTTCTACTTGTGAGCAAAAATATTTGATGTATCTTCTCAAGATCTATCTGAGACAGG	1020
Db	961	GTCAGCCTTCTACTTGTGAGCAAAAATATTTGATGTATCTTCTCAAGATCTATCTGAGACAGG	1020
OY	1021	GCCAGAGAGTATGCTGTTTCTAGCATCATCATCATGTAATTTGCCAGTACTTCTGACTAC	1080
Db	1021	GCCAGAGAGTATGCTGTTTCTAGCATCATCATCATGTAATTTGCCAGTACTTCTGACTAC	1080
OY	1081	AAGAGAAAAAGATGCTAAAAATCTCTTCTGAAACAGCAATCCAGAA	1128
Db	1081	AAGAGAAAAAGATGCTAAAAATCTCTTCTGAAACAGCAATCCAGAA	1128

RESULT 21
 US-09-759-143-368
 : Sequence 368, Application US/09759143
 : Patent No. US2002002248A1
 : GENERAL INFORMATION:
 : APPLICANT: Xu, Jiangchun
 : APPLICANT: Dillon, David C.
 : APPLICANT: Mitcham, Jennifer L.
 : APPLICANT: Harlocker, Susan L.
 : APPLICANT: Jiang, Yugu
 : APPLICANT: Henderson, Robert A.
 : APPLICANT: Kaios, Michael D.
 : APPLICANT: Fanger, Gary R.
 : APPLICANT: Retter, Marc W.
 : APPLICANT: Stolk, John A.
 : APPLICANT: Day, Craig H.
 : APPLICANT: Vedvik, Thomas S.
 : APPLICANT: Carter, Darlick
 : APPLICANT: Li, Samuel
 : APPLICANT: Wang, Aijun
 : APPLICANT: Skelley, Yasir A.W.
 : APPLICANT: Hepler, William
 : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 : FILE REFERENCE: 210121.427C23
 : CURRENT APPLICATION NUMBER: US/09/759,143
 : CURRENT FILING DATE: 2001-01-12
 : NUMBER OF SEQ ID NOS: 934
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO 368
 : LENGTH: 1512
 : TYPE: DNA
 : ORGANISM: Homo sapien
 : US-09-759-143-368

Query Match	Similarity	24.1%	Score 491	DB 10	Length 1512
Best Local	Similarity	94.4%	Pred. No. 8e-180		
Matches	691	Conservative	0	Mismatches	4
				Indels	0
				Gaps	0
QY	34	TCCTCTGTGTAAGAACCATTTTGGTCTCAGACAGCAAGATGGGCAAGTGTGTCGCGTTGC	93		
Db	256	TCCTCTGTGTAAGAACCATTTTGGTCTCAGACAGCAAGATGGGCAAGTGTGTCGCGTTGC	315		
QY	94	TTCCCTCTGCTGCAGGAGAGCGGCGCAAGCAACGTGGGCACTTTCTGGAGACCAAGCAAC	153		
Db	316	TTCCCTCTGCTGCAGGAGAGCGGCGCAAGCAACGTGGGCACTTTCTGGAGACCAAGCAAC	375		
QY	154	TCTGCTATCAACACTCTCGAGAGCAAGATGGGCAAGTGGTGGCGGCACCTGCTCCCTGC	213		
Db	376	TCTGCTATCAACACTCTCGAGAGCAAGATGGGCAAGTGGTGGCGGCACCTGCTCCCTGC	435		
QY	214	TGCAGGGGAGTGGCAAGAGCAACGTGGGCGCTTCTGAGACACAGACACTCTGTATG	273		
Db	436	TGCAGGGGAGTGGCAAGAGCAACGTGGGCGCTTCTGAGACACAGACACTCTGTATG	495		
QY	274	AAGACACTCAGAACACAGATGGGCAAGTGGTCTGCTGCTCTCTCCCTGCTGCAAGGGG	333		
Db	496	AAGACACTCAGAACACAGATGGGCAAGTGGTCTGCTGCTCTCTCCCTGCTGCAAGGGG	555		
QY	334	ACGGCGAAGAGCAAGTGGGCGCTTGGGAGCACTGCGATGACAGTGGCTTCAAGGAGCC	393		
Db	556	ACGGCGAAGAGCAAGTGGGCGCTTGGGAGCACTGCGATGACAGTGGCTTCAAGGAGCC	615		
QY	394	AGGTACCAACGTCTGTGAGAAAGATGTGCAAGCACTGCAAGCAAGTGGCTGTGGGGTAA	453		
Db	616	AGGTACCAACGTCTGTGAGAAAGATGTGCAAGCACTGCAAGCAAGTGGCTGTGGGGTAA	675		
QY	454	GTCGCCAGAAAGATCTCATCTGCTCATGCTCAGGGACACTGACGTGAACAAGAGCAAG	513		
Db	676	GTCGCCAGAAAGATCTCATCTGCTCATGCTCAGGGACACTGACGTGAACAAGAGCAAG	735		
QY	514	CAAAAGAGGACGTCTCATCTGCGCTTGGCAANTGGGAATTCGAATTAATAAAATC	573		
Db	736	CAAAAGAGGACGTCTCATCTGCGCTTGGCAANTGGGAATTCGAATTAATAAAATC	795		
QY	574	CTGCTGACAGACAGATGTCACCTTAATGCTCTTGACAAACAAAAGAGACAGCTGATA	633		
Db	796	CTGCTGACAGACAGATGTCACCTTAATGCTCTTGACAAACAAAAGAGACAGCTGATA	855		
QY	634	AAGCCCGTACAAATGCCAGAGATGAATGGCTTAATGTTCTGGAACATGGCACTGAT	693		
Db	856	AAGCCCGTACAAATGCCAGAGATGAATGGCTTAATGTTCTGGAACATGGCACTGAT	915		
QY	694	CCAAATATTCAGATGATGATGAATACCACTCT	728		
Db	916	CCAAATATTCAGATGATGATGAATACCACTCT	950		

APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 368
LENGTH: 1512
TYPE: DNA
ORGANISM: Homo sapien
US-09-780-669-368

Query Match 24.1%; Score 491; DB 10; Length 1512;
Best Local Similarity 99.4%; Pred. No. 8e-180;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAACCCATTGGTCTCAGAGCAAGATGGCAAGTGGTCTGCCGTTGC 93
DB 256 TCTTCTGTGAAGAACCCATTGGTCTCAGAGCAAGATGGCAAGTGGTCTGCCGTTGC 315
QY 94 TTCCCTGCTGAGGAGGAGGAGGAGCAAGCTGGGCACTTCTGGAGACGACGAC 153
DB 316 TTCCCTGCTGAGGAGGAGGAGGAGCAAGCTGGGCACTTCTGGAGACGACGAC 375
QY 154 TCTGCTATGAGACACTCAGAGAGCAAGATGGGCAAGTGGTCCGCACTGCTTCCCTG 213
DB 376 TCTGCTATGAGACACTCAGAGAGCAAGATGGGCAAGTGGTCCGCACTGCTTCCCTG 435
QY 214 TGCAGGGGAGTGGCAGAGCAAGCTGGGCGCTTCTGAGACCAAGAGCTCTGATG 273
DB 436 TGCAGGGGAGTGGCAGAGCAAGCTGGGCGCTTCTGAGACCAAGAGCTCTGATG 495
QY 274 AAGCACTCAGGAGCAAGATGGGCAAGTGGTCCGCACTGCTTCCCTGCTGAGGGGG 333
DB 496 AAGCACTCAGGAGCAAGATGGGCAAGTGGTCCGCACTGCTTCCCTGCTGAGGGGG 555
QY 334 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTACGATGACAGTGCCTTCATGAGGCC 393
DB 556 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTACGATGACAGTGCCTTCATGAGGCC 615
QY 394 AGTACCAAGCTCCGTGGAGAAAGATGTGACAAGCTCCACAGAGCTGCCTGGTGGGTAA 453
DB 616 AGTACCAAGCTCCGTGGAGAAAGATGTGACAAGCTCCACAGAGCTGCCTGGTGGGTAA 675
QY 454 GTCCCGCAAGAAAGATGTGATGCTATGCTCAGGGGCACTGACGTGAACAAGAGCAAG 513
DB 676 GTCCCGCAAGAAAGATGTGATGCTATGCTCAGGGGCACTGACGTGAACAAGAGCAAG 735
QY 514 CAAAAGAGAGTGTCTCATCTGCGCTCTGCCAATGGGAATTCAGAGTAAACTC 573
DB 736 CAAAAGAGAGTGTCTCATCTGCGCTCTGCCAATGGGAATTCAGAGTAAACTC 795
QY 574 CTGCTGACAGACGATGTCAACTTAATGTCTTGACAACAAAAGAGAGACAGCTGTGATA 633
DB 796 STGCTGGACAGACGATGTCAACTTAATGTCTTGACAACAAAAGAGAGACAGCTGTGATA 855
QY 634 AAGGCCGTACATGCGCAGAGATGAATGTGCGTTAATGTGCTGGAACATGGCACTGAT 693
DB 856 AAGGCCGTACATGCGCAGAGATGAATGTGCGTTAATGTGCTGGAACATGGCACTGAT 915
QY 694 CCAATATTCAGATGAGTATGGAATACCACTCT 728
DB 916 CCAATATTCAGATGAGTATGGAATACCACTCT 950

RESULT 23
US-09-810-936-294

Sequence 294, Application US/09810936
Patent No. US20020068285A1
GENERAL INFORMATION:
APPLICANT: Fridakis, Tony N.
APPLICANT: Reed, Steven G.
APPLICANT: Smith, John M.
APPLICANT: Misher, Linda E.
APPLICANT: Dillon, David C.
APPLICANT: Retter, Marc W.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Harlocker, Susan L.
APPLICANT: Day, Craig H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE REFERENCE: 210121.419C11
CURRENT APPLICATION NUMBER: US/09/810,936
CURRENT FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 334
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 294
LENGTH: 1512
TYPE: DNA
ORGANISM: Homo sapien
US-09-810-936-294

Query Match 24.1%; Score 491; DB 10; Length 1512;
Best Local Similarity 99.4%; Pred. No. 8e-180;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAACCCATTGGTCTCAGAGCAAGATGGGCAAGTGGTCTGCCGTTGC 93
DB 256 TCTTCTGTGAAGAACCCATTGGTCTCAGAGCAAGATGGGCAAGTGGTCTGCCGTTGC 315
QY 94 TTCCCTGCTGAGGAGGAGGAGGAGCAAGCTGGGCACTTCTGGAGACGACGAC 153
DB 316 TTCCCTGCTGAGGAGGAGGAGGAGCAAGCTGGGCACTTCTGGAGACGACGAC 375
QY 154 TCTGCTATGAGACACTCAGAGAGCAAGATGGGCAAGTGGTCCGCACTGCTTCCCTG 213
DB 376 TCTGCTATGAGACACTCAGAGAGCAAGATGGGCAAGTGGTCCGCACTGCTTCCCTG 435
QY 214 TGCAGGGGAGTGGCAGAGCAAGCTGGGCGCTTCTGAGACCAAGAGCTCTGATG 273
DB 436 TGCAGGGGAGTGGCAGAGCAAGCTGGGCGCTTCTGAGACCAAGAGCTCTGATG 495
QY 274 AAGCACTCAGGAGCAAGATGGGCAAGTGGTCCGCACTGCTTCCCTGCTGAGGGGG 333
DB 496 AAGCACTCAGGAGCAAGATGGGCAAGTGGTCCGCACTGCTTCCCTGCTGAGGGGG 555
QY 334 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTACGATGACAGTGCCTTCATGAGGCC 393
DB 556 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTACGATGACAGTGCCTTCATGAGGCC 615
QY 394 AGTACCAAGCTCCGTGGAGAAAGATGTGACAAGCTCCACAGAGCTGCCTGGTGGGTAA 453
DB 616 AGTACCAAGCTCCGTGGAGAAAGATGTGACAAGCTCCACAGAGCTGCCTGGTGGGTAA 675
QY 454 GTCCCGCAAGAAAGATGTGATGCTATGCTCAGGGGCACTGACGTGAACAAGAGCAAG 513
DB 676 GTCCCGCAAGAAAGATGTGATGCTATGCTCAGGGGCACTGACGTGAACAAGAGCAAG 735
QY 514 CAAAAGAGAGTGTCTCATCTGCGCTCTGCCAATGGGAATTCAGAGTAAACTC 573
DB 736 CAAAAGAGAGTGTCTCATCTGCGCTCTGCCAATGGGAATTCAGAGTAAACTC 795
QY 574 CTGCTGACAGACGATGTCAACTTAATGTCTTGACAACAAAAGAGAGACAGCTGTGATA 633
DB 796 STGCTGGACAGACGATGTCAACTTAATGTCTTGACAACAAAAGAGAGACAGCTGTGATA 855
QY 634 AAGGCCGTACATGCGCAGAGATGAATGTGCGTTAATGTGCTGGAACATGGCACTGAT 693
DB 856 AAGGCCGTACATGCGCAGAGATGAATGTGCGTTAATGTGCTGGAACATGGCACTGAT 915


```

; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810.936
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 295
; LENGTH: 1853
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-936-295
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Query Match          12.4%; Score 252; DB 10; Length 1853;
Best Local Similarity 99.7%; Pred. No. 4.5e-88;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 34 TCTTCTGTGAAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGTGCTGCCGTTGC 93
DB 256 TCTTCTGTGAAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGTGCTGCCGTTGC 315
QY 94 TTCCCTGCTGTCAGAGGAGCGGCAAGAGCAAGCTGGCACTTTGTGAGACCAAGAGAGC 153
DB 316 TTCCCTGCTGTCAGAGGAGCGGCAAGAGCAAGCTGGCACTTTGTGAGACCAAGAGAGC 375
QY 154 TCTGCTATGAAGACACACACAGAGCAAGATGGGCAAGTGTGCTGCCGCTGCTATG 213
DB 376 TCTGCTATGAAGACACACACAGAGCAAGATGGGCAAGTGTGCTGCCGCTGCTATG 435
QY 214 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGACCAAGAGCAAGTGTATG 273
DB 436 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGACCAAGAGCAAGTGTATG 495
QY 274 AAGACACTCAGGAACAAGATGGGCAAGTGTGCTGCACTGCTTCCCTGCTGAGGGG 333
DB 496 AAGACACTCAGGAACAAGATGGGCAAGTGTGCTGCACTGCTTCCCTGCTGAGGGG 555
QY 334 AGC 336
DB 556 AGC 558
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RESULT 29
US-09-822-827-369
; Sequence 369, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822.827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 369
; LENGTH: 1853
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-369
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Query Match          12.4%; Score 252; DB 10; Length 1853;
Best Local Similarity 99.7%; Pred. No. 4.5e-88;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 34 TCTTCTGTGAAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGTGCTGCCGTTGC 93
DB 256 TCTTCTGTGAAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGTGCTGCCGTTGC 315
QY 94 TTCCCTGCTGTCAGAGGAGCGGCAAGAGCAAGCTGGCACTTTGTGAGACCAAGAGAGC 153
DB 316 TTCCCTGCTGTCAGAGGAGCGGCAAGAGCAAGCTGGCACTTTGTGAGACCAAGAGAGC 375
QY 154 TCTGCTATGAAGACACACACAGAGCAAGATGGGCAAGTGTGCTGCCGCTGCTATG 213
DB 376 TCTGCTATGAAGACACACACAGAGCAAGATGGGCAAGTGTGCTGCCGCTGCTATG 435
QY 214 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGACCAAGAGCAAGTGTATG 273
DB 436 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGACCAAGAGCAAGTGTATG 495
QY 274 AAGACACTCAGGAACAAGATGGGCAAGTGTGCTGCACTGCTTCCCTGCTGAGGGG 333
DB 496 AAGACACTCAGGAACAAGATGGGCAAGTGTGCTGCACTGCTTCCCTGCTGAGGGG 555
QY 334 AGC 336
DB 556 AGC 558
```

```

RESULT 30
US-09-429-755-295
; Sequence 295, Application US/09429755A
; Patent No. US2002011167A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429.755A
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 295
; LENGTH: 1853
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-295
```

```

Query Match          12.4%; Score 252; DB 10; Length 1853;
Best Local Similarity 99.7%; Pred. No. 4.5e-88;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 34 TCTTCTGTGAAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGTGCTGCCGTTGC 93
DB 256 TCTTCTGTGAAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGTGCTGCCGTTGC 315
QY 94 TTCCCTGCTGTCAGAGGAGCGGCAAGAGCAAGCTGGCACTTTGTGAGACCAAGAGAGC 153
DB 316 TTCCCTGCTGTCAGAGGAGCGGCAAGAGCAAGCTGGCACTTTGTGAGACCAAGAGAGC 375
QY 154 TCTGCTATGAAGACACACACAGAGCAAGATGGGCAAGTGTGCTGCCGCTGCTATG 213
DB 376 TCTGCTATGAAGACACACACAGAGCAAGATGGGCAAGTGTGCTGCCGCTGCTATG 435
QY 214 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGACCAAGAGCAAGTGTATG 273
DB 436 TGCAGGGGAGTGGCAAGAGCAAGTGGGCGCTTCTGAGACCAAGAGCAAGTGTATG 495
QY 274 AAGACACTCAGGAACAAGATGGGCAAGTGTGCTGCACTGCTTCCCTGCTGAGGGG 333
DB 496 AAGACACTCAGGAACAAGATGGGCAAGTGTGCTGCACTGCTTCCCTGCTGAGGGG 555
```

QY	334	AGC	336
Db	556	AGC	558

RESULT 31
US-09-759-143-531
; Sequence 531, Application US/09759143

```

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427023
CURRENT APPLICATION NUMBER: US/09/7759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 531
LENGTH: 879
TYPE: DNA
ORGANISM: Homo sapiens
US-09-759-143--531

```

Query Match	5.9%	Score 120;	DB 10;	length 879;
Best Local Similarity	99.1%	Pred. No. 2.3e-37;		
Matches 220; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0

OY	507	GGACAGCAAAAAGGAGACTGCTTACATCATGTGCCCTTCGCCAATGGGAATTCCAGAAGTAGT	566
Db	333	GGACAAGCAAAAGGAGACTGCTTACATCTTG6CCTCTGCACAATGGGATTCCAGAAGTAGT	392
OY	567	AAAACTCCTGCTGGACAGACGATGTTCAACTTAATGTCTTGACAAACAAAAAGAGGACAGC	626
Db	393	AAAACCTGCTGCTGGACAGACGATGTTCAACTTAATGTCTTGACAAACAAAAAGAGGACAGC	452
OY	627	TCTGATTAAGGCCCTACAAATGCCAGGAAGATGAATGTGCGTTAATGTGTGCTGGACATGG	686
Db	453	TCTACCAAAGCCCTACAAATGCCAGGAAGATGAATGTGCGTTAATGTGTGCTGGACATGG	512
OY	687	CACATGATCCAAATATTCCAGATGSGATNGGAAATACCACACTT	728
Db	513	CACATGATCCAAATATTCCAGATGSGATNGGAAATACCACACTT	554

RESULT 32
US-09-780-669-531
; Sequence 531, Application US/09780669
; Patent No. US20020051977A1

```

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A
; APPLICANT:

```

```

APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stoik, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasar A.W.
APPLICANT: Hepler, William
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427624
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 531
LENGTH: 879
TYPE: DNA
ORGANISM: Homo sapiens
US-09-780-669-531

```

Query Match	5.98;	Score 120;	DB 10;	length 879;
Best Local Similarity	99.18;	Pred. No. 2.3e-37;		
Matches 220;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0

QY	507	GGCAGACAAAAGAGAGATGCTGTACATCTGCGCTTGCCAAATGGGAATTCAGAAAGT	566
QY	567	AAATCTCCTGCTGGACAGACATGTCAACTTAATGTCTTGACAAACAAAAAGAGACAGC	626
Db	333	GGACAGACAAAAGAGAGACTGCTTACATCTTGCCCTCTGCGCAATGGGAATTCAGAAAGT	392
QY	393	AAACTCGTGTGGACAGACAGATGTCAACTTAATGTCTTGACAAACAAAAAGAGACAGC	452
Db	627	TCTGTAAAGGCCGTACACATGCCACAGAGATGAATGTGCGTTAATGTTGCTGGAACTGG	686
QY	453	TCTGCAAAAGGCCGTACATGCCACAGAGATGAATGTGCGTTAATGTTGCTGGAACTGG	512
Db	687	CACGTATCCAAATATTCAGATGAGTATGAGAAATACCACTGT	728
QY	513	CACGTATCCAAATATTCAGATGAGTATGAGAAATACCACTGT	554

RESULT 33
US-09-810-936-314
; Sequence 314, Application US/09810936
; Patent No. US20020068285A1

1 APPLICANT: Frudakis, Tony N.
 2 APPLICANT: Reed, Steven G.
 3 APPLICANT: Smith, John M.
 4 APPLICANT: Misher, Linda E.
 5 APPLICANT: Dillon, Davin C.
 6 APPLICANT: Retter, Marc W.
 7 APPLICANT: Wang, Aijun
 8 APPLICANT: Skeiky, Yasir A.W.
 9 APPLICANT: Harlocker, Susan L.
 10 APPLICANT: Day, Craig H.
 11 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 12 TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST
 13 FILE REFERENCE: 210121.419C11
 14 CURRENT APPLICATION NUMBER: US/09/810,936
 15 CURRENT FILING DATE: 2001-03-16
 16 NUMBER OF SEQ ID NOS: 334
 17 SOFTWARE: FastSeq for Windows Version 3.0
 18 SEQ ID NO 314
 19 LENGTH: 879
 20 TYPE: DNA

```

: ORGANISM: Homo sapiens
US-09-810-936-314

Query Match          5.9%: Score 120; DB 10; Length 879;
Best Local Similarity 99.1%: Pred. No. 2.3e-37;
Matches 220: Conservative 0; Mismatches 2; Indels 0; Gaps 0

OY 507 GGACAGCAAGCAAAAGAGACGCTCTCAATCTGGCCCTCTGCCAATGGGAATTCAGAACTAGT 566
DB 333 GGACAGCAAGCAAAAGAGACGCTCTCAATCTGGCCCTCTGCCAATGGGAATTCAGAACTAGT 392
OY 567 AAAACTCCTGCTGACAGACGATGTCACCTTAATGTCTTGACACAAACAAAAGAGACAGC 626
DB 393 AAAACTCGGCTGGAGACAGACGATGTCACCTTAATGTCTTGACACAAACAAAAGAGACAGC 452
OY 627 TCTGATTAAGAGCGGACATGCGACAGAAATGTCGTTAATGTCTGGAACATGG 686
DB 453 TCTGACAAAGCGCGACATGCGACAGAAATGTCGTTAATGTCTGGAACATGG 512
OY 687 CACTGATCCAAATATTCCAGATGAGTATGGAATACCACTCT 728
DB 513 CACTGATCCAAATATTCCAGATGAGTATGGAATACCACTCT 554

RESULT 34
US-09-822-827-531
: Sequence 531, Application US/09822827
: Patent No. US20020081680A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: CURRENT APPLICATION NUMBER: US/09/822, 827
: CURRENT FILING DATE: 2001-03-28
: NUMBER OF SEQ ID NOS: 982
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 531
: LENGTH: 879
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-822-827-531

Query Match          5.9%: Score 120; DB 10; Length 879;
Best Local Similarity 99.1%: Pred. No. 2.3e-37;
Matches 220: Conservative 0; Mismatches 2; Indels 0; Gaps 0

OY 507 GGACAGCAAGCAAAAGAGACGCTCTCAATCTGGCCCTCTGCCAATGGGAATTCAGAACTAGT 566
DB 333 GGACAGCAAGCAAAAGAGACGCTCTCAATCTGGCCCTCTGCCAATGGGAATTCAGAACTAGT 392
OY 567 AAAACTCCTGCTGACAGACGATGTCACCTTAATGTCTTGACACAAACAAAAGAGACAGC 626
DB 393 AAAACTCGGCTGGAGACAGACGATGTCACCTTAATGTCTTGACACAAACAAAAGAGACAGC 452
OY 627 TCTGATTAAGAGCGGACATGCGACAGAAATGTCGTTAATGTCTGGAACATGG 686
DB 453 TCTGACAAAGCGCGACATGCGACAGAAATGTCGTTAATGTCTGGAACATGG 512
OY 687 CACTGATCCAAATATTCCAGATGAGTATGGAATACCACTCT 728
DB 513 CACTGATCCAAATATTCCAGATGAGTATGGAATACCACTCT 554

RESULT 35
US-09-429-755-314
: Sequence 314, Application US/09429755A
: Patent No. US20020111467A1
: GENERAL INFORMATION:
: APPLICANT: Frudakis, Tony N.
: APPLICANT: Smith, John M.
: APPLICANT: Reed, Steven G.
: APPLICANT: Misher, Lynda

```

```

; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, David C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 314
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-429-755-314

Query Match          5.9%; Score 120; DB 10; Length 879;
Best Local Similarity 99.1%; Pred. No. 2.3e-37;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAGCAAAAGAGAGACTGCTTCATCTGCGCTCTGCGCATGGGAATTCGAAAGTGT 566
Db 333 GGACAGCAAGCAAAAGAGAGAGCTGCTTCATCTGCGCTCTGCGCAATGGGAATTCGAAAGTGT 392
QY 567 AAAACTCTGCTGAGCAGACGATGTCACCTTATGTCCTTGGACAACAAAAGAGACAGC 626
Db 393 AAAACTCGTGGCGAGACAGACGATGTCACCTTATGTCCTTGGACAACAAAAGAGACAGC 452
QY 627 TCTGATTAAGAGCCGTCACAAATGCGCAGAGAGATGTCGGTTAATGTTGCTGGAACATGG 686
Db 453 TCTGACAAAGAGCCGTCACAAATGCGCAGAGAGATGTCGGTTAATGTTGCTGGAACATGG 512
QY 687 CACGTATCCAAATATTCAGATGATGATGGAATTCACACTCT 728
Db 513 CACTGATCCAAATATTCAGATGATGATGGAATTCACACTCT 554

```

```

RESULT 36
US-09-759-143-372
; Sequence 372: Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stoik, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: DIAGNOSIS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427223
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 372
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-372

Query Match          5.9%; Score 120; DB 10; Length 1059;
Best Local Similarity 99.1%; Pred. No. 2.3e-37;

```


Query Match 5.9%; Score 120; DB 10; Length 1059;
Best Local Similarity 99.1%; Pred. No. 2.3e-37;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAAGCAAAAGAGAGCTGCTACATCTGGCCCTGCGCAATGGGAATTGCAAGTAGT 566
DB 276 GGACAAAGCAAAAGAGAGCTGCTACATCTGGCCCTGCGCAATGGGAATTGCAAGTAGT 335
QY 567 AAAACTCTGCTGGACAGAGATGTCACCTTAATGTCCTTGACAAACAAAAAGAGACAGC 626
DB 336 AAAACTCTGCTGGACAGAGATGTCACCTTAATGTCCTTGACAAACAAAAAGAGACAGC 395
QY 627 TCTGATAAAGGCCGTACATGCCAGAGATGATGCGTTAATGTCCTGGAACATGG 686
DB 396 TCTGATAAAGGCCGTACATGCCAGAGATGATGCGTTAATGTCCTGGAACATGG 455
QY 687 CACTGATCCAAATATTCAGATGATGGAATACCACTCT 728
DB 456 CACTGATCCAAATATTCAGATGATGGAATACCACTCT 497

RESULT 40

US-09-429-755-298
; Sequence 298, Application US/09429755A
; Patent No. US2002011467A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 298
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-298

Query Match 5.9%; Score 120; DB 10; Length 1059;
Best Local Similarity 99.1%; Pred. No. 2.3e-37;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAAGCAAAAGAGAGCTGCTACATCTGGCCCTGCGCAATGGGAATTGCAAGTAGT 566
DB 276 GGACAAAGCAAAAGAGAGCTGCTACATCTGGCCCTGCGCAATGGGAATTGCAAGTAGT 335
QY 567 AAAACTCTGCTGGACAGAGATGTCACCTTAATGTCCTTGACAAACAAAAAGAGACAGC 626
DB 336 AAAACTCTGCTGGACAGAGATGTCACCTTAATGTCCTTGACAAACAAAAAGAGACAGC 395
QY 627 TCTGATAAAGGCCGTACATGCCAGAGATGATGCGTTAATGTCCTGGAACATGG 686
DB 396 TCTGATAAAGGCCGTACATGCCAGAGATGATGCGTTAATGTCCTGGAACATGG 455
QY 687 CACTGATCCAAATATTCAGATGATGGAATACCACTCT 728
DB 456 CACTGATCCAAATATTCAGATGATGGAATACCACTCT 497

RESULT 41

US-09-825-301-1/C
; Sequence 1, Application US/09825301
; Patent No. US20020009738A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Dillon, Davin C.

; APPLICANT: Molesh, David A.
; APPLICANT: Xu, Jianshun
; APPLICANT: Zehentner, Barbara
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
; FILE REFERENCE: 210121.513
; CURRENT APPLICATION NUMBER: US/09/825,301
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-825-301-1

Query Match 5.9%; Score 120; DB 10; Length 1851;
Best Local Similarity 99.1%; Pred. No. 2.2e-37;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAAGCAAAAGAGAGCTGCTACATCTGGCCCTGCGCAATGGGAATTGCAAGTAGT 566
DB 791 GGACAAAGCAAAAGAGAGCTGCTACATCTGGCCCTGCGCAATGGGAATTGCAAGTAGT 732
QY 567 AAAACTCTGCTGGACAGAGATGTCACCTTAATGTCCTTGACAAACAAAAAGAGACAGC 626
DB 731 AAAACTCTGCTGGACAGAGATGTCACCTTAATGTCCTTGACAAACAAAAAGAGACAGC 672
QY 627 TCTGATAAAGGCCGTACATGCCAGAGATGATGCGTTAATGTCCTGGAACATGG 686
DB 671 TCTGATAAAGGCCGTACATGCCAGAGATGATGCGTTAATGTCCTGGAACATGG 612
QY 687 CACTGATCCAAATATTCAGATGATGGAATACCACTCT 728
DB 611 CACTGATCCAAATATTCAGATGATGGAATACCACTCT 570

RESULT 42

US-09-759-143-366/C
; Sequence 366, Application US/09759143
; Patent No. US2002022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 366
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-366

Query Match 5.9%; Score 120; DB 10; Length 1851;
Best Local Similarity 99.1%; Pred. No. 2.2e-37;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAGAGAGAGACTGCTCTACATCTGGCCCTGCCAATGGGAATTCAGAACTAGT 566
|||||
DB 791 GGACAGCAAGAGAGAGACTGCTCTACATCTGGCCCTGCCAATGGGAATTCAGAACTAGT 732

QY 567 AAACTCTGCTGGACAGACGATGTCACCTTAATGCTTGACACAAAAGAGACAGC 626
|||||
DB 731 AAACTCTGCTGGACAGACGATGTCACCTTAATGCTTGACACAAAAGAGACAGC 672

QY 627 TCTGATAAAGGCCGTACATGCGCAGGAAGATGATGCGTTAATGTTGCTGGAACATGG 686
|||||
DB 671 TCTGATAAAGGCCGTACATGCGCAGGAAGATGATGCGTTAATGTTGCTGGAACATGG 612

QY 687 CACTGATCCAAATATTCAGATGAGTATGAAATACCACTCT 728
|||||
DB 611 CACTGATCCAAATATTCAGATGAGTATGAAATACCACTCT 570

RESULT 43
US-09-780-669-366/c
; Sequence 366, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jjiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Rafter, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 366
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-780-669-366

Query Match 5.9%; Score 120; DB 10; Length 1851;
Best Local Similarity 99.1%; Pred. No. 2.2e-37;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAGAGAGAGACTGCTCTACATCTGGCCCTGCCAATGGGAATTCAGAACTAGT 566
|||||
DB 791 GGACAGCAAGAGAGAGACTGCTCTACATCTGGCCCTGCCAATGGGAATTCAGAACTAGT 732

QY 567 AAACTCTGCTGGACAGACGATGTCACCTTAATGCTTGACACAAAAGAGACAGC 626
|||||
DB 731 AAACTCTGCTGGACAGACGATGTCACCTTAATGCTTGACACAAAAGAGACAGC 672

QY 627 TCTGATAAAGGCCGTACATGCGCAGGAAGATGATGCGTTAATGTTGCTGGAACATGG 686
|||||

DB 671 TCTGCAAAAGCCGTACATGCGCAGGAAGATGATGCGTTAATGTTGCTGGAACATGG 612
QY 687 CACTGATCCAAATATTCAGATGAGTATGAAATACCACTCT 728
|||||
DB 611 CACTGATCCAAATATTCAGATGAGTATGAAATACCACTCT 570

RESULT 44
US-09-810-936-291/c
; Sequence 291, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 291
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-936-291

Query Match 5.9%; Score 120; DB 10; Length 1851;
Best Local Similarity 99.1%; Pred. No. 2.2e-37;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 791 GGACAGCAAGAGAGAGACTGCTCTACATCTGGCCCTGCCAATGGGAATTCAGAACTAGT 732

QY 567 AAACTCTGCTGGACAGACGATGTCACCTTAATGCTTGACACAAAAGAGACAGC 626
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DB 731 AAACTCTGCTGGACAGACGATGTCACCTTAATGCTTGACACAAAAGAGACAGC 672

QY 627 TCTGATAAAGGCCGTACATGCGCAGGAAGATGATGCGTTAATGTTGCTGGAACATGG 686
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DB 671 TCTGATAAAGGCCGTACATGCGCAGGAAGATGATGCGTTAATGTTGCTGGAACATGG 612

QY 687 CACTGATCCAAATATTCAGATGAGTATGAAATACCACTCT 728
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DB 611 CACTGATCCAAATATTCAGATGAGTATGAAATACCACTCT 570

RESULT 45
US-09-810-936-292/c
; Sequence 292, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER

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; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: fbsSeq For Windows Version 3.0.
; SEQ ID NO 292
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-936-292

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Query Match	5.9%	Score 120	DB 10	length 1851
Best Local Similarity	99.1%	Pred. No. 2.2e-37		
Matches 220; Conservative	0	Mismatches 2	Indels 0	Gaps 0

QY	507	GGACAGCAAAAAGAGGACGTGCTTCACTACATCTGACCTTGCCAAATGGGAATTCAGAAAGT	566
Db	791	GGACAGCAAAAAGAGGACGTGCTTCACTACATCTGACCTTGCCAAATGGGAATTCAGAAAGT	732
QY	567	AAACCTCCTGCTGGACAGACGATGTCAACTTAATGTCTTGACAAACAAAAGAGGACAGC	626
Db	731	AAACCTCCTGCTGGACAGACGATGTCAACTTAATGTCTTGACAAACAAAAGAGGACAGC	672
QY	627	TCTGATTAAGGCGGTACCAATGCCAGGAAGATGAATGTGCGCTTAATGTTGCTGGACATGG	686
Db	671	TCTGCAAAAGGCGGTACCAATGCCAGGAAGATGTGCGCTTAATGTTGCTGGACATGG	612
QY	687	CACGTGATCCAATATTTCAGATGAGATGTGGAATAACCACTCT	728
Db	611	CACGTGATCCAATATTTCAGATGAGATGTGGAATAACCACTCT	570

Search completed: November 8, 2002, 15:54:04
Job time : 115.871 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2002, 09:07:24 : Search time 4021.43 seconds
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Title: US-09-924-400-303
Perfect score: 2040
Sequence: 1 atgtgtgtgtgagtgatc.....aaaaaaaaaaaaaaaaaaaaa 2040

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_NA_Main.*

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3	2040	100.0	2040	16	US-09-289-198-303	Sequence 303, App	
4	2040	100.0	2040	18	US-09-429-755-303	Sequence 303, App	
5	2040	100.0	2040	18	US-09-443-686-375	Sequence 375, App	
6	2040	100.0	2040	18	US-09-483-672A-375	Sequence 375, App	
7	2040	100.0	2040	20	US-09-534-825A-303	Sequence 303, App	
8	2040	100.0	2040	20	US-09-536-857-375	Sequence 375, App	
9	2040	100.0	2040	22	US-09-568-100A-375	Sequence 375, App	
10	2040	100.0	2040	22	US-09-577-055B-303	Sequence 303, App	
11	2040	100.0	2040	22	US-09-590-583-303	Sequence 303, App	
12	2040	100.0	2040	22	US-09-593-793A-375	Sequence 375, App	
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15	2040	100.0	2040	25	US-09-651-236-375	Sequence 375, App	
16	2040	100.0	2040	25	US-09-657-279-375	Sequence 375, App	
17	2040	100.0	2040	26	US-09-679-272-375	Sequence 375, App	
18	2040	100.0	2040	26	US-09-679-426-375	Sequence 375, App	
19	2040	100.0	2040	27	US-09-685-166-375	Sequence 375, App	
20	2040	100.0	2040	27	US-09-685-166A-375	Sequence 375, App	
21	2040	100.0	2040	27	US-09-699-295-303	Sequence 303, App	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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25 2040 100.0 2040 31 US-09-810-936-303 Sequence 303, App
26 2040 100.0 2040 31 US-09-822-827-375 Sequence 375, App
27 2040 100.0 2040 31 US-09-825-301-7 Sequence 7, App
28 2040 100.0 2040 32 US-09-852-911-375 Sequence 375, App
29 2040 100.0 2040 33 US-09-895-793-375 Sequence 375, App
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33 2040 100.0 2040 38 US-10-010-940-375 Sequence 375, App
34 2040 100.0 2040 38 US-10-012-896-375 Sequence 375, App
35 2040 100.0 2040 39 US-10-079-137B-303 Sequence 303, App
36 2040 100.0 2040 40 US-10-144-678A-375 Sequence 375, App
37 2040 100.0 2040 42 US-10-212-679-303 Sequence 303, App
38 1551 76.0 2000 1 PCT-US02-24917-302 Sequence 302, App
39 1551 76.0 2000 16 US-09-288-946-374 Sequence 374, App
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ALIGNMENTS

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RESULT 1
PCT-US02-24917-303
; Sequence 303, Application PC/FUS0224917
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, Davin C.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.41931PC
; CURRENT APPLICATION NUMBER: PCT/US02/24917
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-24917-303
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Query Match 100.0%; Score 2040; DB 1; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2.7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 ATGGTGGTTAGGTGATTCATCCAGCGGCTCTTCTGTGAAGAAGCCATTGGCTC 60
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Db 121 AGCAAGTGGGCACTTCTGAGACACAGAGACTCTGCTATGAAGACACTCAGAGCA 180
QY 181 ATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
Db 181 ATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
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Db 241 GGGCTTCTGAGAGCACAGACTCTGTATGAAGACACTCAGAAACAGATGGGCAAG 300
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QY 361 GAGAGCTACAGATGACAGTGGCTTCATAGGAGCCAGGATCCGCTGGAGAAATCTG 420
Db 361 GAGAGCTACAGATGACAGTGGCTTCATAGGAGCCAGGATCCGCTGGAGAAATCTG 420
QY 421 GACAAAGCTCCACAGAGCTGCTGGTGGGTTAAGTCCCAAGAAAGATCTCATCTCATG 480
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Db 781 TATGTCGTATATTCGAATCAAAAAACAGATGAGGCTCACACAGCTGTTACTTGGTGA 840
QY 841 CATGAGCAAAACAGCAAGTGTGGAATTTTATATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAACAGCAAGTGTGGAATTTTATATCAAGAAAAAGCAATTTAAATGCA 900
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QY 961 GTGAGCTTCTACTTGAAGCAAAATATGATATCTTCTCAAGATCTATCTGACAGAGC 1020
Db 961 GTGAGCTTCTACTTGAAGCAAAATATGATATCTTCTCAAGATCTATCTGACAGAGC 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATATTTTGGCAGTTACTTGTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATATTTTGGCAGTTACTTGTGACTAC 1080
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QY 1141 CTGACATCAGAGAGAGAGTCCAAAGGCTTCAAGGCAAGTGAAGTGGCAGCCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGAGTCCAAAGGCTTCAAGGCAAGTGAAGTGGCAGCCAGAGAA 1200
QY 1201 ATGTCTCAAGAACCAAAATTAATAGATGTGATAGAGAGTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAAATTAATAGATGTGATAGAGAGTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGTAAATATGAGGATTAATGAAGAAACCTGATATGATGCTGCTGGC 1320
Db 1261 AAGCATGAAGTAAATATGAGGATTAATGAAGAAACCTGATATGATGCTGCTGGC 1320
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Db 1321 AATGGTAAATGATTAATTCCTCAAGAGAGAGACACACCTGMAAATCAGCAATT 1380
OY 1381 CCTGACACGAAAGTGAAGATATCAGCAATTTGGCAATTAGTTTCTGACTACAAAGAA 1440
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Db 1381 CCTGACACGAAAGTGAAGATATCAGCAATTTGGCAATTAGTTTCTGACTACAAAGAA 1440
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Db 1441 AAACGATGCCAAAATACCTCTCTGMAAAGACCAACCCAGAACACACTTAAAGCTGACA 1500
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Db 1501 TCAGAGAGAGATGCACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCAGAGAAAGATCT 1560
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Db 1561 CAAGAACCGAAATTAATTAAGATGCTGATAGAGCTTGAAATTTATGGCTATCGAA 1620
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Db 1801 AAGCAATTTTGAAGACAGACACTGGAATTTACAGATGAGATTCGATTCATGAA 1860
OY 1861 GAAAGCAGATAGAAAGTGTGMAAATGAATTCAGACTTCTCTTGAAGTGAAGAA 1920
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Db 1861 GAAAGCAGATAGAAAGTGTGMAAATGAATTCAGACTTCTCTTGAAGTGAAGAA 1920
OY 1921 GAAAAAGACATCTGTCATGAAATAGTACGTCGGGAAAGAAATTCCTGCTAAGACTG 1980
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Db 1921 GAAAAAGACATCTGTCATGAAATAGTACGTCGGGAAAGAAATTCCTGCTAAGACTG 1980
OY 1981 GAGCTAGACATGAAATGATCAGAGCCAGCTAAAAAAGAAAAAAGAAAAA 2040
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Db 1981 GAGCTAGACATGAAATGATCAGAGCCAGCTAAAAAAGAAAAAAGAAAAA 2040

RESULT 2

US-09-288-946-375
; Sequence 375, Application US/09288946
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C7
; CURRENT APPLICATION NUMBER: US/09/288,946
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-288-946-375

Query Match 100.0%; Score 2040; DB 16; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2.7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGGTGTTGAGTGTGATTCATGCGCGCTGCCTCTTGTGMAAGAACCATTTGGCTC 60
OY 61 AGGAGCAAGATGGGCAATGTGTGCTCCGTTGCTTCCCTGTCAGGAGAGACGGCAAG 120
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Db 61 AGGAGCAAGATGGGCAATGTGTGCTCCGTTGCTTCCCTGTCAGGAGAGACGGCAAG 120
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Db 121 AGCAAGTGGGCACTTCTGGAGACCAAGACGACTGCTGATGAAAGCACTCAGAGACAAG 180
OY 181 ATGGGCAAGTGGGCGCCGCACTCTCCCTGCTGAGGGGAGATGGCAAGACAGT 240
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OY 241 GGGCTTCTGGAGACCAAGACGACTGCTGATGAAAGCACTCAGAGACAAGATGGCAAG 300
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Db 241 GGGCTTCTGGAGACCAAGACGACTGCTGATGAAAGCACTCAGAGACAAGATGGCAAG 300
OY 301 TGGTGTGCACTGCTTCCCTGCTGAGGGGAGAGGGGCAAGGAGTGGCGCTTGG 360
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OY 361 GGAGACTAGATGACAGTGCCTTCATGAGCCAGGATACACGCTCCGTGGAGAAATCTG 420
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Db 361 GGAGACTAGATGACAGTGCCTTCATGAGCCAGGATACACGCTCCGTGGAGAAATCTG 420
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Db 421 GACAGCTCCACAGAGCTGCTGCTGGGGTAAAGTCCCGAAGAAAGATCTCATGCTATG 480
OY 481 CTCAGGACACAGTACGCTGAACAAAGAGACCAAGAGAGAGCTCTACATCTGGCC 540
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Db 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTCTGAGAGAGATGCACTTAAT 600
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Db 601 GTCTTTGACAAACAAAGAGAGAGCTGTGATTAAGGCGGTACATGCCAGAAATGAA 660
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Db 661 TGTGCGTTAATGTTGTGGAACAATGGCACTGATCCAAATTTCCAGATGATGTAAT 720
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Db 721 ACCACTGTCACATGCTATCTAATGAAGATTAATGAGCAAGCACTGCTTGA 780
OY 781 TATGTTGCTGATATGAAATCAAAAAACAGCATGGCCTCACACACTGTTACTTGGTGA 840
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Db 781 TATGTTGCTGATATGAAATCAAAAAACAGCATGGCCTCACACACTGTTACTTGGTGA 840
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Db 841 CATGACCAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
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Db 1021 GCCAGAGATATGCTTTTCTAGTCAATCATGTAATTTGCCAGTTACTTTGTGCTAC 1080
OY 1081 AAAGAAACAGATGCTTAAAAATCTCTTGAAAGACAGCAATCCAGAACACTTAAAG 1140

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Db	1141	CTGACATCAGAGGAAGAGTCCACAAGGTTTCAAAAGCAGTGAATAATAGCCAGCCAGAGAAA	1200
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Db	1201	ATGCTCAAGAACCGAATAAATTAATTAAGGATGGGTGATAGGACGTTGAAGAAGAAATGAG	1260
Qy	1261	AAGCATGAAGTATATATGTGGGATTACTAGAAACCTGACATAATAGTGTCAGTCTGCTGC	1320
Db	1261	AAGCATGAAGTATATATGTGGGATTACTAGAAACCTGACATAATAGTGTCAGTCTGCTGC	1320
Qy	1321	AATGCTGATTAATGGATTAAATTCCTCAAAGAGAGACAGAACCTGGAATAATCAGCAATTT	1380
Db	1321	AATGCTGATTAATGGATTAAATTCCTCAAAGAGAGACAGAACCTGGAATAATCAGCAATTT	1380
Qy	1381	CCTGACACAGGAAGTGAAGGTATCAGACGAATTTGGATTGTTTGACATACCAAGAA	1440
Db	1381	CCTGACACAGGAAGTGAAGGTATCAGACGAATTTGGATTGTTTGACATACCAAGAA	1440
Qy	1441	AAACAGATGCCAAATATCTTCTTGTGA AAAACAGCAACCCAGAACCAAGACTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAATATCTTCTTGTGA AAAACAGCAACCCAGAACCAAGACTTAAAGCTGACA	1500
Qy	1501	TCACAGGAAGAGTCCACAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAGAAAAAGATCT	1560
Db	1501	TCACAGGAAGAGTCCACAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAGAAAAAGATCT	1560
Qy	1561	CAAGAACACAGAAATTAATTAAGATGGGTAGATAGAGACTGGAATAATTTATGCTATCGAA	1620
Db	1561	CAAGAACACAGAAATTAATTAAGATGGGTAGATAGAGACTGGAATAATTTATGCTATCGAA	1620
Qy	1621	GAAATGAAGAAGCAGCGAAGTACTCATGTGCGATTTCCAGAAAACCTGACTAATGTGTCC	1680
Db	1621	GAAATGAAGAAGCAGCGAAGTACTCATGTGCGATTTCCAGAAAACCTGACTAATGTGTCC	1680
Qy	1681	ACTGCTGGCAATGGTGTATGATGATTAATTTCCCTCCAGGAAGAGAGCAACCTGAAAGC	1740
Db	1681	ACTGCTGGCAATGGTGTATGATGATTAATTTCCCTCCAGGAAGAGAGCAACCTGAAAGC	1740
Qy	1741	CAGCAATTTCTGACACTGGAATGAAGATATCAGATGAGAGCAAAATGATACTCAG	1800
Db	1741	CAGCAATTTCTGACACTGGAATGAAGATATCAGATGAGAGCAAAATGATACTCAG	1800
Qy	1801	AAGCAATTTTGTGAGAACAGAACTCGAATTTACACAGATGAGATTTCTGATTCATGAA	1860
Db	1801	AAGCAATTTTGTGAGAACAGAACTCGAATTTACACAGATGAGATTTCTGATTCATGAA	1860
Qy	1861	GAAAGACAGATAGAAAGTGTGAAAAAATGAATTCGACCTTCTGTTAGTTGTAAGAA	1920
Db	1861	GAAAGACAGATAGAAAGTGTGAAAAAATGAATTCGACCTTCTGTTAGTTGTAAGAA	1920
Qy	1921	GAAAAAGACATCTTGATGAAATAATAGCTTGCGGGAAGAAATTCGCATGCTAAGACTG	1980
Db	1921	GAAAAAGACATCTTGATGAAATAATAGCTTGCGGGAAGAAATTCGCATGCTAAGACTG	1980
Qy	1981	GAGCTAGACACATGAAACATCAGACCCAGCTTAAAAAATTTTTTTTTTTTTTTTTTTTTTTT	2040
Db	1981	GAGCTAGACACATGAAACATCAGACCCAGCTTAAAAAATTTTTTTTTTTTTTTTTTTTTTTT	2040

RESULT 3
US-09-289-198-303
Sequence 303, Application US/09289198
GENERAL INFORMATION:
APPLICANT: FRUDAKIS, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

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TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419CS
CURRENT APPLICATION NUMBER: US/09/289,198
CURRENT FILING DATE: 1999-04-09
EARLIER APPLICATION NUMBER: US 09/062,451
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: US 08/991,789
EARLIER FILING DATE: 1997-12-11
EARLIER APPLICATION NUMBER: US 08/838,762
EARLIER FILING DATE: 1997-04-09
EARLIER APPLICATION NUMBER: PCT/US97/00485
EARLIER FILING DATE: 1997-01-10
EARLIER APPLICATION NUMBER: US 08/700,014
EARLIER FILING DATE: 1996-08-20
EARLIER APPLICATION NUMBER: US 08/585,392
EARLIER FILING DATE: 1996-01-01
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 303
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-289-198-303
Query Match      100.0%; Score 2040; DB 16; Length 2040;
Best Local Similarity 100.0%; Pred. NO. 2.7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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[illegible]

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Db 661 TGTGGTAAATGTTGCTGGACATGGCACTGATCCAAATATTTCCAGATGATGGAAT 720
Qy 721 ACCACTGCACTACGCTATCATTAATGAAGTAATTAATGAGCCCAAGCACTGCTTA 780
Db 721 ACCACTGCACTACGCTATCATTAATGAAGTAATTAATGAGCCCAAGCACTGCTTA 780
Qy 781 TATGCTGATATGCAATCAAAAAAACAAGCATGGCTCACACCACTGTTACTTGCTGA 840
Db 781 TATGCTGATATGCAATCAAAAAAACAAGCATGGCTCACACCACTGTTACTTGCTGA 840
Qy 841 CATGAGCAAAAAACAGCAAGCTGTAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGCTGTAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
Qy 901 CTGGATATATGGAAGAGCTGCTCATCTACTGCTGATGCTGATGCTGATGCTGATG 960
Db 901 CTGGATATATGGAAGAGCTGCTCATCTACTGCTGATGCTGATGCTGATGCTGATG 960
Qy 961 GTCAGCCTTCTACTGAGCAAAATATGATGATCTCTCAAGATCTATCTGAGACAG 1020
Db 961 GTCAGCCTTCTACTGAGCAAAATATGATGATCTCTCAAGATCTATCTGAGACAG 1020
Qy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTCTG 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTCTG 1080
Qy 1081 AAAGAAAAAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCCAAACTTAAAG 1140
Db 1081 AAAGAAAAAGATGCTAAAAATCTCTCTGAAAAACAGCAATCCCAAACTTAAAG 1140
Qy 1141 CTGACATCAGAGAAAGCTCAAAAGTTCAAAAGCAGTGAATAATGAGCAGCAGAGA 1200
Db 1141 CTGACATCAGAGAAAGCTCAAAAGTTCAAAAGCAGTGAATAATGAGCAGCAGAGA 1200
Qy 1201 ATGCTCAAGAACAGAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGCTCAAGAACAGAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAATTAATTAATGCTGGATTAAGTAAACCTGACTAATGCTGCTGCTG 1320
Db 1261 AAGCATGAAATTAATTAATGCTGGATTAAGTAAACCTGACTAATGCTGCTGCTG 1320
Qy 1321 AATGGTAAATGATTAATCTCTCAAGAAAGACAGCAACCTGAAATATGCAATTT 1380
Db 1321 AATGGTAAATGATTAATCTCTCAAGAAAGACAGCAACCTGAAATATGCAATTT 1380
Qy 1381 CCTGACAAGAAAGTGAAGATATCAGAAATTTGCGAATTAATGTTGACTACAAAGA 1440
Db 1381 CCTGACAAGAAAGTGAAGATATCAGAAATTTGCGAATTAATGTTGACTACAAAGA 1440
Qy 1441 AAACGATGCCAAATTAATCTCTGAAAAACAGCAACCAAGAAAGCTTAAGCTGACA 1500
Db 1441 AAACGATGCCAAATTAATCTCTGAAAAACAGCAACCAAGAAAGCTTAAGCTGACA 1500
Qy 1501 TCAGAGAAAGTCAAAAGCTTGAAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1560
Db 1501 TCAGAGAAAGTCAAAAGCTTGAAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1560
Qy 1561 CAAGAACAGAAATTAATTAAGATGCTGATAGAGACTAGAAATTTATGCTATCGAA 1620
Db 1561 CAAGAACAGAAATTAATTAAGATGCTGATAGAGACTAGAAATTTATGCTATCGAA 1620
Qy 1621 GAATGAAAGAGCAGGAAGTCTATGCTGATTCAGAAAGCTGATATGCTGCTG 1680
Db 1621 GAATGAAAGAGCAGGAAGTCTATGCTGATTCAGAAAGCTGATATGCTGCTGCTG 1680
Qy 1681 ACTGCTGCAATGCTGATGATGATTAATCTCTCAAGAAAGAGCAGAAACCTGATG 1740
Db 1681 ACTGCTGCAATGCTGATGATGATTAATCTCTCAAGAAAGAGCAGAAACCTGATG 1740
Qy 1741 CAGCAATTTCTGACACTGAGAAATGATCACTGAGCAAAATGATGCTGAG 1800
Db 1741 CAGCAATTTCTGACACTGAGAAATGATCACTGAGCAAAATGATGCTGAG 1800
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Db 1741 CAGCAATTTCTGACACTGAGAAATGATCACTGAGCAAAATGATGCTGAG 1800
Qy 1801 AAGCAATTTTGGAAAGACAGAACTGGAATTAATCAAGATGATGATGATGATGAA 1860
Db 1801 AAGCAATTTTGGAAAGACAGAACTGGAATTAATCAAGATGATGATGATGATGAA 1860
Qy 1861 GAAAGCAGATGAAAGTGGTGAATAATGAAATTTGATGACTTTCTTATGTTAAAGAA 1920
Db 1861 GAAAGCAGATGAAAGTGGTGAATAATGAAATTTGATGACTTTCTTATGTTAAAGAA 1920
Qy 1921 GAAAGCAGATGAAAGTGGTGAATAATGAAATTTGATGACTTTCTTATGTTAAAGAA 1980
Db 1921 GAAAGCAGATGAAAGTGGTGAATAATGAAATTTGATGACTTTCTTATGTTAAAGAA 1980
Qy 1981 GAGCTAGACACATGAATCAATGAGCCAGCTAAAAAATGAGTGAAGTGAAGTGA 2040
Db 1981 GAGCTAGACACATGAATCAATGAGCCAGCTAAAAAATGAGTGAAGTGAAGTGA 2040

RESULT 4
US-09-429-755-303
; Sequence 303, Application US/09429755A
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, David C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-303

Query Match 100.0%; Score 2040; DB 18; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2,7e-264; Indels 0; Gaps 0;
Matches 2040; Conservative 0; Mismatches 0;

Qy 1 AATGTTGTTGAGTTGATTCATGCGGCTGCTCTTCTGTAAGAACCATTTGCTC 60
Db 1 AATGTTGTTGAGTTGATTCATGCGGCTGCTCTTCTGTAAGAACCATTTGCTC 60
Qy 61 AGGACCAAGATGGCGAAGTGGTGGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Db 61 AGGACCAAGATGGCGAAGTGGTGGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Qy 121 AGCAAGTGGGCACTTCTGAGACACAGACGACGCTGCTGATGAAGACACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACACAGACGACGCTGCTGATGAAGACACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGGTGGCGCACTGCTTCCCTGCTCAGGGGAGTGGCAAGAGCAAGCTG 240
Db 181 ATGGGCAAGTGGTGGCGCACTGCTTCCCTGCTCAGGGGAGTGGCAAGAGCAAGCTG 240
Qy 241 GGGCTTCTGGAGACACAGAGACTCTGCTATGAAGACACTAGAGAACAAATGGGCAAG 300
Db 241 GGGCTTCTGGAGACACAGAGACTCTGCTATGAAGACACTAGAGAACAAATGGGCAAG 300
Qy 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGGGAGCGCAAGAGAGTGGGCGCTTGG 360
Db 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGGGAGCGCAAGAGAGTGGGCGCTTGG 360
Qy 361 GGAGACTACGATGACAGTGGCTTCAATGAGAGCCAGGATACACGCTCGTGGAGAAATG 420
Db 361 GGAGACTACGATGACAGTGGCTTCAATGAGAGCCAGGATACACGCTCGTGGAGAAATG 420
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QY 421 GACAAAGTCCACAGAGTGGCTGGGGGTAAAGTCCCCAGAAAAGATCTCATGTCATG 480
 |||||
 Db 421 GACAAAGTCCACAGAGTGGCTGGGGGTAAAGTCCCCAGAAAAGATCTCATGTCATG 480
 QY 481 CTGAGGACACCTGACGTGAACAAAGAGACAGCAAAAAGAGACTGCTTACATGCGCC 540
 |||||
 Db 481 CTGAGGACACCTGACGTGAACAAAGAGACAGCAAAAAGAGACTGCTTACATGCGCC 540
 QY 541 TGTGCCAATGGGAATTCAGAAAGTAAACCTGCTGACAGAGATGCAACTTAAT 600
 |||||
 Db 541 TGTGCCAATGGGAATTCAGAAAGTAAACCTGCTGACAGAGATGCAACTTAAT 600
 QY 601 GTCCCTTGACAAACAAAAGAGAGAGAGCTGTATAAAGCCCTACAAATGCCAGGAAGTAA 660
 |||||
 Db 601 GTCCCTTGACAAACAAAAGAGAGAGAGCTGTATAAAGCCCTACAAATGCCAGGAAGTAA 660
 QY 661 TGTGCGTTAATGTTGCTGGAACATGGCAGTGAATCCAAATATTCAGATGATGAAAT 720
 |||||
 Db 661 TGTGCGTTAATGTTGCTGGAACATGGCAGTGAATCCAAATATTCAGATGATGAAAT 720
 QY 721 ACCACTGTGCACTACGCTATCTTAATGAAGATTAATTAATGGCAAGAGAGCTGCTTA 780
 |||||
 Db 721 ACCACTGTGCACTACGCTATCTTAATGAAGATTAATTAATGGCAAGAGAGCTGCTTA 780
 QY 781 TATGCTGCTGATATCGAATCAAAAACAGCATGGCCTCACACCACTGTTACTTGTGTA 840
 |||||
 Db 781 TATGCTGCTGATATCGAATCAAAAACAGCATGGCCTCACACCACTGTTACTTGTGTA 840
 QY 841 CATGACGCAAAAACAGCAGCTGCGAATTTTATATCAAGAAAAAGCAATTTAATGCA 900
 |||||
 Db 841 CATGACGCAAAAACAGCAGCTGCGAATTTTATATCAAGAAAAAGCAATTTAATGCA 900
 QY 901 CTGGATGATGATGAAGAGAGCTGCTCATCTGCTGTATGTTGTGATAGCAAGTATA 960
 |||||
 Db 901 CTGGATGATGATGAAGAGAGCTGCTCATCTGCTGTATGTTGTGATAGCAAGTATA 960
 QY 961 GTGAGCCTTCTACTTGAGCAAAATATTGATGTATCTTCTCAAGATCTATCTGACAGAG 1020
 |||||
 Db 961 GTGAGCCTTCTACTTGAGCAAAATATTGATGTATCTTCTCAAGATCTATCTGACAGAG 1020
 QY 1021 GCCAGAGAGTATGCTGTTTGTAGTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
 |||||
 Db 1021 GCCAGAGAGTATGCTGTTTGTAGTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
 QY 1081 AAAGAAAAACAGATGCTAAATCTCTTGTGAAGACAGCAATCCAGAAAGAGCTTAAG 1140
 |||||
 Db 1081 AAAGAAAAACAGATGCTAAATCTCTTGTGAAGACAGCAATCCAGAAAGAGCTTAAG 1140
 QY 1141 CTGACATCAGAGAGAGAGTCAAAAGGTTCAAAAGCAGTGAATAATGACCCAGAGAGAA 1200
 |||||
 Db 1141 CTGACATCAGAGAGAGAGTCAAAAGGTTCAAAAGCAGTGAATAATGACCCAGAGAGAA 1200
 QY 1201 ATGTCTCAGAACACAGAAATTAATTAAGATGGTATGAGAGGTTGAAGAAAGATGAAG 1260
 |||||
 Db 1201 ATGTCTCAGAACACAGAAATTAATTAAGATGGTATGAGAGGTTGAAGAAAGATGAAG 1260
 QY 1261 AAGCATGAAGATATATGTTGGGATTAATGCTGAATAACCTGCTATGCTGCTGCTGCTG 1320
 |||||
 Db 1261 AAGCATGAAGATATATGTTGGGATTAATGCTGAATAACCTGCTATGCTGCTGCTGCTG 1320
 QY 1321 AATGCTGATTAATGATTAATTTCTCAAGAGAGAGAGAGACACCTGAAATTCAGCAATTT 1380
 |||||
 Db 1321 AATGCTGATTAATGATTAATTTCTCAAGAGAGAGAGAGACACCTGAAATTCAGCAATTT 1380
 QY 1381 CCTGACACAGAAAGTGAAGAGTATCACAGATTTGGCAATTTAGTTCTGACTCAAAAGAA 1440
 |||||
 Db 1381 CCTGACACAGAAAGTGAAGAGTATCACAGATTTGGCAATTTAGTTCTGACTCAAAAGAA 1440
 QY 1441 AAACAGATGCAAAATATCTTCTGAAAACAGAACCCAGAACAGCAAGCTTAAGCTGACA 1500
 |||||
 Db 1441 AAACAGATGCAAAATATCTTCTGAAAACAGAACCCAGAACAGCAAGCTTAAGCTGACA 1500

QY 1501 TCAGAGAGAGAGTCCACAAAGCTTGAAGGAGTGAAGAAATGGCCAGAGAGAAAGATCT 1560
 |||||
 Db 1501 TCAGAGAGAGAGTCCACAAAGCTTGAAGGAGTGAAGAAATGGCCAGAGAGAAAGATCT 1560
 QY 1561 CAAGAACACAGAAATTAATTAAGATGGTATGATGAGAGAGTAAAGAAATTTATGCTATCGAA 1620
 |||||
 Db 1561 CAAGAACACAGAAATTAATTAAGATGGTATGATGAGAGAGTAAAGAAATTTATGCTATCGAA 1620
 QY 1621 GAATGAAGAGAGAGAGAGTACTCATGTCGATGTTCCAGAAAACCTGACTAATGGTCC 1680
 |||||
 Db 1621 GAATGAAGAGAGAGAGAGTACTCATGTCGATGTTCCAGAAAACCTGACTAATGGTCC 1680
 QY 1681 ACTGTGCGCAATGGTATGATGATTAATTTCTTCCAGAAAGAGAGAGACCTGAAAGC 1740
 |||||
 Db 1681 ACTGTGCGCAATGGTATGATGATTAATTTCTTCCAGAAAGAGAGAGACCTGAAAGC 1740
 QY 1741 CAGCAATTTCTGACACTGAGATGAAGATATCACAGTATGACAGCAAAATGATCTCAG 1800
 |||||
 Db 1741 CAGCAATTTCTGACACTGAGATGAAGATATCACAGTATGACAGCAAAATGATCTCAG 1800
 QY 1801 AAGCAATTTTGTGAAGAGAGAGACACTGGAATATTAACAGATGAGATTTGATTCATGAA 1860
 |||||
 Db 1801 AAGCAATTTTGTGAAGAGAGAGACACTGGAATATTAACAGATGAGATTTGATTCATGAA 1860
 QY 1861 GAAAAGCAGATGAGAGAGTGTGAAGAAATGAATTTGAGCTTCTCTTACTGTAAGAAA 1920
 |||||
 Db 1861 GAAAAGCAGATGAGAGAGTGTGAAGAAATGAATTTGAGCTTCTCTTACTGTAAGAAA 1920
 QY 1921 GAAAAGACATCTTGTGCAATGAAGAAATGATGCTTCCGGGAAAGAAATGGCAAGTAAAGCTG 1980
 |||||
 Db 1921 GAAAAGACATCTTGTGCAATGAAGAAATGATGCTTCCGGGAAAGAAATGGCAAGTAAAGCTG 1980
 QY 1981 GAGCTAGACACATGAAGACATCAGAGCCAGCTTAAAAAATTTAAAAAATTTAAAAA 2040
 |||||
 Db 1981 GAGCTAGACACATGAAGACATCAGAGCCAGCTTAAAAAATTTAAAAAATTTAAAAA 2040

RESULT 5
 US-09-443-686-375
 ; Sequence 375, Application US/09443686
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, JIANGCHUN
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan Louise
 ; APPLICANT: Jiang Yuxui
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Kalos, Michael
 ; APPLICANT: Fanger, Gary
 ; APPLICANT: Retter, Mark
 ; APPLICANT: Solk, John
 ; APPLICANT: Day, Craley
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
 ; FILE REFERENCE: 210121.427C9A
 ; CURRENT APPLICATION NUMBER: US/09/443,686
 ; NUMBER OF SEQ ID NOS: 551
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 375
 ; LENGTH: 2040
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-09-443-686-375

Query Match 100.0%; Score 2040; DB 18; Length 2040;
 Best local Similarity 100.0%; Pred. No. 2,7e-264;
 Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGTGTTAGAGTTGATTCATGCGGCTGCTCTTCTGTGAAGAACATTTGGCTC 60
 |||||
 Db 1 ATGTGTTAGAGTTGATTCATGCGGCTGCTCTTCTGTGAAGAACATTTGGCTC 60

Qy	61	AGAGCAAGATGGGGCAAGTGTGTCTCCCTTGTCTTCCCTGCTGCGAGGAGAGCGGCAAG	120
Dp	61	AGGAGCAAGATGGGGCAAGTGTGTCTCCCTTGTCTTCCCTGCTGCGAGGAGAGCGGCAAG	120
Qy	121	AGCAAGCTGGGGCACTTCTTGAGAGCCAGCAGACGACTGCTGATGAGACACTCAGACACTCGAGGAGCAAG	180
Dp	121	AGCAAGCTGGGGCACTTCTTGAGAGCCAGCAGACGACTGCTGATGAGACACTCAGACACTCGAGGAGCAAG	180
Qy	181	ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGCGAGGGGAGTGGCAAGCAAGCTG	240
Dp	181	ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGCGAGGGGAGTGGCAAGCAAGCTG	240
Qy	241	GGCCCTTCTTGAGAGCCAGCAGCAGACTGCTGATGAGACACTCAGACACTGATGGGCAAG	300
Dp	241	GGCCCTTCTTGAGAGCCAGCAGCAGACTGCTGATGAGACACTCAGACACTGATGGGCAAG	300
Qy	301	TGGTGTGGCCAGTGTCTTCCCTGCTGCGAGGGGAGCGGCAAGCAAGTGGGGCTTGG	360
Dp	301	TGGTGTGGCCAGTGTCTTCCCTGCTGCGAGGGGAGCGGCAAGCAAGTGGGGCTTGG	360
Qy	361	GGAGACTTACGATGACAGTGGCTTTCATGAGAGCCAGGTACACAGTCCGTGGAGAAATGTG	420
Dp	361	GGAGACTTACGATGACAGTGGCTTTCATGAGAGCCAGGTACACAGTCCGTGGAGAAATGTG	420
Qy	421	GACAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAGATCTATCGTCATG	480
Dp	421	GACAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAGATCTATCGTCATG	480
Qy	481	CTCGGGGACACTACGCGAACAAGAGAGCAAGCAAAAGAGACTGTCTACATCTGGCC	540
Dp	481	CTCGGGGACACTACGCGAACAAGAGAGCAAGCAAAAGAGACTGTCTACATCTGGCC	540
Qy	541	TCTGCCAATGGGAATTCAGAAAGTAGTAAAACTCTGCTGGAGAGACGATGCAACTTAT	600
Dp	541	TCTGCCAATGGGAATTCAGAAAGTAGTAAAACTCTGCTGGAGAGACGATGCAACTTAT	600
Qy	601	GTCCTTGACAAACAAAAGAGAGACGCTGTGATPAAAGCCGTACATGGCCAGGAAGATGA	660
Dp	601	GTCCTTGACAAACAAAAGAGAGACGCTGTGATPAAAGCCGTACATGGCCAGGAAGATGA	660
Qy	661	TGTGCGTAAATGTTGCGGGAACATGGGCACTGATCCAAATATTCAGATGATGATGGAAT	720
Dp	661	TGTGCGTAAATGTTGCGGGAACATGGGCACTGATCCAAATATTCAGATGATGATGGAAT	720
Qy	721	ACCACCTTGACATACGCTATCTATATGAGAGATPAAATTTATGGCAAGCACTGCTTGA	780
Dp	721	ACCACCTTGACATACGCTATCTATATGAGAGATPAAATTTATGGCAAGCACTGCTTGA	780
Qy	781	TATGTGCTGATATCGAATCAAAAACAAGCATGGGCTTCACACCACTGTACTTGGTGTA	840
Dp	781	TATGTGCTGATATCGAATCAAAAACAAGCATGGGCTTCACACCACTGTACTTGGTGTA	840
Qy	841	CATAGCAAAAACAGCAAGCTGTGAATTTTATATCAGAAAAAGCGAATTTAATATCA	900
Dp	841	CATAGCAAAAACAGCAAGCTGTGAATTTTATATCAGAAAAAGCGAATTTAATATCA	900
Qy	901	CTGGATATGATGGAAGAGACTGCTGCTCATACTTGGTGTGTGGATCAGCAAGATTA	960
Dp	901	CTGGATATGATGGAAGAGACTGCTGCTCATACTTGGTGTGTGGATCAGCAAGATTA	960
Qy	961	GTCAGCTTCTACTTGAGCAAAAATATTTGATGTATCTTCAAGATCTATCTGGACAGCG	1020
Dp	961	GTCAGCTTCTACTTGAGCAAAAATATTTGATGTATCTTCAAGATCTATCTGGACAGCG	1020
Qy	1021	GGCAGAGATATCTGTTCTACTCATCATATGTAATTTGCCAATCTACTTCTGCACTAC	1080
Dp	1021	GGCAGAGATATCTGTTCTACTCATCATATGTAATTTGCCAATCTACTTCTGCACTAC	1080
Qy	1081	AAAGAAATAAGATGCTAAATAAACTCTTCTGAAAACAGAAATCCAGAAACAAGACTTAAG	1140
Dp	1081	AAAGAAATAAGATGCTAAATAAACTCTTCTGAAAACAGAAATCCAGAAACAAGACTTAAG	1140
Qy	1141	CTGACATCAGAGAGAGTACAAAAGTTCAAAAGGCTGAATAATAGCCAGCGAGATA	1200

Db	1141	CTGACATCAGAGGAAGAGTCACAAAGGTTCAAAAGGCACAGTGAATAATGACAGCAAGAAA	1200
Qy	1201	ATGTCCTAAAGAACCCAGAAATAATTAAGTAGGTGTGATAGAGAGCTTGAAAGAATAATGAAG	1260
Db	1201	ATGTCTCAAGAACCCAGAAATAATTAAGTAGGTGTGATAGAGAGCTTGAAAGAATAATGAAG	1260
Qy	1261	AAGCATGAAAGTAATTAATGTGGGATTACTAGAAAACCTGACTAATGTGTCTACTGTGGC	1320
Db	1261	AAGCATGAAAGTAATTAATGTGGGATTACTAGAAAACCTGACTAATGTGTCTACTGTGGC	1320
Qy	1321	AATGGTGATTAATGGATTATTTCTCTCAAGAGAACAGACAGAACCCGTAATAATCAGCAATTT	1380
Db	1321	AATGGTGATTAATGGATTATTTCTCTCAAGAGAACAGACAGAACCCGTAATAATCAGCAATTT	1380
Qy	1381	CCTGCACAACGAAAGGAAAGATGATCATCAGAAATTTGCGAATTTAGTTCTGTACTACAAAGAA	1440
Db	1381	CCTGCACAACGAAAGGAAAGATGATCATCAGAAATTTGCGAATTTAGTTCTGTACTACAAAGAA	1440
Qy	1441	AAACAGATGCCAAAATACTCTTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAAATACTCTTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA	1500
Qy	1501	TCAGAGGAAAGATCACAAGGCTTGAAGGCGAATGAAAAATGGCCACCAGAGAAAAAGATCT	1560
Db	1501	TCAGAGGAAAGATCACAAGGCTTGAAGGCGAATGAAAAATGGCCACCAGAGAAAAAGATCT	1560
Qy	1561	CAAGAACCCAGAAATTAATTAAGGATGGTGATAGAGAGCTAGAAAATTTTATGGCTATCGAA	1620
Db	1561	CAAGAACCCAGAAATTAATTAAGGATGGTGATAGAGAGCTAGAAAATTTTATGGCTATCGAA	1620
Qy	1621	GAATTAAGAAAGCCACGGAAGTACTCATGTGCGATTCCAGAAAACCTGACTAATGTGGCC	1680
Db	1621	GAATTAAGAAAGCCACGGAAGTACTCATGTGCGATTCCAGAAAACCTGACTAATGTGGCC	1680
Qy	1681	ACTGCTGGCAATGGATGATGATGATTAATTTCTCCACAGGAAGAGCAACACTGTAAGGC	1740
Db	1681	ACTGCTGGCAATGGATGATGATGATTAATTTCTCCACAGGAAGAGCAACACTGTAAGGC	1740
Qy	1741	CAGCAATTTTCCCTGCACACTGAGAAATGAAGGTATCAGACTGACGAACAAATGATACTGAG	1800
Db	1741	CAGCAATTTTCCCTGCACACTGAGAAATGAAGGTATCAGACTGACGAACAAATGATACTGAG	1800
Qy	1801	AAGCAATTTTGTGAAGAACACAGACACCTGGAATATTACACGATGAGATTCTGATTCATGAA	1860
Db	1801	AAGCAATTTTGTGAAGAACACAGACACCTGGAATATTACACGATGAGATTCTGATTCATGAA	1860
Qy	1861	GAAAGACGATGGAAGTGGTTGAAAAAATGAAATTCGTAGCTTCTCTTAGTTGTAAAGAA	1920
Db	1861	GAAAGACGATGGAAGTGGTTGAAAAAATGAAATTCGTAGCTTCTCTTAGTTGTAAAGAA	1920
Qy	1921	GAAGAAAGACATCTTGATGATAAATAGTACGTGTGCGGGAAGAAATTCGCTAGTAAAGCTG	1980
Db	1921	GAAGAAAGACATCTTGATGATAAATAGTACGTGTGCGGGAAGAAATTCGCTAGTAAAGCTG	1980
Qy	1981	GAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTTTTTT	2040
Db	1981	GAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAAATTTTTTTTTTTTTTTTTTTTTT	2040

RESULT 6
US-09-403-672A-375
: Sequence 375, Application US/09483672A
: GENERAL INFORMATION:
: APPLICANT: Xu, Jlangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlockam, Susan Louise
: APPLICANT: Jiang Yiqui
: APPLICANT: Reed, Steven G.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.

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; APPLICANT: Solk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Wang, Aljun
; APPLICANT: Meagher, Madeleine
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.42711C11
; CURRENT APPLICATION NUMBER: US/09/483,672A
; CURRENT FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-483-672A-375

Query Match      100.0%; Score 2040; DB 18; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2.7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAGTGGTTGAGGTGATTCATCCATGCGCGGCTCTTCTGTGAAGAACCATTTGGTCTC 60
DB 1 ATGGTGGTTGAGGTGATTCATCCATGCGCGGCTCTTCTGTGAAGAACCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCTCCCTCCCTGCTGCAAGGAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCTCCCTCCCTGCTGCAAGGAGAGCGGCAAG 120
QY 121 AGCAAGCTGGGCACTTCTGAGACACAGACACTCTGCTATGAAAGACTCAGAGCAAG 180
DB 121 AGCAAGCTGGGCACTTCTGAGACACAGACACTCTGCTATGAAAGACTCAGAGCAAG 180
QY 181 ATGGCAAGTGGTGGCCGACCTGCTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGCTG 240
DB 181 ATGGCAAGTGGTGGCCGACCTGCTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGCTG 240
QY 241 GGGGCTTCTGAGACACAGACACTGCTGATGAAAGCACTCAGAAACAGATGGGCAAG 300
DB 241 GGGGCTTCTGAGACACAGACACTGCTGATGAAAGCACTCAGAAACAGATGGGCAAG 300
QY 301 TGTGCTGCTGCACTGCTTCCCTGCTGCAAGGAGGAGGAGCAAGGAGTGGGCTTGG 360
DB 301 TGTGCTGCTGCACTGCTTCCCTGCTGCAAGGAGGAGGAGCAAGGAGTGGGCTTGG 360
QY 361 GGAGACTAGAGTACAGTGGCTTCATGAGGCCAGGTACACAGTCCGCTGGAAGAAATCTG 420
DB 361 GGAGACTAGAGTACAGTGGCTTCATGAGGCCAGGTACACAGTCCGCTGGAAGAAATCTG 420
QY 421 GACAAAGCTCCACAGAGCTGCTGCTGGTGGGTAAAGTCCCGCAAGAAAGATCTCATCTGATG 480
DB 421 GACAAAGCTCCACAGAGCTGCTGCTGGTGGGTAAAGTCCCGCAAGAAAGATCTCATCTGATG 480
QY 481 CTCAGGAGACACTGACCTGGAACAAGAGCAAGCAAAAGGAGGACTCTCTACATCTGGGCC 540
DB 481 CTCAGGAGACACTGACCTGGAACAAGAGCAAGCAAAAGGAGGACTCTCTACATCTGGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTATGAAAACTCTGCTGGACAGAGATGTCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAAGTATGAAAACTCTGCTGGACAGAGATGTCAACTTAAT 600
QY 601 GTCCCTTGCACAAACAAAAGAGAGAGCTGTGATAAAGCCGCTACAAATGCGCAGAAAGATGAA 660
DB 601 GTCCCTTGCACAAACAAAAGAGAGAGCTGTGATAAAGCCGCTACAAATGCGCAGAAAGATGAA 660
QY 661 TGTGCTTATGTGCTGGAACATGACACTGATCAAAATATTCACAGATGATGGAAT 720
DB 661 TGTGCTTATGTGCTGGAACATGACACTGATCAAAATATTCACAGATGATGGAAT 720
QY 721 ACCACTCTGACACTAGCTATCTATATGAAGATAATTAATGAGCCAAAGCACTGCTCTTA 780
DB 721 ACCACTCTGACACTAGCTATCTATATGAAGATAATTAATGAGCCAAAGCACTGCTCTTA 780
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QY 781 TATGTGCTGATATCGAATCAAAAACAAACATGCGCTCACACACTGTACTGTGTGA 840
DB 781 TATGTGCTGATATCGAATCAAAAACAAACATGCGCTCACACACTGTACTGTGTGA 840
QY 841 CATGAGCAAAAACAGCAAGCTGGAATTTTATATCAAGAAAAAGCAATTTAAATGCA 900
DB 841 CATGAGCAAAAACAGCAAGCTGGAATTTTATATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGGATATGATATGGAAGAGTGGCTTCATCTGCTGATGATGTTGFGATAGCAAGTATA 960
DB 901 CTGGATATGATATGGAAGAGTGGCTTCATCTGCTGATGATGTTGFGATAGCAAGTATA 960
QY 961 GTCAGCCTTCTACTTGGACAAAATATTTGATGATCTTCTCCAGATCTATCTGACAGAGC 1020
DB 961 GTCAGCCTTCTACTTGGACAAAATATTTGATGATCTTCTCCAGATCTATCTGACAGAGC 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGATTAATTTGCCAGTTACTTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGATTAATTTGCCAGTTACTTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAAAATCTCTTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
DB 1081 AAGAAAAACAGATGCTAAAAATCTCTTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCACAAAGGTTCAAGGCAAGTGAATAAGCCAGCCAGAGAAA 1200
DB 1141 CTGACATCAGAGAGAGAGTCACAAAGGTTCAAGGCAAGTGAATAAGCCAGCCAGAGAAA 1200
QY 1201 ATGTCTCAGAACCCAGAAATTAATTAAGATGTGATAGAGAGTTGAAGAAATGAAAG 1260
DB 1201 ATGTCTCAGAACCCAGAAATTAATTAAGATGTGATAGAGAGTTGAAGAAATGAAAG 1260
QY 1261 AAGCATGAAGATTAATATGAGGATTAATCTGAAACCTGCTAATGAGTGCACCTGCTGGC 1320
DB 1261 AAGCATGAAGATTAATATGAGGATTAATCTGAAACCTGCTAATGAGTGCACCTGCTGGC 1320
QY 1321 AATGGTATTAATGATTAATTTCTCAAAAGGAGAGCAAGAACACTGAAATACAGCAATTT 1380
DB 1321 AATGGTATTAATGATTAATTTCTCAAAAGGAGAGCAAGAACACTGAAATACAGCAATTT 1380
QY 1381 CTTGACACAGAAAGTGAAGATATCACAGAAATTTGGCAATTTAGTTTCTGACTCAAGAA 1440
DB 1381 CTTGACACAGAAAGTGAAGATATCACAGAAATTTGGCAATTTAGTTTCTGACTCAAGAA 1440
QY 1441 AAGCAGATGCGCAAAATACCTTCTGAAAAACAGAACCCAGAACAGACTTAAGAGTGA 1500
DB 1441 AAGCAGATGCGCAAAATACCTTCTGAAAAACAGAACCCAGAACAGACTTAAGAGTGA 1500
QY 1501 TCAGAGGAAGAGTCACAAAGGCTTGAAGGCAATGAATGAGCCAGAGCAAGAAAGATCT 1560
DB 1501 TCAGAGGAAGAGTCACAAAGGCTTGAAGGCAATGAATGAGCCAGAGCAAGAAAGATCT 1560
QY 1561 CAAGAACCCAGAAATTAATTAAGATGTGATAGAGACTGAGAAATTTTATGGCTATCGAA 1620
DB 1561 CAAGAACCCAGAAATTAATTAAGATGTGATAGAGACTGAGAAATTTTATGGCTATCGAA 1620
QY 1621 GAAATGAAGAGCAGGAAGTACTCATGTCGAGTTCCAGAAAACTGACTTAATGGTGGC 1680
DB 1621 GAAATGAAGAGCAGGAAGTACTCATGTCGAGTTCCAGAAAACTGACTTAATGGTGGC 1680
QY 1681 ACTGTGGCAATGATGATGATTAATTTCTCAAGGAAGAGCAAGAACCTGGAAGC 1740
DB 1681 ACTGTGGCAATGATGATGATTAATTTCTCAAGGAAGAGCAAGAACCTGGAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGATGAAGATATCACAGTATGAGCAACAAATGATACTCAG 1800
DB 1741 CAGCAATTTCTGACACTGAGATGAAGATATCACAGTATGAGCAACAAATGATACTCAG 1800
QY 1801 AAGCAATTTTGAAGAACAGAACTGGAATTTACAGATGAGATTTGATTCATGAA 1860
DB 1801 AAGCAATTTTGAAGAACAGAACTGGAATTTACAGATGAGATTTGATTCATGAA 1860
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QY	1861	GAACACAGATGAAATGGTTGAAAAAAGATTTGAGCTTCTCTTAGTTGTAAGAA	1920
Db	1861	GAAAACAGATGAATGGTTGTAAAAAAAGAAATTCGTGAGCTTCTCTTAGTTGTAAGAA	1920
QY	1921	GAAAAAGACATCTGTCATGAAAATAGTACCTTGCGGGAAGAAATTCGCATCTAAGACTG	1980
Db	1921	GAAAAAGACATCTGTCATGAAAATAGTACCTTGCGGGAAGAAATTCGCATCTAAGACTG	1980
QY	1981	GAGCTGACACAAATGAACATCAGAGCCAGCTAAAAAAGAAAAAAGAAAAAAGAAAA	2040
Db	1981	GAGCTGACACAAATGAACATCAGAGCCAGCTAAAAAAGAAAAAAGAAAAAAGAAAA	2040

RESULT 7

US-09-534-825A-303
; Sequence 303, Application US/09534825A
SEVENTH INNOVATION

```

? APPLICANT: Fridakis, Tony N.
? APPLICANT: Smith, John M.
? APPLICANT: Reed, Steven G.
? APPLICANT: Misher, Lynda
? APPLICANT: Retter, Marc W.
? APPLICANT: Dillon, Davin C.
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
? TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
? FILE REFERENCE: 210121.419c7
? CURRENT APPLICATION NUMBER: US/09/534,825A
? CURRENT FILING DATE: 2000-03-23
? NUMBER OF SEQ ID NOS: 317
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 303
? LENGTH: 2040
? TYPE: DNA
? ORGANISM: Homo sapien
? US-09-534-825A-303

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Query Match	100.0%	Score 2040:	DB 20:	Length 2040:
Best Local Similarity	100.0%	Pred. No. 2,7e-254:		
Matches 2040:	Conservative	0:	Mismatches	0:
			Indels	0:
			Gaps	0:

OY	1	ATGTGGTTAGAGTGAATTCATGACCGGGCGCTCTTGTGAAAGAACCATTTGGCTC	60
Db	1	ATGTGGTTAGAGTGAATTCATGACCGGGCGCTCTTGTGAAAGAACCATTTGGCTC	60
OY	61	AGGAGCAAGATGGGCAAGTGGTGTGCTGCTTCCCTGCTGCAAGGAGACGGCAAG	120
Db	61	AGGAGCAAGATGGGCAAGTGGTGTGCTGCTTCCCTGCTGCAAGGAGACGGCAAG	120
OY	121	AGCAAGCTGGGCACTTGTGGAGACACAGACGACTCTGCTATTGAAGACTTCAGAGCAAG	180
Db	121	AGCAAGCTGGGCACTTGTGGAGACACAGACGACTCTGCTATTGAAGACTTCAGAGCAAG	180
OY	181	ATGGGCAAGTGTGTCGCCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGTG	240
Db	181	ATGGGCAAGTGTGTCGCCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGTG	240
OY	241	GCGGCTTCTGAGACACAGACGACTCTGCTATTGAAGACTTCAGGAACAAGATGGCAAG	300
Db	241	GCGGCTTCTGAGACACAGACGACTCTGCTATTGAAGACTTCAGGAACAAGATGGCAAG	300
OY	301	TGGTGTGCGGCACCTCTTCCCTGCTGGAAGGGGGAGCGGCAAGAGCAAGTGGGCGCTGG	360
Db	301	TGGTGTGCGGCACCTCTTCCCTGCTGGAAGGGGGAGCGGCAAGAGCAAGTGGGCGCTGG	360
OY	361	GGAGACTACGATGACAGTGCCTTCATGAGAGCCAGGTACACAGTCCGTGGAGAAGATCTG	420
Db	361	GGAGACTACGATGACAGTGCCTTCATGAGAGCCAGGTACACAGTCCGTGGAGAAGATCTG	420
OY	421	GACAAAGTCCACAGAGGTGGCTGGTGGGGTAAAGTCCCCGAAAGAAAGATCTCATGCTCATG	480
Db	421	GACAAAGTCCACAGAGGTGGCTGGTGGGGTAAAGTCCCCGAAAGAAAGATCTCATGCTCATG	480
OY	481	CTCAGGAGACACTGCATGAACAGAAAGAGACAGCAAAAGAGGAGTGCCTTCATCTTGGCC	540

Db	481	CTCAGGGACACTGCAGCTGATACAGAAAGGACACAAAGGAGGATCGCTACATCTGGCC	540
Qy	541	TCCTGCCAATGGGAATTCAGAAAGTACTAAACCTCCTGCTGGACAGACGATGTCACATTAA	600
Db	541	TCCTGCCAATGGGAATTCAGAAAGTACTAAACCTCCTGCTGGACAGACGATGTCACATTAA	600
Qy	601	GTCCTTGACACAAACAAAGAGGACGACTTGATTAAGGCGGTACAACTGCCAGGAAGATGAA	660
Db	601	GTCCTTGACACAAACAAAGAGGACGACTTGATTAAGGCGGTACAACTGCCAGGAAGATGAA	660
Qy	661	TGTGGTTAAAGTGTCTGGAAACATGGCAGCTGTCCAAATATTCCAGATGAGTATGGAAAT	720
Db	661	TGTGGTTAAAGTGTCTGGAAACATGGCAGCTGTCCAAATATTCCAGATGAGTATGGAAAT	720
Qy	721	ACCACTCTGCACATAGCTATCTATATATAGATTAATTAATGAGCCAAAGCAGCTGCTCTTA	780
Db	721	ACCACTCTGCACATAGCTATCTATATATAGATTAATTAATGAGCCAAAGCAGCTGCTCTTA	780
Qy	781	TATGGTCTGATATTCGAATCAAAAAACAGCATGGCGCTCACACCACTGTACTTGGTGA	840
Db	781	TATGGTCTGATATTCGAATCAAAAAACAGCATGGCGCTCACACCACTGTACTTGGTGA	840
Qy	841	CATGAGCAAAAAACACCAAGCTGTGAATTTTAAATCAAGAAAAAAGCAATTTAAATGCA	900
Db	841	CATGAGCAAAAAACACCAAGCTGTGAATTTTAAATCAAGAAAAAAGCAATTTAAATGCA	900
Qy	901	CTGGATAGATATGTAAGAGACGTCTCCATYACTGCTGATGTTGGATTCAGCAAGTATA	960
Db	901	CTGGATAGATATGTAAGAGACGTCTCTCATCTGCTGTATGTTGGATTCAGCAAGTATA	960
Qy	961	GTCAGCCCTTCTACTTGAGCAAAATATGATGTATCTTCTCAAGATCTATCTGGACAGCG	1020
Db	961	GTCAGCCCTTCTACTTGAGCAAAATATGATGTATCTTCTCAAGATCTATCTGGACAGCG	1020
Qy	1021	GCCAAAGATATGCTGTTTCTAGTCATATCATGTAATTTGGCAATTCTTTGACACTAC	1080
Db	1021	GCCAAAGATATGCTGTTTCTAGTCATATCATGTAATTTGGCAATTCTTTGACACTAC	1080
Qy	1081	AAAGAAAAACAGATCTTAAAAATCTCTCTGAAAACAGCAATCCAGAACAGACTTAAG	1140
Db	1081	AAAGAAAAACAGATCTTAAAAATCTCTCTGAAAACAGCAATCCAGAACAGACTTAAG	1140
Qy	1141	CTGACATCAGAGGAAGAGTCACAAAGGTTCAAAGGCACTGAAATATGGCCAGCAGAGAA	1200
Db	1141	CTGACATCAGAGGAAGAGTCACAAAGGTTCAAAGGCACTGAAATATGGCCAGCAGAGAA	1200
Qy	1201	ATGTCTCAAGAACCAAGAAATTAATTAAGATGTGATACAGAGTTGAAAGAAATGAAG	1260
Db	1201	ATGTCTCAAGAACCAAGAAATTAATTAAGATGTGATACAGAGTTGAAAGAAATGAAG	1260
Qy	1261	AAGCATGGAAGTAATTAATGTGGGATTACTAGAAAACCTGCAGTAATGGTGTACTGTGGC	1320
Db	1261	AAGCATGGAAGTAATTAATGTGGGATTACTAGAAAACCTGCAGTAATGGTGTACTGTGGC	1320
Qy	1321	AATGGTGAATATGATTTAATTCCTTCAAGAGGACAGACAACTCGAAATATCAGCAATTT	1380
Db	1321	AATGGTGAATATGATTTAATTCCTTCAAGAGGACAGACAACTCGAAATATCAGCAATTT	1380
Qy	1381	CCCTGACAAAGAAAGTGAAGAGTATCACAGAAATTTGCGAATTAAGTTTCTGACTACAAAGAA	1440
Db	1381	CCCTGACAAAGAAAGTGAAGAGTATCACAGAAATTTGCGAATTAAGTTTCTGACTACAAAGAA	1440
Qy	1441	AAACGATGGCCAAATACTCTCTTCCAAAACAGCAACCCAGAAACAAAGACTTAAAGCTTGACA	1500
Db	1441	AAACGATGGCCAAATACTCTCTTCCAAAACAGCAACCCAGAAACAAAGACTTAAAGCTTGACA	1500
Qy	1501	TCAGAGGAAGATCTCAAAAGCGTTGAGGGCAGTGAATAATGGCCAGCCAGAGAAAAGATCT	1560
Db	1501	TCAGAGGAAGATCTCAAAAGCGTTGAGGGCAGTGAATAATGGCCAGCCAGAGAAAAGATCT	1560
Qy	1561	CAAGAACCAGAAATTAATTAAGATGGTGAATAGAGACTAGAAAATTTTATGGCTATCGAA	1620
Db	1561	CAAGAACCAGAAATTAATTAAGATGGTGAATAGAGACTAGAAAATTTTATGGCTATCGAA	1620

Db 1561 CAAGAACAGAAATTAATGAATGCTGATAGAGAGCTAGAAAAATTTTATGCTATTCGAA 1620
QY 1621 GAATGAGAAAGCAGGAACTACTCATGTCGATTCAGAAAACTGACTAAATGATGCC 1680
Db 1621 GAATGAGAAAGCAGGAACTACTCATGTCGATTCAGAAAACTGACTAAATGATGCC 1680
QY 1681 ACTGCTGGCAATGCTGATGATGATTAATTCCTCCAGAGAGACAGACACCTGAAAGC 1740
Db 1681 ACTGCTGGCAATGCTGATGATGATTAATTCCTCCAGAGAGACAGACACCTGAAAGC 1740
QY 1741 CACCAATTTCTCAGACTGAGATGAAGAGATATCACAGTACCAACCAAAATGATATCAG 1800
Db 1741 CACCAATTTCTCAGACTGAGATGAAGAGATATCACAGTACCAACCAAAATGATATCAG 1800
QY 1801 AACCAATTTTGTAGAGAACAGAACACTGGAATTTACACAGATGATTCGATTCATGAA 1860
Db 1801 AACCAATTTTGTAGAGAACAGAACACTGGAATTTACACAGATGATTCGATTCATGAA 1860
QY 1861 GAAAGCAGATAGAGTGTGTAAGAAAAATGAAATTCGAGCTTTCTTACTGTTAAGAAA 1920
Db 1861 GAAAGCAGATAGAGTGTGTAAGAAAAATGAAATTCGAGCTTTCTTACTGTTAAGAAA 1920
QY 1921 GAAAAAGACATCTTCATGATAAATAGTACTTCGCGGAGAAATTCGACATGCTAAGCTG 1980
Db 1921 GAAAAAGACATCTTCATGATAAATAGTACTTCGCGGAGAAATTCGACATGCTAAGCTG 1980
QY 1981 GACCTAGACACATGAACATCAGAGCAGCTAAAAAATGAAAAAATGAAAAAATGAAAA 2040
Db 1981 GACCTAGACACATGAACATCAGAGCAGCTAAAAAATGAAAAAATGAAAAAATGAAAA 2040

RESULT 8

US-09-536-857-375

Sequence 375, Application US/09536857

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiaod, Yuxui
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael D.
APPLICANT: Ranger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.42712C12
CURRENT APPLICATION NUMBER: US/09/536, 857
CURRENT FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 592
SOFTWARE: Fastseq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-536-857-375

Query Match 100.0%; Score 2040; DB 20; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2,7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTTGAGTGTGATTCATGCGGCTGCTCTTCTGTGAAGAACCATTTGGTCTG 60
Db 1 ATGTGTTGAGTGTGATTCATGCGGCTGCTCTTCTGTGAAGAACCATTTGGTCTG 60
QY 61 AGGAGCAAGATGGCAAGTGTGCTGCTCCCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGCAAGTGTGCTGCTCCCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACCAAGACGACTGTGCTATGAAGACACTCAGAGCAAG 180
Db 121 ATGTCTCAAGAACCAAGAAATTAATGAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260

Db 121 AGCAAGTGGGCACTTCTGAGACCAAGACGACTGTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGACCAAGTGT 240
Db 181 ATGGGCAAGTGTGCGGCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGACCAAGTGT 240
QY 241 GGGCGTTTCTGAGAACCAAGCAAGCACTGTGCTATGAAGCACTCAGGAACAAGATGGCAAG 300
Db 241 GGGCGTTTCTGAGAACCAAGCAAGCACTGTGCTATGAAGCACTCAGGAACAAGATGGCAAG 300
QY 301 TGTGCTGCGCACGCTTCCCTGCTGCTGCAAGGGGAGGCGGCAAGAGTGGGCGCTGG 360
Db 301 TGTGCTGCGCACGCTTCCCTGCTGCTGCAAGGGGAGGCGGCAAGAGTGGGCGCTGG 360
QY 361 GGAGACTACGATGACAGTGTGCTTCATGAGACCCAGGATACACGCTCCGTGGAAGAAATCTG 420
Db 361 GGAGACTACGATGACAGTGTGCTTCATGAGACCCAGGATACACGCTCCGTGGAAGAAATCTG 420
QY 421 GACAAAGCTCCAGAGCTGCTGCTGGGTAAAGTCCCGAGAAAGATCTCATCTGATG 480
Db 421 GACAAAGCTCCAGAGCTGCTGCTGGGTAAAGTCCCGAGAAAGATCTCATCTGATG 480
QY 481 CTGAGGGACACTGACGTGGAACAAGAAAGACAAACCAAAAGAGACTGCTACATCTGGCC 540
Db 481 CTGAGGGACACTGACGTGGAACAAGAAAGACAAACCAAAAGAGACTGCTACATCTGGCC 540
QY 541 TCTGCGCAATGGGAATTCAGAAATGATTAATGAAATCTGCTGAGACAGAGATGCAACTTAAT 600
Db 541 TCTGCGCAATGGGAATTCAGAAATGATTAATGAAATCTGCTGAGACAGAGATGCAACTTAAT 600
QY 601 GTCCCTTGACAAACAAAGAGACAGCTGTGATTAAGGCGCTACATGCCAGAAATGAA 660
Db 601 GTCCCTTGACAAACAAAGAGAGACAGCTGTGATTAAGGCGCTACATGCCAGAAATGAA 660
QY 661 TGTGCGTATGTTGCTGCGAACAATGGACATGATCCAAATTTCCACATGATGATGAAT 720
Db 661 TGTGCGTATGTTGCTGCGAACAATGGACATGATCCAAATTTCCACATGATGATGAAT 720
QY 721 ACCACTGTGCACTACGCTATCTATTAATGAAGATTAATGAGCCAAAGCAGCTGCTTA 780
Db 721 ACCACTGTGCACTACGCTATCTATTAATGAAGATTAATGAGCCAAAGCAGCTGCTTA 780
QY 781 TATGTGCTGATATTCGAATCAAAACCAAGATGGCCCTACACCACTGTTACTTGGTGA 840
Db 781 TATGTGCTGATATTCGAATCAAAACCAAGATGGCCCTACACCACTGTTACTTGGTGA 840
QY 841 CATGAGCAAAACAGCAAGTCGGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAACAGCAAGTCGGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGGATGATATGGAAGGAGTGTCTCATCTGCTGATGATGTTGGATCAGCAAGTATA 960
Db 901 CTGGATGATATGGAAGGAGTGTCTCATCTGCTGATGATGTTGGATCAGCAAGTATA 960
QY 961 GTGAGCCTTCTACTTGAAGCAAAATATTGATGATCTTCTCAGATCTATCTGAGCAGAG 1020
Db 961 GTGAGCCTTCTACTTGAAGCAAAATATTGATGATCTTCTCAGATCTATCTGAGCAGAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGATTAATTTGCCAGTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGATTAATTTGCCAGTACTTCTGACTAC 1080
QY 1081 AAGGAAAAACAGATGCTAAATAATCTTCTGAAACAGCAATCACAACAAAGACTTAAG 1140
Db 1081 AAGGAAAAACAGATGCTAAATAATCTTCTGAAACAGCAATCACAACAAAGACTTAAG 1140
QY 1141 CTGACATCAGAGGAAGATCACAAGGTTCAAAGGAGTGAATAATAGCCAGCAGAGAAA 1200
Db 1141 CTGACATCAGAGGAAGATCACAAGGTTCAAAGGAGTGAATAATAGCCAGCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATGAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAGAAATTAATGAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260

QY 541 TCTGCCAATGGGAATTCAGAAAGTAGTAAACCTCTGTCGACAGAGATGTCAACTTAAT 600
 Db 541 TCTGCCAATGGGAATTCAGAAAGTAGTAAACCTCTGTCGACAGAGATGTCAACTTAAT 600
 QY 601 GTCTCTTGACACAAAAAAGAGACAGCTGTGATTAAGGCCGTACAAATGCCAGGAATGAA 660
 Db 601 GTCTCTTGACACAAAAAAGAGACAGCTGTGATTAAGGCCGTACAAATGCCAGGAATGAA 660
 QY 661 TGTGGCTTAATGTGTGTGAACATGGCAGTCCAAATATTTCCAGATGATGTGAAAT 720
 Db 661 TGTGGCTTAATGTGTGTGAACATGGCAGTCCAAATATTTCCAGATGATGTGAAAT 720
 QY 721 ACCACTCTGACATGACCTATCTATATGAAGATTAATATGAGCCAAAGCAGTCTCTTA 780
 Db 721 ACCACTCTGACATGACCTATCTATATGAAGATTAATATGAGCCAAAGCAGTCTCTTA 780
 QY 781 TATGTGTGATATGCAATCAAAAAAAGCATGGCCTCACACACTGTTACTTGGTGA 840
 Db 781 TATGTGTGATATGCAATCAAAAAAAGCATGGCCTCACACACTGTTACTTGGTGA 840
 QY 841 CATGACCAAAAAACAGCAATCGTGAATTTTATATCAAGAAAAACGAATTTAATGCA 900
 Db 841 CATGACCAAAAAACAGCAATCGTGAATTTTATATCAAGAAAAACGAATTTAATGCA 900
 QY 901 CTGGATAGATATGGAAGAGCTGCTCATCTGTTGATGTTGGATCAGCAAGTATA 960
 Db 901 CTGGATAGATATGGAAGAGCTGCTCATCTGTTGATGTTGGATCAGCAAGTATA 960
 QY 961 GTACGCCCTTCTACTTGAGCAAAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
 Db 961 GTACGCCCTTCTACTTGAGCAAAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
 QY 1021 GCCAGAGATATGCTCTTCTACTCATCATGATGATTTTGGCAGTTACTTTGTGACTAC 1080
 Db 1021 GCCAGAGATATGCTCTTCTACTCATCATGATGATTTTGGCAGTTACTTTGTGACTAC 1080
 QY 1081 AAGAGAAAAACAGATGCTAAAAATCTCTTCAAAAAACAGCAATCCAGCAAGCTTAAG 1140
 Db 1081 AAGAGAAAAACAGATGCTAAAAATCTCTTCAAAAAACAGCAATCCAGCAAGCTTAAG 1140
 QY 1141 CTGACATCAGAGAGAGAGTACAAAGGTTCAAGGCAAGTGAATAATGCCAGCAGAGAAA 1200
 Db 1141 CTGACATCAGAGAGAGAGTACAAAGGTTCAAGGCAAGTGAATAATGCCAGCAGAGAAA 1200
 QY 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
 Db 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
 QY 1261 AAGCATGAAGATTAATATGAGGATTAAGAAACCTGACTAATGTTGCACTGCTGAGC 1320
 Db 1261 AAGCATGAAGATTAATATGAGGATTAAGAAACCTGACTAATGTTGCACTGCTGAGC 1320
 QY 1321 AATGATGATTAATGATTAATCTCTCAAGAGAGAGCAGAAACACTTAAATATCGCAATTT 1380
 Db 1321 AATGATGATTAATGATTAATCTCTCAAGAGAGAGCAGAAACACTTAAATATCGCAATTT 1380
 QY 1381 CCTGACAAAGAAAGTGAAGATATCACAGAAATTTGCAATTAATTTCTGACTCAAAAGAA 1440
 Db 1381 CCTGACAAAGAAAGTGAAGATATCACAGAAATTTGCAATTAATTTCTGACTCAAAAGAA 1440
 QY 1441 AAACAGATGCAAAATACTCTTCTGAAAAACAGCAACCCAGAAACAGACTTAAGCTGACA 1500
 Db 1441 AAACAGATGCAAAATACTCTTCTGAAAAACAGCAACCCAGAAACAGACTTAAGCTGACA 1500
 QY 1501 TCAGAGAGAGAGTACAAAGGCTTGAAGGCGAGTGAATAATGCGCAGCAGAGAAAGATCT 1560
 Db 1501 TCAGAGAGAGAGTACAAAGGCTTGAAGGCGAGTGAATAATGCGCAGCAGAGAAAGATCT 1560
 QY 1561 CAAGAACGAGAAATTAATAGATGATGATGAGAGAGTGAAGAAATTTTATGCTATCGAA 1620
 Db 1561 CAAGAACGAGAAATTAATAGATGATGATGAGAGAGTGAAGAAATTTTATGCTATCGAA 1620

QY 1621 GAAATGAGAAGCAGCAGAGTACTCATGTGCGATTCCAGAAAACTGACTAATGCTGCC 1680
 Db 1621 GAAATGAGAAGCAGCAGAGTACTCATGTGCGATTCCAGAAAACTGACTAATGCTGCC 1680
 QY 1681 ACTGTGGCAATGTGATGATGATTAATTTCTCCAGAGAAAGCAGAAACACTGAAAGC 1740
 Db 1681 ACTGTGGCAATGTGATGATGATTAATTTCTCCAGAGAAAGCAGAAACACTGAAAGC 1740
 QY 1741 CAGCAATTTCCGACACTGAGATGAAGATATCACAGTGAAGCAAAAAATGATTAATCAG 1800
 Db 1741 CAGCAATTTCCGACACTGAGATGAAGATATCACAGTGAAGCAAAAAATGATTAATCAG 1800
 QY 1801 AAGCAATTTTGTGAAGAGAGAAACACTGGAATATTAACAGATGAGATGATGATTCAGAA 1860
 Db 1801 AAGCAATTTTGTGAAGAGAGAAACACTGGAATATTAACAGATGAGATGATGATTCAGAA 1860
 QY 1861 GAAAGCAGATGAGATGATGATGATTAATTAATGATGATGATGATGATGATGATGATG 1920
 Db 1861 GAAAGCAGATGAGATGATGATGATTAATTAATGATGATGATGATGATGATGATGATG 1920
 QY 1921 GAAAGCAGATGATGATGATGATGATTAATTAATGATGATGATGATGATGATGATGATG 1980
 Db 1921 GAAAGCAGATGATGATGATGATGATTAATTAATGATGATGATGATGATGATGATGATG 1980
 QY 1981 GAGCTGACACAAATGAACATCAGACAGCTGAAAAAATGATGATGATGATGATGATGATG 2040
 Db 1981 GAGCTGACACAAATGAACATCAGACAGCTGAAAAAATGATGATGATGATGATGATGATG 2040

RESULT 11
 US-09-590-583-303
 : Sequence 303, Application US/09590583
 : GENERAL INFORMATION:
 : APPLICANT: Frudakis, Tony N.
 : APPLICANT: Reed, Steven G.
 : APPLICANT: Smith, John M.
 : APPLICANT: Misher, Linda E.
 : APPLICANT: Dillon, David C.
 : APPLICANT: Retter, Marc W.
 : APPLICANT: Wang, Aljun
 : APPLICANT: Skelky, Yasir A.W.
 : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 : FILE REFERENCE: 210121.419C9
 : CURRENT APPLICATION NUMBER: US/09/590,583
 : CURRENT FILING DATE: 2000-06-08
 : NUMBER OF SEQ ID NOS: 324
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO: 303
 : LENGTH: 2040
 : TYPE: DNA
 : ORGANISM: Homo sapien
 US-09-590-583-303
 Query Match 100.0%; Score 2040; DB 22; Length 2040;
 Best Local Similarity 100.0%; Pred. No. 2,7e+264;
 Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTTGAGGTGATTCATGCGGCTGCTCTTCTGTGAAGAACCATTTGCTC 60
 Db 1 ATGTGTTGAGGTGATTCATGCGGCTGCTCTTCTGTGAAGAACCATTTGCTC 60
 QY 61 AGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGAGAGCAG 120
 Db 61 AGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGAGAGCAG 120
 QY 121 AGCAAGTGGGCACTTCTGAGACCAAGAGACTGCTGTGAAGCACTCAGAGCAAG 180
 Db 121 AGCAAGTGGGCACTTCTGAGACCAAGAGACTGCTGTGAAGCACTCAGAGCAAG 180
 QY 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAAGCTG 240
 Db 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAAGCTG 240

QY 241 GGCCTTCTGGAGACACGAGACTGCTGATGAAGACACTCAGGAACAGATGGGCAAG 300
|||||
Db 241 GGCCTTCTGGAGACACGAGACTGCTGATGAAGACACTCAGGAACAGATGGGCAAG 300
QY 301 TGGTGCTGCCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGAGTGGGCTTGG 360
|||||
Db 301 TGGTGCTGCCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGTGGGCTTGG 360
QY 361 GGAGACTACGATGACAGTGCCTTCATGAGAGCCAGGTACACAGTCCGCTGAGAGATCTG 420
|||||
Db 361 GGAGACTACGATGACAGTGCCTTCATGAGAGCCAGGTACACAGTCCGCTGAGAGATCTG 420
QY 421 GACAGCTCCACAGAGCTGCTGCTGGGGTAAAGTCCCGAGAAAAGATCTCATGCTATG 480
|||||
Db 421 GACAGCTCCACAGAGCTGCTGCTGGGGTAAAGTCCCGAGAAAAGATCTCATGCTATG 480
QY 481 CTCAGGACACTGACGTGAACAAAGAGACAAAGAAAAGAGACTGCTCATCTGCCCC 540
|||||
Db 481 CTCAGGACACTGACGTGAACAAAGAGACAAAGAAAAGAGACTGCTCATCTGCCCC 540
QY 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCCTGCTGACAGACGATGCTCACTTAAT 600
|||||
Db 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCCTGCTGACAGACGATGCTCACTTAAT 600
QY 601 GTCTTGAACAACAAAAGAGACAGCTCTGATAAAGCCGTACAAATGCCAGGAAGATGAA 660
|||||
Db 601 GTCTTGAACAACAAAAGAGACAGCTCTGATAAAGCCGTACAAATGCCAGGAAGATGAA 660
QY 661 TGTGCGTTAATGTTGCGGAACATGCACTGATCCAAATATTCAGATGATGATGAAAT 720
|||||
Db 661 TGTGCGTTAATGTTGCGGAACATGCACTGATCCAAATATTCAGATGATGATGAAAT 720
QY 721 ACCACTGTGCACTAGCTATCTATATGAAGATAAATTAATGGCCAAAGCACTGCTCTTA 780
|||||
Db 721 ACCACTGTGCACTAGCTATCTATATGAAGATAAATTAATGGCCAAAGCACTGCTCTTA 780
QY 781 TATGCTGCTGATATCGAATCAAAAACAGCATGGCCTCACACCACTGTTACTTGGTGA 840
|||||
Db 781 TATGCTGCTGATATCGAATCAAAAACAGCATGGCCTCACACCACTGTTACTTGGTGA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAAGGAATTTAAATGCA 900
|||||
Db 841 CATGAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAAGGAATTTAAATGCA 900
QY 901 CTGATAGATATGGAAGAGACTGCTCTCATACTTCTGATGTTGGATCGACAATATA 960
|||||
Db 901 CTGATAGATATGGAAGAGACTGCTCTCATACTTCTGATGTTGGATCGACAATATA 960
QY 961 GTGAGCTTCTACTTGAACAAAATATTGATGTATCTTCAAGATCTATCTGACAGAG 1020
|||||
Db 961 GTGAGCTTCTACTTGAACAAAATATTGATGTATCTTCAAGATCTATCTGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTTGTAGTCATCATCATGTAATTTGGCCGATTACTTTGACATAC 1080
|||||
Db 1021 GCCAGAGATATGCTGTTTGTAGTCATCATCATGTAATTTGGCCGATTACTTTGACATAC 1080
QY 1081 AAAAGAAAAACAGATGCTAAAAATCTCTTCTGAAGAACAGCAATCCAGAAACAGACTTAAG 1140
|||||
Db 1081 AAAAGAAAAACAGATGCTAAAAATCTCTTCTGAAGAACAGCAATCCAGAAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGTCACAAAAGTTCAAGGAGAGTGAATAATAGCCAGAGAGAAA 1200
|||||
Db 1141 CTGACATCAGAGAGAGTCACAAAAGTTCAAGGAGAGTGAATAATAGCCAGAGAGAAA 1200
QY 1201 ATGCTCTAAGAGAACAGAAATTAATAGAGTGTATAGAGAGTTGAAGAAAGAAATGAG 1260
|||||
Db 1201 ATGCTCTAAGAGAACAGAAATTAATAGAGTGTATAGAGAGTTGAAGAAAGAAATGAG 1260
QY 1261 AAGCATGAAGATTAATATGTTGGGATTAATGAAAAACCTGACTAATGTTGCTACTGCTGGC 1320
|||||
Db 1261 AAGCATGAAGATTAATATGTTGGGATTAATGAAAAACCTGACTAATGTTGCTACTGCTGGC 1320

QY 1321 AATGCTAATTAATGATTAATTCCTCAAGAGAGACAGAACACTGAAATCAGCAATTT 1380
|||||
Db 1321 AATGCTAATTAATGATTAATTCCTCAAGAGAGACAGAACACTGAAATCAGCAATTT 1380
QY 1381 CCTGCAACGAAGTGAAGAGTATCAGAAATTTGGCAATTAGTTTCTGACTACAAAGAA 1440
|||||
Db 1381 CCTGCAACGAAGTGAAGAGTATCAGAAATTTGGCAATTAGTTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCAAAATACTCTTCTGAAGAACAGCAACCCAGAACAGACTTAAGCTGACA 1500
|||||
Db 1441 AAACAGATGCAAAATACTCTTCTGAAGAACAGCAACCCAGAACAGACTTAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGTCACAAAAGCTTGAGGGCAGTGAATAATGGCCAGCCAGAGAAAATCT 1560
|||||
Db 1501 TCAGAGAGAGAGTCACAAAAGCTTGAGGGCAGTGAATAATGGCCAGCCAGAGAAAATCT 1560
QY 1561 CAAGAACAGAAATTAATTAAGAGTGTATGAGAGCTAGAGAAATTTATGGCTATGGA 1620
|||||
Db 1561 CAAGAACAGAAATTAATTAAGAGTGTATGAGAGCTAGAGAAATTTATGGCTATGGA 1620
QY 1621 GAAATGAAGAGACAGGAACTACTCATGTGCGATTCCAGAAAACCTGACTAATGTGCC 1680
|||||
Db 1621 GAAATGAAGAGACAGGAACTACTCATGTGCGATTCCAGAAAACCTGACTAATGTGCC 1680
QY 1681 ACTGCTGCAATGGTGATGATGATTAATTCCTCAAGAGAGACAGAACCTGAAAAC 1740
|||||
Db 1681 ACTGCTGCAATGGTGATGATGATTAATTCCTCAAGAGAGACAGAACCTGAAAAC 1740
QY 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCACAGTGCAGAACAAATGATACTCAG 1800
|||||
Db 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCACAGTGCAGAACAAATGATACTCAG 1800
QY 1801 AAGCAATTTTGTGAAGAACACAGACACTGGAATATTACACGATGATGATTCATGAA 1860
|||||
Db 1801 AAGCAATTTTGTGAAGAACACAGACACTGGAATATTACACGATGATGATTCATGAA 1860
QY 1861 GAAAAAGCAGATAGAGTGTGTTGAAAAATGCAATTCAGCTTCTCTTAGTTGAAGAA 1920
|||||
Db 1861 GAAAAAGCAGATAGAGTGTGTTGAAAAATGCAATTCAGCTTCTCTTAGTTGAAGAA 1920
QY 1921 GAAAAAGCAGATGCAATGAATAGTACGTTGGGGAGAAATTTGCCATGCTAAGACTG 1980
|||||
Db 1921 GAAAAAGCAGATGCAATGAATAGTACGTTGGGGAGAAATTTGCCATGCTAAGACTG 1980
QY 1981 GAGCTAGACCAATGAACATCAGAGCCAGCTAAAAAAGAAAAAAGAAAAAAGAAAAA 2040
|||||
Db 1981 GAGCTAGACCAATGAACATCAGAGCCAGCTAAAAAAGAAAAAAGAAAAAAGAAAAA 2040

RESULT 12
US-09-593-793A-375
Sequence 375, Application US/09593793A
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Helper, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42715C15

; CURRENT APPLICATION NUMBER: US/09/593,793A
; CURRENT FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 814
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-593-793A-375

Query Match 100.0%; Score 2040; DB 22; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2,7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGTTGAGTGGATTCATGCCGGTGGCTCTCTCTGTGAAGAAGCATTTGGTCTC 60
DB 1 ATGGTGTTGAGTGGATTCATGCCGGTGGCTCTCTCTGTGAAGAAGCATTTGGTCTC 60
QY 61 AGGACCAAGATGGGCAAGGTGTGTCGCTGCTCCCTGCTGAGGAGAGCGGCAAG 120
DB 61 AGGACCAAGATGGGCAAGGTGTGTCGCTGCTCCCTGCTGAGGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGGAGACCAAGCACTCTGTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTGGAGACCAAGCACTCTGTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGGCACCTGCTTCCCTGCTGAGGAGAGTGGCAAGCACTG 240
DB 181 ATGGGCAAGTGGTGGCGGCACCTGCTTCCCTGCTGAGGAGAGTGGCAAGCACTG 240
QY 241 GGGCTTCTGGAGACCAAGCACTCTGTATGAAGACACTCAGAGCAAGTGGGCAAG 300
DB 241 GGGCTTCTGGAGACCAAGCACTCTGTATGAAGACACTCAGAGCAAGTGGGCAAG 300
QY 301 TGGTCTGCACTGCTTCCCTGCTGAGGAGAGCGGCAAGCAAGTGGGCGCTTG 360
DB 301 TGGTCTGCACTGCTTCCCTGCTGAGGAGAGCGGCAAGCAAGTGGGCGCTTG 360
QY 361 GGAGACTACGATGACAGTCCCTTCATGAGCCAGGTACCAAGTGGGCAAGTGG 420
DB 361 GGAGACTACGATGACAGTCCCTTCATGAGCCAGGTACCAAGTGGGCAAGTGG 420
QY 421 GACAAGCTCCACAGAGCTCTGTGGGGTAAAGTCCCGAAGAGATCTCATCTGATG 480
DB 421 GACAAGCTCCACAGAGCTCTGTGGGGTAAAGTCCCGAAGAGATCTCATCTGATG 480
QY 481 CTCAGGGACACTGACGTGAACAAGAGCAAGCAAGAGAGTCTCTACATCTGGCC 540
DB 481 CTCAGGGACACTGACGTGAACAAGAGCAAGCAAGAGAGTCTCTACATCTGGCC 540
QY 541 TGTGCAATGGGAATTCAGAAATAGTAAATCTCTGCTGAGACAGATGCTAATTA 600
DB 541 TGTGCAATGGGAATTCAGAAATAGTAAATCTCTGCTGAGACAGATGCTAATTA 600
QY 601 GTCTTGAACAAGAAAGAGACAGCTGTATAAAGCCGTCAATGCCAGAGATGAA 660
DB 601 GTCTTGAACAAGAAAGAGACAGCTGTATAAAGCCGTCAATGCCAGAGATGAA 660
QY 661 TGTGCGTTAATGTGCTGAGACATGGCACTGATCCAAATATTCAGATGATGAAT 720
DB 661 TGTGCGTTAATGTGCTGAGACATGGCACTGATCCAAATATTCAGATGATGAAT 720
QY 721 ACCACTCTGACCTAGCTCTTATATGAAGTAAATTAATGGCCAAACACTGCTTA 780
DB 721 ACCACTCTGACCTAGCTCTTATATGAAGTAAATTAATGGCCAAACACTGCTTA 780
QY 781 TATGTTGCTGATATGAAATCAAAAAACAGCATGGCTCACAACACTGTACTGTGTA 840
DB 781 TATGTTGCTGATATGAAATCAAAAAACAGCATGGCTCACAACACTGTACTGTGTA 840
QY 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGA 900
DB 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGA 900

QY 901 CTGATATGATATGAAGACCTGCTCATACTTGGTATGTTGTGATCAGCAAGTATA 960
DB 901 CTGATATGATATGAAGACCTGCTCATACTTGGTATGTTGTGATCAGCAAGTATA 960
QY 961 GTACAGCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGACAG 1020
DB 961 GTACAGCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGACAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCAATCATATGTAATTTGGCAGTACTTTCTGACT 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCAATCATATGTAATTTGGCAGTACTTTCTGACT 1080
QY 1081 AAGAGAAACACATGCTAAATATCTTGTGAAGACAGCAATCCAGAAAGCTTAAAG 1140
DB 1081 AAGAGAAACACATGCTAAATATCTTGTGAAGACAGCAATCCAGAAAGCTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAAGGAGTGAATAATAGCCAGCAGAGAA 1200
DB 1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAAGGAGTGAATAATAGCCAGCAGAGAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATGAATGATGATAGAGAGTTGAGAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACCAAGAAATTAATGAATGATGATAGAGAGTTGAGAGAAATGAAG 1260
QY 1261 AAGCATGAAGTAAATATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
DB 1261 AAGCATGAAGTAAATATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
QY 1321 AATGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
DB 1321 AATGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1381 CCTGACAAACGAAAGTGAAGATATCAAGAAATTTGGCAATTTAGTTTCTGACTCA 1440
DB 1381 CCTGACAAACGAAAGTGAAGATATCAAGAAATTTGGCAATTTAGTTTCTGACTCA 1440
QY 1441 AAGAGATGCCAAATATCTCTGTAAGACCAAGCAAGCAAGCAAGCAAGCAAGCA 1500
DB 1441 AAGAGATGCCAAATATCTCTGTAAGACCAAGCAAGCAAGCAAGCAAGCAAGCA 1500
QY 1501 TCAGAGAGAGTCAACAAAGCTTGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1560
DB 1501 TCAGAGAGAGTCAACAAAGCTTGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1560
QY 1561 CAAGAACCAAGAAATTAATGAAGTGTGATGAGAGCTGAGAAATTTTATGCTATCG 1620
DB 1561 CAAGAACCAAGAAATTAATGAAGTGTGATGAGAGCTGAGAAATTTTATGCTATCG 1620
QY 1621 GAAATGAAGAACAGAGTACTCATGTCGATTCAGAAACCTGACTAATGCTG 1680
DB 1621 GAAATGAAGAACAGAGTACTCATGTCGATTCAGAAACCTGACTAATGCTG 1680
QY 1681 ACTGCTGCAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
DB 1681 ACTGCTGCAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
QY 1741 CAGCAATTTCTGACACTGAGATGAAGTATCAACAGTGAAGCAACAAATGATCTAG 1800
DB 1741 CAGCAATTTCTGACACTGAGATGAAGTATCAACAGTGAAGCAACAAATGATCTAG 1800
QY 1801 AAGCAATTTTGAAGAACAGAACTGGAATATTCAGAGATGATGATGATGATG 1860
DB 1801 AAGCAATTTTGAAGAACAGAACTGGAATATTCAGAGATGATGATGATGATGATG 1860
QY 1861 GAAAGCAGATAGAGTGTGTAATAATATTCAGACTTCTTCTTATGTTGAAGAA 1920
DB 1861 GAAAGCAGATAGAGTGTGTAATAATATTCAGACTTCTTCTTATGTTGAAGAA 1920
QY 1921 GAAAAAGACATCTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1980
DB 1921 GAAAAAGACATCTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1980

QY 1981 GACCTAGACACATGAAACATCATGAGCCAGCTAAAAA 2040
DB 1981 GACCTAGACACATGAAACATCATGAGCCAGCTAAAAA 2040

RESULT 13

US-09-605-783A-375

Sequence 375, Application US/09605783A

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqun.
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Reiter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,783A
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-605-783A-375

Query Match

100.0%; Score 2040; DB 23; Length 2040;

Best Local Similarity 100.0%; Pred. No. 2.7e-264; Mismatches 0; Indels 0; Gaps 0;

Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTGGAGTGAATTCATGCCGCTGCTCTGTGAAGAACCCATTTGTCTC 60
DB 1 ATGGTGGTGGAGTGAATTCATGCCGCTGCTCTGTGAAGAACCCATTTGTCTC 60
QY 61 AGAGCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGAGAGAGCGGCAAG 120
DB 61 AGAGCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGAGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTGTGAGACACGAGACCTGCTATGAAGACACACAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTGTGAGACACGAGACCTGCTATGAAGACACACAGAGCAAG 180
QY 181 ATGGGCAAGTGTGAGACACGAGACCTGCTATGAAGACACACAGAGCAAG 240
DB 181 ATGGGCAAGTGTGAGACACGAGACCTGCTATGAAGACACACAGAGCAAG 240
QY 241 GGGGCTTGTGAGACACGAGACCTGCTATGAAGACACACAGAGCAAG 300
DB 241 GGGGCTTGTGAGACACGAGACCTGCTATGAAGACACACAGAGCAAG 300
QY 301 TGTGCTGCGCACTGCTTCCCTGCTGAGGGGAGCGGCAAGAGCAAGTGGGCTTG 360
DB 301 TGTGCTGCGCACTGCTTCCCTGCTGAGGGGAGCGGCAAGAGCAAGTGGGCTTG 360
QY 361 GGAGACTACGATGACAGTGTGCTTATGAGAGCCAGAGTACAGCTCCGTGGAGAGATCTG 420
DB 361 GGAGACTACGATGACAGTGTGCTTATGAGAGCCAGAGTACAGCTCCGTGGAGAGATCTG 420
QY 421 GACAGCTCAGACAGAGTGTGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
DB 421 GACAGCTCAGACAGAGTGTGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATGTCATG 480

DB 421 GACAGCTCAGACAGAGTGTGCTGCTGAGGAGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
QY 481 CTCAGGACACTGACGTGACACAAAGAGACAGCAAGAGAGACTGCTACATCTGACC 540
DB 481 CTCAGGACACTGACGTGACACAAAGAGACAGCAAGAGAGACTGCTACATCTGACC 540
QY 541 TCTGCCAATGGGAATTCAGAGTATGAATTAACCTCTGAGACAGAGATCTCAATTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAGTATGAATTAACCTCTGAGACAGAGATCTCAATTAAT 600
QY 601 GTCCCTTACACAAAGAGAGACAGCTGATTAAGCCCTTACAAATCCGAGAAAGATGAA 660
DB 601 GTCCCTTACACAAAGAGAGAGACAGCTGATTAAGCCCTTACAAATCCGAGAAAGATGAA 660
QY 661 TGTGCGTAAATGTTGCTGGAACATGGACATGATCCAAATATTCAGATGATGAGAAAT 720
DB 661 TGTGCGTAAATGTTGCTGGAACATGGACATGATCCAAATATTCAGATGATGAGAAAT 720
QY 721 ACCACTGTGACATACGCTATCTATTAATGAAGATTAATTAATGAGCAAGCTGCTTGA 780
DB 721 ACCACTGTGACATACGCTATCTATTAATGAAGATTAATTAATGAGCAAGCTGCTTGA 780
QY 781 TATGCTGCTATATCGAATCAAAAAACAGATGAGCTCACACACCTGTTACTTGTGTA 840
DB 781 TATGCTGCTATATCGAATCAAAAAACAGATGAGCTCACACACCTGTTACTTGTGTA 840
QY 841 CATGAGCAAAACAGCAAGTGTGGAATTTTATATCAAGAAAAAGCAATTTAAATGCA 900
DB 841 CATGAGCAAAACAGCAAGTGTGGAATTTTATATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATGATATGGAAGAGAGCTGCTCATCTGCTGATGTTGTGATGATGAGCAAGTATA 960
DB 901 CTGATGATATGGAAGAGAGCTGCTCATCTGCTGATGTTGTGATGATGAGCAAGTATA 960
QY 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGTCTATATGAGCAAGC 1020
DB 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGTCTATATGAGCAAGC 1020
QY 1021 GCCAGAGATATGCTGTTTATGATCATCATCATGATTAATTTGCCAGTACTTTCAGTAC 1080
DB 1021 GCCAGAGATATGCTGTTTATGATCATCATCATGATTAATTTGCCAGTACTTTCAGTAC 1080
QY 1081 AAAGAAAAAGATGCTAAAAATCTCTTGTGAAGACAGCAATCCAGCAAGACTTAAAG 1140
DB 1081 AAAGAAAAAGATGCTAAAAATCTCTTGTGAAGACAGCAATCCAGCAAGACTTAAAG 1140
QY 1141 CTGACATCAAGAGAGAGTCAAAAGGTTCAAGGCGATGAATAATACCGACAGAGAAA 1200
DB 1141 CTGACATCAAGAGAGAGTCAAAAGGTTCAAGGCGATGAATAATACCGACAGAGAAA 1200
QY 1201 ATGCTCAAGAACAGAAATTAATTAAGATGATGATGAGAGTGAAGAAATGAAG 1260
DB 1201 ATGCTCAAGAACAGAAATTAATTAAGATGATGATGAGAGTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTAAATATGAGGATTAATTAAGAAACCTGACTAATGCTGACAGCTG 1320
DB 1261 AAGCATGAAAGTAAATATGAGGATTAATTAAGAAACCTGACTAATGCTGACAGCTG 1320
QY 1321 AATGCTATTAATGATTAATTCCTCAAGAGAGAGCAAGACCTGAAATTAAGCAATTT 1380
DB 1321 AATGCTATTAATGATTAATTCCTCAAGAGAGAGCAAGACCTGAAATTAAGCAATTT 1380
QY 1381 CTTGACACAGAAAGTGAAGATATCAAGATTTGCAATTAATGTTTGTGACTACAAAGAA 1440
DB 1381 CTTGACACAGAAAGTGAAGATATCAAGATTTGCAATTAATGTTTGTGACTACAAAGAA 1440
QY 1441 AAACAGATGCAAAATATCTTCTGAAAGACAGCAACCCAGACAGACTTAAAGCTGACA 1500
DB 1441 AAACAGATGCAAAATATCTTCTGAAAGACAGCAACCCAGACAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGGAAGAGTCAAAAGCTTGAAGGAGAGTGAATGAGCCAGCCAGAGAAAGATCT 1560
DB 1501 TCAGAGGAAGAGTCAAAAGCTTGAAGGAGAGTGAATGAGCCAGCCAGAGAAAGATCT 1560

Qy 1561 CAGAACGAGAAATTAATAGAGTGTATAGAGCTAGAGAAATTTTATGGCTATCGAA 1620
|||||
Db 1561 CAGAACGAGAAATTAATAGAGTGTATAGAGCTAGAGAAATTTTATGGCTATCGAA 1620
Qy 1621 GAAATGAAGAGCAGCGAGAGTACTCATGTCCGATTTCCAGAGAAACCTGACTAATGTGCC 1680
|||||
Db 1621 GAAATGAAGAGCAGCGAGAGTACTCATGTCCGATTTCCAGAGAAACCTGACTAATGTGCC 1680
Qy 1681 ACTGCTGCAATGCTGATGATGATTAATTCCTCCAGAGAGAGAGAACACCTGAAAGC 1740
|||||
Db 1681 ACTGCTGCAATGCTGATGATGATTAATTCCTCCAGAGAGAGAGAACACCTGAAAGC 1740
Qy 1741 CAGCAATTTCTGACACTGAGAGATGAGATATCATCACTGACGAAACAAATGATCTCAG 1800
|||||
Db 1741 CAGCAATTTCTGACACTGAGAGATGAGATATCATCACTGACGAAACAAATGATCTCAG 1800
Qy 1801 AAGCAATTTTGTGAAGAGACAGACACTGGAATATACAGATGATCTGATTCATGAA 1860
|||||
Db 1801 AAGCAATTTTGTGAAGAGACAGACACTGGAATATACAGATGATCTGATTCATGAA 1860
Qy 1861 GAAAAAGCAGATAGAGAGTGTGAAAAAATGAATTCGACTTTCTTAGTTGAAGAA 1920
|||||
Db 1861 GAAAAAGCAGATAGAGAGTGTGAAAAAATGAATTCGACTTTCTTAGTTGAAGAA 1920
Qy 1921 GAAAAAGCAGATCTGCAATGAAATATGATACGTTGCGGAGAGAAATGCCATGCTAAGACTG 1980
|||||
Db 1921 GAAAAAGCAGATCTGCAATGAAATATGATACGTTGCGGAGAGAAATGCCATGCTAAGACTG 1980
Qy 1981 GAGCTAGACACAATGAACATTCAGGCCAGCTAATAAAAAAAAAAAAAAAAAAAAAA 2040
|||||
Db 1981 GAGCTAGACACAATGAACATTCAGGCCAGCTAATAAAAAAAAAAAAAAAAAAAAAA 2040

RESULT 14

US-09-636-215-375
; Sequence 375; Application US/09636215
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuguí
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-636-215-375

Query Match 100.0%; Score 2040; DB 24; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2,7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTGGTTGAGTTGATTCATGCGCGGCTGCTCTTCTGTGAAGAACCATTTGGTCTC 60

Db 1 ATGGTGGTTGAGTTGATTCATGCGCGGCTGCTCTTCTGTGAAGAACCATTTGGTCTC 60
Qy 61 AGGACGAAGATGGGCAAGGAGTGCCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Db 61 AGGACGAAGATGGGCAAGGAGTGCCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Qy 121 AGCAACGTGGGCACTTGTGAGACCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTGTGAGACCAAGCAAGCACTGCTATGAAGCACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGTGG 240
Db 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAAGTGG 240
Qy 241 GCGGCTTGGAGACACAGACACTGCTGATGAAGACACTGAGAAACAAGATGGGCAAG 300
Db 241 GCGGCTTGGAGACACAGACACTGCTGATGAAGACACTGAGAAACAAGATGGGCAAG 300
Qy 301 TGGTCTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGCAAGTGGGCGCTTGG 360
Db 301 TGGTCTGCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGCAAGTGGGCGCTTGG 360
Qy 361 GGAGACTACGATGACAGTGCCTTTCATGAGGCCAGGTACCACAGTCCGTGGAGAAATCTG 420
Db 361 GGAGACTACGATGACAGTGCCTTTCATGAGGCCAGGTACCACAGTCCGTGGAGAAATCTG 420
Qy 421 GACAAGCTCCACAGAGCTGCTGAGGGGTAAAGTCCCGAAGAGATTCATGCTCATG 480
Db 421 GACAAGCTCCACAGAGCTGCTGAGGGGTAAAGTCCCGAAGAGATTCATGCTCATG 480
Qy 481 CTCAGGAGACTGAGCTGTAACAAGAGCAACAAGAGAGCTGCTACATCTGGCC 540
Db 481 CTCAGGAGACTGAGCTGTAACAAGAGCAACAAGAGAGCTGCTACATCTGGCC 540
Qy 541 TCTGCCAATGGCAATTCAGAGTAAATCTCTGCTGAGACAGATGTCAGTTAAT 600
Db 541 TCTGCCAATGGCAATTCAGAGTAAATCTCTGCTGAGACAGATGTCAGTTAAT 600
Qy 601 GTCCTTGACAAACAAAAGAGCAGCTGATAAAGGCCCTCAATGCCAGAGATGAA 660
Db 601 GTCCTTGACAAACAAAAGAGCAGCTGATAAAGGCCCTCAATGCCAGAGATGAA 660
Qy 661 TGTGGCTTAATGTTCTGTAACATGGCAGCTGATCCAAATATTCAGATGATGAAAT 720
Db 661 TGTGGCTTAATGTTCTGTAACATGGCAGCTGATCCAAATATTCAGATGATGAAAT 720
Qy 721 ACCACTCTGCACTACGCTATCTATATGAAGTAAATTAATGGCCAAAGCACTGCTTAA 780
Db 721 ACCACTCTGCACTACGCTATCTATATGAAGTAAATTAATGGCCAAAGCACTGCTTAA 780
Qy 781 TATGGCTGATATGCAATCAAAAAACAGCTGGCTCACACCACTGTTACTGGTGA 840
Db 781 TATGGCTGATATGCAATCAAAAAACAGCTGGCTCACACCACTGTTACTGGTGA 840
Qy 841 CATGAGCAAAAACAGCAAGTCTGAAATTTTATCAAGAAAAAGCGAATTTAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGTCTGAAATTTTATCAAGAAAAAGCGAATTTAATGCA 900
Qy 901 CTGGATAGATATGAAGAGCTGCTCATATCTTGTCTGATGTTGGATCAGCAAGTATA 960
Db 901 CTGGATAGATATGAAGAGCTGCTCATATCTTGTCTGATGTTGGATCAGCAAGTATA 960
Qy 961 GTCAGCTTCTACTGAGCAAAAATTTGATGATCTTCAAGATCTATGAGACAGAG 1020
Db 961 GTCAGCTTCTACTGAGCAAAAATTTGATGATCTTCAAGATCTATGAGACAGAG 1020
Qy 1021 GCCAGAGATATGCTTTTCTAGTATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTTTTCTAGTATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Qy 1081 AAAGAAAAACAGATCTTAAAAATCTCTGTGAAGAACAGCAATCCAGAACAGCTTAAAG 1140
|||||

```

Db 1081 AAAAAAAAAACAGATGCTAAAAATCTCTCTGAAAAACGCAATCCAGAACAGACTTAAG 1140
Qy 1141 CTGACATCAGAGAGAGATGCACAAAGTTCAAGGCGAGTGAATAGCCAGCCAGAGAA 1200
Db 1141 CTTGACATCAGAGAGAGATGCACAAAGTTCAAGGCGAGTGAATAGCCAGCCAGAGAA 1200
Qy 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGTGATAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGTGATAGAGAGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAGATTAATATGTGGATTAAGAAAACCTGACTAATGTGTCACTGTGCC 1320
Db 1261 AAGCATGAAGATTAATATGTGGATTAAGAAAACCTGACTAATGTGTCACTGTGCC 1320
Qy 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGAGAAACCTGAAATGAGCAATTT 1380
Db 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGAGAAACCTGAAATGAGCAATTT 1380
Qy 1381 CCTGACAGAGAAAGTGAAGAGATATCAGAAATTTGGCAATTTAGTTCTGACTCAAGAA 1440
Db 1381 CCTGACAGAGAAAGTGAAGAGATATCAGAAATTTGGCAATTTAGTTCTGACTCAAGAA 1440
Qy 1441 AAGCATGCCAAATATCTCTTGTGAAAACAGCAACCCAGACAGACTTAAGAGTACA 1500
Db 1441 AAGCATGCCAAATATCTCTTGTGAAAACAGCAACCCAGACAGACTTAAGAGTACA 1500
Qy 1501 TCAGAGAGAGATGCACAAAGGCTTGAAGGCGAGTGAATGGCCAGAGAGAAAGTCT 1560
Db 1501 TCAGAGAGAGATGCACAAAGGCTTGAAGGCGAGTGAATGGCCAGAGAGAAAGTCT 1560
Qy 1561 CAAGAACAGAAATTAATTAAGATGTGATAGAGACTAGAAATTTATGGCTATCGAA 1620
Db 1561 CAAGAACAGAAATTAATTAAGATGTGATAGAGACTAGAAATTTATGGCTATCGAA 1620
Qy 1621 GAAATTAAGAGAGAGAGAGTACTCATGTGCGATTTCCCAAGAAACCTGACTAATGTGCC 1680
Db 1621 GAAATTAAGAGAGAGAGAGTACTCATGTGCGATTTCCCAAGAAACCTGACTAATGTGCC 1680
Qy 1681 ACTGCTGCAATGTGATGATGATTAATCTCTCAAGAGAGAGAGAGAGAGAGAGAG 1740
Db 1681 ACTGCTGCAATGTGATGATGATTAATCTCTCAAGAGAGAGAGAGAGAGAGAGAG 1740
Qy 1741 CAGCAATTTCTGACACTGAGAAATGAGAGATATCAGAGTGAAGAAATGATGACTCAG 1800
Db 1741 CAGCAATTTCTGACACTGAGAAATGAGAGATATCAGAGTGAAGAAATGATGACTCAG 1800
Qy 1801 AAGCAATTTTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
Db 1801 AAGCAATTTTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
Qy 1861 GAAAGAGAGATGAAGTGTGTTGAAATTAATGATGAGCTTCTGATGATTAAGAA 1920
Db 1861 GAAAGAGAGATGAAGTGTGTTGAAATTAATGATGAGCTTCTGATGATTAAGAA 1920
Qy 1921 GAAAAAGAGATCTTGTGATGAAATTAATGATGAGCTTCTGATGATTAAGAA 1980
Db 1921 GAAAAAGAGATCTTGTGATGAAATTAATGATGAGCTTCTGATGATTAAGAA 1980
Qy 1981 GAGCTGACAGAGATGAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040
Db 1981 GAGCTGACAGAGATGAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040

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RESULT 15
US-09-651-236-375

; Sequence 375, Application US/09651236
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.

```

; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42718C18
; CURRENT APPLICATION NUMBER: US/09/651,236
; NUMBER OF SEQ ID NOS: 865
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-651-236-375

Query Match 100.0%; Score 2040; DB 25; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2,7e+264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGCTTGAAGTGTGATTCATATGCGGCTGCTCTTCTGTGAAGAACCATTTGCTCTC 60
Db 1 ATGTGCTTGAAGTGTGATTCATATGCGGCTGCTCTTCTGTGAAGAACCATTTGCTCTC 60
Qy 61 AGGAGCAAGATGGGCAAGTGGTCTGCGCTGCTCCCTGCTGCAAGGAGAGAGAGAGAG 120
Db 61 AGGAGCAAGATGGGCAAGTGGTCTGCGCTGCTCCCTGCTGCAAGGAGAGAGAGAGAG 120
Qy 121 AGCAAGTGGGCACTCTTGTGAGACACAGAGACTGTGATGAAGACACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTCTTGTGAGACACAGAGACTGTGATGAAGACACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Db 181 ATGGGCAAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Qy 241 GGGGCTTCTGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Db 241 GGGGCTTCTGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Qy 301 TGTGCTGCGGCACTGCTTCCCTGCTGCGAGGGGAGGCGGCAAGAGTGGGCGCTGG 360
Db 301 TGTGCTGCGGCACTGCTTCCCTGCTGCGAGGGGAGGCGGCAAGAGTGGGCGCTGG 360
Qy 361 GAGAGACTAGATATACAGTGTGCTTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 361 GAGAGACTAGATATACAGTGTGCTTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Qy 421 GAGAGCTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 421 GAGAGCTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Qy 481 CTCAGGAGACAGTACGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 481 CTCAGGAGACAGTACGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Qy 541 TCTGCAATGGGAATTCAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
Db 541 TCTGCAATGGGAATTCAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
Qy 601 GTCCCTGACAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 601 GTCCCTGACAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Qy 661 TGTGCTTAATGTTGCTGGAACAGTGCATCAATTAATTAATTAATTAATTAATTAATTA 720

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Db 661 TGTGGTTAAATGTTGCTGGAACTGGCACTGATCCAAATATTCAGATGATGGAAT 720
Qy 721 AACACTGCACTACGCTATCATTAATGAAGTAATTAATGAGCCAAAGCACTGCTTA 780
Db 721 AACACTGCACTACGCTATCATTAATGAAGTAATTAATGAGCCAAAGCACTGCTTA 780
Qy 781 TATGCTGCTGATATGCAATCAAAAACAAGCATGGCTCACACCACTGTTACTTGGTGA 840
Db 781 TATGCTGCTGATATGCAATCAAAAACAAGCATGGCTCACACCACTGTTACTTGGTGA 840
Qy 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAAAGCAATTTAAATGCA 900
Qy 901 CTGGATATATGGAAGAGCTGCTCATCTGATGCTGATATGCTGATGATCAGCAATGA 960
Db 901 CTGGATATATGGAAGAGCTGCTCATCTGATGCTGATGCTGATGATCAGCAATGA 960
Qy 961 GTCAAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGACAG 1020
Db 961 GTCAAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGACAG 1020
Qy 1021 GCCAGAGATATGCTGTTCTAGTATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTCTAGTATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Qy 1081 AAAGAAAAAGATGCTTAAAAATCTCTCTGAAAACAGCAATCCCAAGCAACTTAAAG 1140
Db 1081 AAAGAAAAAGATGCTTAAAAATCTCTCTGAAAACAGCAATCCCAAGCAACTTAAAG 1140
Qy 1141 CTGACATCAGAGAGAGTCAAAAGTTCAAAGAGCAGTGAAGAAATAGCCAGCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTCAAAAGTTCAAAGAGCAGTGAAGAAATAGCCAGCAGAGAA 1200
Qy 1201 ATGCTCAAGAACAGAAATTAATTAAGATGCTGATAGAGAGTGAAGAAATGAAG 1260
Db 1201 ATGCTCAAGAACAGAAATTAATTAAGATGCTGATAGAGAGTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAGATTAATTAATGCTGATTAAGAAACCTGAAATAGTCTGCTGCTGCTG 1320
Db 1261 AAGCATGAAGATTAATTAATGCTGATTAAGAAACCTGAAATAGTCTGCTGCTGCTG 1320
Qy 1321 AATGCTGATTAATGATTAATTCCTCAAGAGAGCAGAAACCTGAAATAGCAATTT 1380
Db 1321 AATGCTGATTAATGATTAATTCCTCAAGAGAGCAGAAACCTGAAATAGCAATTT 1380
Qy 1381 CCTGACAAAGAAAGTGAAGATATCACAGAAATTTGCAATTAAGTTCTGACTACAAAGA 1440
Db 1381 CCTGACAAAGAAAGTGAAGATATCACAGAAATTTGCAATTAAGTTCTGACTACAAAGA 1440
Qy 1441 AAACGATGCCAAATACTCTTCTAAAAACAGCAACCCAGAAACAGACTTAAAGCTGACA 1500
Db 1441 AAACGATGCCAAATACTCTTCTAAAAACAGCAACCCAGAAACAGACTTAAAGCTGACA 1500
Qy 1501 TCAGAGAGAGTCAAAAGCTTGAAGGCTGAGGAGTGAAGATGGCCAGCAGAGAAAGATCT 1560
Db 1501 TCAGAGAGAGTCAAAAGCTTGAAGGCTGAGGAGTGAAGATGGCCAGCAGAGAAAGATCT 1560
Qy 1561 CAAGAAGCAGAAATTAATTAAGATGCTGATAGAGCTAGAAATTTTATGCTATCGAA 1620
Db 1561 CAAGAAGCAGAAATTAATTAAGATGCTGATAGAGCTAGAAATTTTATGCTATCGAA 1620
Qy 1621 GAAATGAAGAAAGCAGGAGTACTCATGTCGATCCAGAAACCTGACTAATGCTGCC 1680
Db 1621 GAAATGAAGAAAGCAGGAGTACTCATGTCGATCCAGAAACCTGACTAATGCTGCC 1680
Qy 1681 ACTGCTGCAATGCTGATGATGATTAATTCCTCAAGGAGAGAGCAACACTGAAAGC 1740
Db 1681 ACTGCTGCAATGCTGATGATGATTAATTCCTCAAGGAGAGAGCAACACTGAAAGC 1740
Qy 1741 CAGCAATTTCTGACACTGAGAAAGTATCAACAGTGAAGCAAAATATATCTCAG 1800
Db 1741 CAGCAATTTCTGACACTGAGAAAGTATCAACAGTGAAGCAAAATATATCTCAG 1800

```

```

Db 1741 CAGCAATTTCTGACACTGAGAAATGAGATATCAACAGTGAAGCAAAATGATCTCAG 1800
Qy 1801 AAGCAATTTTGTGAAGACAGAACTGGAAATTAACAGATGATGATCTGATTCATGA 1860
Db 1801 AAGCAATTTTGTGAAGACAGAACTGGAAATTAACAGATGATGATCTGATTCATGA 1860
Qy 1861 GAAAGCAGATGAAGTGTGAAAAAATGAATTCAGACTTCTTCTTGTAGTGAAGAA 1920
Db 1861 GAAAGCAGATGAAGTGTGAAAAAATGAATTCAGACTTCTTCTTGTAGTGAAGAA 1920
Qy 1921 GAAAAAGACATTTCTGATGAAAAATAGTACGTTGCGGAGAAATTCCTGCTAAGACTG 1980
Db 1921 GAAAAAGACATTTCTGATGAAAAATAGTACGTTGCGGAGAAATTCCTGCTAAGACTG 1980
Qy 1981 GAGCTAGACACATGAATGAATCAGAGCCAGCTTAAAAAATGAAAAAATGAAAAA 2040
Db 1981 GAGCTAGACACATGAATGAATCAGAGCCAGCTTAAAAAATGAAAAAATGAAAAA 2040

```

```

RESULT 16
US-09-657-279-375
; Sequence 375, Application US/09657279
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitchem, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuxin
; APPLICANT: Henderson, Robert A.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C19
; CURRENT APPLICATION NUMBER: US/09/657,279
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 877
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-657-279-375

```

```

Query Match 100.0%; Score 2040; DB 25; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2,7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 ATGCTGTTGAGTGTGATTCATGCGGCTGCTCTTCTGTGAAGAGCCATTTGCTTC 60
Db 1 ATGCTGTTGAGTGTGATTCATGCGGCTGCTCTTCTGTGAAGAGCCATTTGCTTC 60
Qy 61 AGGAGCAATGAGGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 61 AGGAGCAATGAGGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Qy 121 AGCAAGTGGGCACTTCTGAGACCAAGCAAGTGTATGAAGCACTGAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACCAAGCAAGTGTATGAAGCACTGAGAGCAAG 180
Qy 181 ATGGCAAGTGTGCGGCACTGCTTCCCTGCTGAGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGCAAGTGTGCGGCACTGCTTCCCTGCTGAGGGAGTGGCAAGCAAGCTG 240

```

QY 241 GCGCTTCTGGAGACACGACGACTGCTATGAGACACTCAGGAACAAGATGGGCAAG 300
 |||||||
 Db 241 GGGGCTTCTGGAGACACGACGACTGCTATGAGACACTCAGGAACAAGATGGGCAAG 300
 QY 301 TGGTGGCCACTGCTTCCCTGCTGAGGGGGAGGGGCAAGAGCGAGGGCGCTGG 360
 |||||||
 Db 301 TGGTGGCTGCGACGCTTCCCTGCTGAGGGGGAGGGGCAAGAGCGAGGGCGCTGG 360
 QY 361 GGAGACTAGAGTACAGTGGCTTCAATGAGGCCAGGTACACGCTCCGTGGAGAGATCTG 420
 |||||||
 Db 361 GGAGACTAGAGTACAGTGGCTTCAATGAGGCCAGGTACACGCTCCGTGGAGAGATCTG 420
 QY 421 GACAGCTCCACAGAGCTGCTGGTGGGTAAGTCCCGCAAGAGATCTCATGTCATG 480
 |||||||
 Db 421 GACAGCTCCACAGAGCTGCTGGTGGGTAAGTCCCGCAAGAGATCTCATGTCATG 480
 QY 481 CTCAGGAGACCTAGCTGTAAGCAAGAGACAAAGAGGAGCTGCTACATCTGAGCC 540
 |||||||
 Db 481 CTCAGGAGACCTAGCTGTAAGCAAGAGACAAAGAGGAGCTGCTACATCTGAGCC 540
 QY 541 TCTGCCAATGGGAATTCAGAACTAGTAAACCTCTGCTGACAGAGAGTCAACTTAAT 600
 |||||||
 Db 541 TCTGCCAATGGGAATTCAGAACTAGTAAACCTCTGCTGACAGAGAGTCAACTTAAT 600
 QY 601 GTCTTTCACACAAACAAAGAGAGAGCTCTGATATAAGGCGGTACATGCCAGAAATGAA 660
 |||||||
 Db 601 GTCTTTCACACAAACAAAGAGAGAGCTCTGATATAAGGCGGTACATGCCAGAAATGAA 660
 QY 661 TGTGCTTATGTGTGCTGGAACTGGACCTGATCAAAATTTCCAGATGATGTAAGAAAT 720
 |||||||
 Db 661 TGTGCTTATGTGTGCTGGAACTGGACCTGATCAAAATTTCCAGATGATGTAAGAAAT 720
 QY 721 ACCACTCTGCACACTACCTATCTATTAATGAAGATTAATTAAGGCCAAAGCAGCTCTTA 780
 |||||||
 Db 721 ACCACTCTGCACACTACCTATCTATTAATGAAGATTAATTAAGGCCAAAGCAGCTCTTA 780
 QY 781 TATGTCGTGATATTCGAATCAACAAACAAAGCAGTGGCTCAGACACTGTTACTTGGTGA 840
 |||||||
 Db 781 TATGTCGTGATATTCGAATCAACAAACAAAGCAGTGGCTCAGACACTGTTACTTGGTGA 840
 QY 841 CATGACCAACAAACAGCAAGCTGTAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
 |||||||
 Db 841 CATGACCAACAAACAGCAAGCTGTAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
 QY 901 CTGGATAGATATGGAAGAGAGCTGCTCATATCTGCTATGTTGTGGATCAGCAAGTATA 960
 |||||||
 Db 901 CTGGATAGATATGGAAGAGAGCTGCTCATATCTGCTATGTTGTGGATCAGCAAGTATA 960
 QY 961 GTCAGGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAGAGATCTATCTGACAGAGC 1020
 |||||||
 Db 961 GTCAGGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAGAGATCTATCTGACAGAGC 1020
 QY 1021 GCCAGAGATATGCTTCTTCTAGTCAATCATGATTAATTTGCCAGTACTTCTGACTAC 1080
 |||||||
 Db 1021 GCCAGAGATATGCTTCTTCTAGTCAATCATGATTAATTTGCCAGTACTTCTGACTAC 1080
 QY 1081 AAGAAAAACAGATGCTAAAAATCTCTTCTGAAACAGCAATCCAGAACAGACTTAAAG 1140
 |||||||
 Db 1081 AAGAAAAACAGATGCTAAAAATCTCTTCTGAAACAGCAATCCAGAACAGACTTAAAG 1140
 QY 1141 CTGACATCAGAGAGAGTACACAAAGGTTCAAGGCAAGGAAATGAGCCAGCCAGAGAA 1200
 |||||||
 Db 1141 CTGACATCAGAGAGAGTACACAAAGGTTCAAGGCAAGGAAATGAGCCAGCCAGAGAA 1200
 QY 1201 ATGTCTCAAGAACAGAAATTAATAGATGATGATAGAGAGTTAAGAGAAATGAAG 1260
 |||||||
 Db 1201 ATGTCTCAAGAACAGAAATTAATAGATGATGATAGAGAGTTAAGAGAAATGAAG 1260
 QY 1261 AAGCATGAAAGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
 |||||||
 Db 1261 AAGCATGAAAGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
 QY 1321 AATGTGATATATGATATATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380

Db 1321 AATGTGATATATGATATATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
 |||||||
 QY 1381 CTTGACACAGAAAGTGAAGATATACAGAAATTTGGCAATTTAGTTCTGACTCAAGAA 1440
 |||||||
 Db 1381 CTTGACACAGAAAGTGAAGATATACAGAAATTTGGCAATTTAGTTCTGACTCAAGAA 1440
 QY 1441 AACAGATGCCAAATATCTTCTGAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
 |||||||
 Db 1441 AACAGATGCCAAATATCTTCTGAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
 QY 1501 TCAAGAGAGAGTACACAAAGGCTTGAAGGCAATGAAATGGCCAGACAGAGAAATCT 1560
 |||||||
 Db 1501 TCAAGAGAGAGTACACAAAGGCTTGAAGGCAATGAAATGGCCAGACAGAGAAATCT 1560
 QY 1561 CAAGAACCCAGAAATTAATAGATGATGATGATGATGATGATGATGATGATGATGATG 1620
 |||||||
 Db 1561 CAAGAACCCAGAAATTAATAGATGATGATGATGATGATGATGATGATGATGATGATG 1620
 QY 1621 GAATGAGAGAGACAGAGAACTGATGATGATGATGATGATGATGATGATGATGATGATG 1680
 |||||||
 Db 1621 GAATGAGAGAGACAGAGAACTGATGATGATGATGATGATGATGATGATGATGATGATG 1680
 QY 1681 ACTGCTGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
 |||||||
 Db 1681 ACTGCTGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1740
 QY 1741 CAGCAATTTCTGACACTGAGATGAGATGATGATGATGATGATGATGATGATGATGATG 1800
 |||||||
 Db 1741 CAGCAATTTCTGACACTGAGATGAGATGATGATGATGATGATGATGATGATGATGATG 1800
 QY 1801 AAGCAATTTTGTGAAG 1860
 |||||||
 Db 1801 AAGCAATTTTGTGAAG 1860
 QY 1861 GAAAGACAGATAGAGTGGTGAAGAAATGATGATGATGATGATGATGATGATGATGATG 1920
 |||||||
 Db 1861 GAAAGACAGATAGAGTGGTGAAGAAATGATGATGATGATGATGATGATGATGATGATG 1920
 QY 1921 GAAAAAGACATCTTGCATGAAATATGATGATGATGATGATGATGATGATGATGATGATG 1980
 |||||||
 Db 1921 GAAAAAGACATCTTGCATGAAATATGATGATGATGATGATGATGATGATGATGATGATG 1980
 QY 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTAAAAAAGAGAGAGAGAGAGAGAGAG 2040
 |||||||
 Db 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTAAAAAAGAGAGAGAGAGAGAGAGAG 2040

RESULT 17
 US-09-679-272-375
 ; Sequence 375, Application US/09679272
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Skelky, Yasir
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Cheever, Martin
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE REFERENCE: 210121.534
 ; CURRENT APPLICATION NUMBER: US/09/679,272
 ; NUMBER OF SEQ ID NOS: 476
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 375
 ; LENGTH: 2040
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-09-679-272-375

Query Match 100.0%; Score 2040; DB 26; Length 2040;
 Best Local Similarity 100.0%; Pred. No. 2,76-264;
 Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATATGGTTAGAGTTATTTCCATACGCCGGCTGGCTCTCTGTGTGAAGAAACCACTTTGGTCTC	60
Db	1	ATATGGTTAGAGTTATTTCCATACGCCGGCTGGCTCTCTGTGTGAAGAAACCACTTTGGTCTC	60
QY	61	AGGAGCAAGATGGGGCAAGTGGTGGCTGGCTTCCCTGGCTGGAGGAGGGGCAAG	120
Db	61	AGGAGCAAGATGGGGCAAGTGGTGGCTGGCTTCCCTGGCTGGAGGAGGGGCAAG	120
QY	121	AGCAACGTGGGGCACTTCTGTGAGACCAAGCAAGCACTGTGTATGAAAGACACTGAGGACAG	180
Db	121	AGCAACGTGGGGCACTTCTGTGAGACCAAGCAAGCACTGTGTATGAAAGACACTGAGGACAG	180
QY	181	ATTGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAAGTGG	240
Db	181	ATTGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAAGTGG	240
QY	241	GGGCGTTCTGTGAGACCAAGCAAGCACTGTGTATGAAAGACACTGAGAACAGATGGGCAAG	300
Db	241	GGGCGTTCTGTGAGACCAAGCAAGCACTGTGTATGAAAGACACTGAGAACAGATGGGCAAG	300
QY	301	TGGTGTGCCACTGCTTCCCTGCTCAGGGGGAGGGGCAAGCAAGGTTGGGCGCTTGG	360
Db	301	TGGTGTGCCACTGCTTCCCTGCTCAGGGGGAGGGGCAAGCAAGGTTGGGCGCTTGG	360
QY	361	GGAGACTACGATGACAGTGGCTTATGATGAGCCAGGTACACAGTCCGTGGAGAAAGATGTG	420
Db	361	GGAGACTACGATGACAGTGGCTTATGATGAGCCAGGTACCAAGTCCGTGGAGAAAGATGTG	420
QY	421	GACAAAGCTCACAAGAGGTGGCTGGTGGGGTAAAGTCCCAAGAAAGATCTATGTCTATG	480
Db	421	GACAAAGCTCACAAGAGGTGGCTGGTGGGGTAAAGTCCCAAGAAAGATCTATGTCTATG	480
QY	481	CTCAGGACACTACAGTGAACAAGAGGACAAGCAAAAAGAGACTGCTACATATGGCC	540
Db	481	CTCAGGACACTACAGTGAACAAGAGGACAAGCAAAAAGAGACTGCTACATATGGCC	540
QY	541	TCGTCCATGGGAATTCAGAAAGTAGTAAATCTCGCTGGAGACAGATGTCAACTTAAT	600
Db	541	TCGTCCATGGGAATTCAGAAAGTAGTAAATCTCGCTGGAGACAGATGTCAACTTAAT	600
QY	601	GTCCTGTACAACAAAAAGAGAGAGTGTGATTAAGGCCGTCAATGGCCAGGAAAGATGAA	660
Db	601	GTCCTGTACAACAAAAAGAGAGAGTGTGATTAAGGCCGTCAATGGCCAGGAAAGATGAA	660
QY	661	TGTGCGTTAATGTTGTCGGAACATATGGCACTGTATCCAAATATCCAGATGAGATGGAAT	720
Db	661	TGTGCGTTAATGTTGTCGGAACATATGGCACTGTATCCAAATATTCAGATGATGATGGAAT	720
QY	721	ACCACTGTGACACTACGCTATCTAATTAATGAAGATTAATATGAGCAAGCACTGCTCTTA	780
Db	721	ACCACTGTGACACTACGCTATCTAATTAATGAAGATTAATATGAGCAAGCACTGCTCTTA	780
QY	781	TATGGTGTCTGATATCCAAATTAATAAACCAAGCATGGCTTACACCACTGTACTTGGTGTGA	840
Db	781	TATGGTGTCTGATATCCAAATTAATAAACCAAGCATGGCTTACACCACTGTACTTGGTGTGA	840
QY	841	CATGAGCAAAAAACAGCAAGCTGTGAATTTTATCAAGAAAAAGCGAATTTAATTAATCA	900
Db	841	CATGAGCAAAAAACAGCAAGCTGTGAATTTTATCAAGAAAAAGCGAATTTAATTAATCA	900
QY	901	CTGTAGATATATGGAAGAGACTGCTCATACTGTGCTATGTTGTGTGATCAGCAAGTATA	960
Db	901	CTGTAGATATATGGAAGAGACTGCTCATACTGTGCTATGTTGTGTGATCAGCAAGTATA	960
QY	961	GTCAGCCTTCTACTTGAAGCAAAATATTGATGTAATCTTCAAGATCTATCTGGAGACAGC	1020
Db	961	GTCAGCCTTCTACTTGAAGCAAAATATTGATGTAATCTTCAAGATCTATCTGGAGACAGC	1020
QY	1021	GCCAGAGATATGCTGTTTCTAGTCAATCAATGTAATTTGGCAGTTACTTTGACATAC	1080
Db	1021	GCCAGAGATATGCTGTTTCTAGTCAATCAATGTAATTTGGCAGTTACTTTGACATAC	1080
QY	1081	AAAGAAAAACAGATGCTTAAATCTCTTGTGAAGACAGCAATCCAGAACAGACTTAAAG	1140

Db	1081	AAAGAAAAAGATGCTAAAAAATCTCTTCGAAAACAGCAATCCGAACAGACTTAAAG	1140
Qy	1141	CTGACATCAGAGGAAAGATGCACAAAGGTTCCAAAGGCAGTAAATAAGCCAGCCAGAGAA	1200
Db	1141	CTGACATCAGAGGAAAGATGCACAAAGGTTCCAAAGGCAGTAAATAAGCCAGCCAGAGAA	1200
Qy	1201	ATGTCTCAGAACCCAGAAATAAATAAGGATGGTGATAGAGAGTTGAAGAGAAATGAAG	1260
Db	1201	ATGTCTCAGAACCCAGAAATAAATAAGGATGGTGATAGAGAGTTGAAGAGAAATAAGAG	1260
Qy	1261	AAGCATGAAGTAAATATGTGGGATTACTATGAAAACCTGACTAAATGGTGTCACCTGCGC	1320
Db	1261	AAGCATGAAGTAAATATGTGGGATTACTATGAAAACCTGACTAAATGGTGTCACCTGCGC	1320
Qy	1321	AATGGTGAATAATGATTAATTCCTCAAAAGGAAAGCAGAAACCTGAAAATCAGCAATTT	1380
Db	1321	AATGGTGAATAATGATTAATTCCTCAAAAGGAAAGCAGAAACCTGAAAATCAGCAATTT	1380
Qy	1381	CCTGACAAACGAAATGAAAGATATCACAGAAATTTGGGAAATTAAGTTTCTGTACTACAAATA	1440
Db	1381	CCTGACAAACGAAATGAAAGATATCACAGAAATTTGGGAAATTAAGTTTCTGTACTACAAATA	1440
Qy	1441	AAACGATGCCCAAAATACTCTTCGAAAACACGAAACCCAGCAACAAAGACTTAAGCTGACA	1500
Db	1441	AAACGATGCCCAAAATACTCTTCGAAAACACGAAACCCAGCAACAAAGACTTAAGCTGACA	1500
Qy	1501	TCAGAGAAAGATGCACAAAGGCTTGAAGGCACTGAAAATATGGCCAGCCAGAGAAAAGATCT	1560
Db	1501	TCAGAGAAAGATGCACAAAGGCTTGAAGGCACTGAAAATATGGCCAGCCAGAGAAAAGATCT	1560
Qy	1561	CAAGACACCAAGAAATAAATAAGATGGTGATAGAGACTTGAATAATTTATGGCTATCGAA	1620
Db	1561	CAAGACACCAAGAAATAAATAAGATGGTGATAGAGACTTGAATAATTTATGGCTATCGAA	1620
Qy	1621	GAATGAAGAGACACGGAAGTACTCATGTGCGAATGCCAGAAAACCTGCAATATGGTGCC	1680
Db	1621	GAATGAAGAGACACGGAAGTACTCATGTGCGAATGCCAGAAAACCTGCAATATGGTGCC	1680
Qy	1681	ACTGCTGGCAATGGTGAATGATGATTAATTCCTCCAAAGAGACAGAACACCTGAAGC	1740
Db	1681	ACTGCTGGCAATGGTGAATGATGATTAATTCCTCCAAAGAGAGACAGAACACCTGAAGC	1740
Qy	1741	CAGCAATTCCTGACACTGTGAAGATGAAGATATCACAGTGAAGAACAAAATGATACTGAG	1800
Db	1741	CAGCAATTCCTGACACTGTGAAGATGAAGATATCACAGTGAAGAACAAAATGATACTGAG	1800
Qy	1801	AAGCAATTTTGTGAAGAACAGAACACTGGAATTTTACAGATGAGATTTCTGATTCATGAA	1860
Db	1801	AAGCAATTTTGTGAAGAACAGAACACTGGAATTTTACAGATGAGATTTCTGATTCATGAA	1860
Qy	1861	GAAGAGCAGATAGAAAGTGTTGAAAAAATGAAATTCAGACTTTCTCTTAGTTGTAAAGAA	1920
Db	1861	GAAGAGCAGATAGAAAGTGTTGAAAAAATGAAATTCAGACTTTCTCTTAGTTGTAAAGAA	1920
Qy	1921	GAAGAAAGACATCTTGATGAAATAATAGTACCTGCGGAGAAATTTGCCATGCTAAGACTG	1980
Db	1921	GAAGAAAGACATCTTGATGAAATAATAGTACCTGCGGAGAAATTTGCCATGCTAAGACTG	1980
Qy	1981	GAGCTAGACACAAATGAACATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAAATGAAAA	2040
Db	1981	GAGCTAGACACAAATGAACATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAAATGAAAA	2040

```

RESULT:18
US-09-679-426-375
; Sequence 375, Application US/09679426
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocke, Susan L.
; APPLICANT: Jiang, Yuqi

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|||||
Db 1741 CAGCATTTCCTGACACTGAGATGAAGTATCACAGTGCAGCAACAAATGATCTCAG 1800
OY 1801 AAGCATTTCGTGAAGACAGAACTGGAATTTACAGATGAGATTCGATCTCATGAA 1860
Db 1801 AAGCATTTCGTGAAGACAGAACTGGAATTTACAGATGAGATTCGATCTCATGAA 1860
OY 1861 GAAAAGCAGATGAGATGCTTGAAGAAATTAATTCGATCTTCCTTGTAGTGAAGAA 1920
Db 1861 GAAAAGCAGATGAGATGCTTGAAGAAATTAATTCGATCTTCCTTGTAGTGAAGAA 1920
OY 1921 GAAAAGCAGATCTTCGATGAAAAATAGTACGTTGCGGGAAGAAATTCGATCTGTAAGACTG 1980
Db 1921 GAAAAGCAGATCTTCGATGAAAAATAGTACGTTGCGGGAAGAAATTCGATCTGTAAGACTG 1980
OY 1981 GAGCTGAGACATGAAATCATGAGCCAGCTGTAAGAAAAATGAAAAATGAAAAATGAAAA 2040
Db 1981 GAGCTGAGACATGAAATCATGAGCCAGCTGTAAGAAAAATGAAAAATGAAAAATGAAAA 2040

RESULT 19
US-09-685-166-375
; Sequence 375, Application US/09685166
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Micham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jjiang, Yuqul
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-685-166-375

Query Match 100.0%; Score 2040; DB 27; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2,7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 241 GGCCTTCGAGACACGACGACTGCTATGAAGCACTCAGGAACAAGATGGCAAG 300
Db 241 GGCCTTCGAGACACGACGACTGCTATGAAGCACTCAGGAACAAGATGGCAAG 300
OY 301 TGGTGTGACACTGCTCCCTCCTCAGGAGGAGGCGCAAGCAAGTGGGCGTTGG 360
Db 301 TGGTGTGACACTGCTCCCTCCTCAGGAGGAGGCGCAAGCAAGTGGGCGTTGG 360
OY 361 GGAGACTAGATGACAGTGGCTTCATGAGAGCCAGTACCAGTCCGTGGAGAAATCTG 420
Db 361 GGAGACTAGATGACAGTGGCTTCATGAGAGCCAGTACCAGTCCGTGGAGAAATCTG 420
OY 421 GACAACTCCACAGAGCTGCTGGTGGGGTAAAGTCCCGAAGAAAGATCATGCTGATG 480
Db 421 GACAACTCCACAGAGCTGCTGGTGGGGTAAAGTCCCGAAGAAAGATCATGCTGATG 480
OY 481 CTCAGGAGACACTGACGTGAACAAGAGACAAAGCAAGAGAGACTGCTACATCTGGCC 540
Db 481 CTCAGGAGACACTGACGTGAACAAGAGACAAAGCAAGAGAGACTGCTACATCTGGCC 540
OY 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGACAGACAGATGCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGACAGACAGATGCAACTTAAT 600
OY 601 GTCCCTTGACAAACAAAAGAGAGACGCTGATAAAGGCGCTACAAATGCCAGAAATGAA 660
Db 601 GTCCCTTGACAAACAAAAGAGAGACGCTGATAAAGGCGCTACAAATGCCAGAAATGAA 660
OY 661 TGTGCGTTAATGTTGCTGGAACATGACAGTATCAAAATTTCCAGATGATGGAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGACAGTATCAAAATTTCCAGATGATGGAAT 720
OY 721 ACCACTGTGACATGACGATCTATTAATGAAGATTAATTAATGAGCAAGCACTGCTTA 780
Db 721 ACCACTGTGACATGACGATCTATTAATGAAGATTAATTAATGAGCAAGCACTGCTTA 780
OY 781 TATGTCGTGATATGCAATCAAAAACAGCAGGCGCTCACACAGCTGACTGATGTA 840
Db 781 TATGTCGTGATATGCAATCAAAAACAGCAGGCGCTCACACAGCTGACTGATGTA 840
OY 841 CATGACCAAAAACAGCAGAGTGTGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGACCAAAAACAGCAGAGTGTGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
OY 901 CTGAGATGATGAGAGAGACTGCTCATATCTGCTGATGTTGTGATCAGCAAGTATA 960
Db 901 CTGAGATGATGAGAGAGACTGCTCATATCTGCTGATGTTGTGATCAGCAAGTATA 960
OY 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAAATATCTGAGCAGAG 1020
Db 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAAATATCTGAGCAGAG 1020
OY 1021 GCCAGAGATGCTGTTTCTAGTCATCATGATTAATTTGCCAGTACTTTTGACTAC 1080
Db 1021 GCCAGAGATGCTGTTTCTAGTCATCATGATTAATTTGCCAGTACTTTTGACTAC 1080
OY 1081 AAGAAAAACAGATGCTAAAAATCTCTGAAACAGCAATCCAGAAACAGACTTAAG 1140
Db 1081 AAGAAAAACAGATGCTAAAAATCTCTGAAACAGCAATCCAGAAACAGACTTAAG 1140
OY 1141 CTGACATCAGAGAGAAAGTCAAAAGTTCAAAGGCAAGTAAATAGCCGCAAGAAA 1200
Db 1141 CTGACATCAGAGAGAAAGTCAAAAGTTCAAAGGCAAGTAAATAGCCGCAAGAAA 1200
OY 1201 ATGCTCAAGAACCAAAATTAATTAAGATGAGTGAAGAGGTTGAAGAAAGAAAG 1260
Db 1201 ATGCTCAAGAACCAAAATTAATTAAGATGAGTGAAGAGGTTGAAGAAAGAAAG 1260
OY 1261 AAGCATGAAAGTAAATATGAGGATTAAGAAACCTGACTAATGATGCTGCTGGC 1320
Db 1261 AAGCATGAAAGTAAATATGAGGATTAAGAAACCTGACTAATGATGCTGCTGGC 1320
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Db 541 TCTGCCAATGGGAATTCAGAAAGTAATAAATCTCTGCGACAGACATGTCAACTTAAT 600
QY 601 GTCTTGCACAAACAAAAGAGACAGCTCTGATAAAGCCCGTACAAATCCAGAGATGAA 660
Db 601 GTCTTGCACAAACAAAAGAGACAGCTCTGATAAAGCCCGTACAAATCCAGAGATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGSCATGTCACAAATATTTCCAGATGAGTAAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGSCATGTCACAAATATTTCCAGATGAGTAAAT 720
QY 721 ACCGCTGCACTACGCTATCTATATGAAGATAAATTAATGGCAAAAGCATGCTCTTA 780
Db 721 ACCGCTGCACTACGCTATCTATATGAAGATAAATTAATGGCAAAAGCATGCTCTTA 780
QY 781 TATGTCCTGATATCGAATCAAAAACAGCATGGCTCACACACTGTTACTTGTTA 840
Db 781 TATGTCCTGATATCGAATCAAAAACAGCATGGCTCACACACTGTTACTTGTTA 840
QY 841 CATGAGCAAAAACAGCAAGTCGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGTCGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATGATATGTAAGAGACTGCTCTCATCTTCTGATGTTGATGATCAGCAAGTATA 960
Db 901 CTGATGATATGTAAGAGACTGCTCTCATCTTCTGATGTTGATGATCAGCAAGTATA 960
QY 961 GTCAGCCTTCTACTTGAAGCAAAATATGATGATCTCTCAAGATCTATCGACAGACG 1020
Db 961 GTCAGCCTTCTACTTGAAGCAAAATATGATGATCTCTCAAGATCTATCGACAGACG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTCGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTCGACTAC 1080
QY 1081 AAAAGAAAAAGATGCTAAAAATCTCTTGAAAAACAGCAATCCAGAAACAGATTTAAAG 1140
Db 1081 AAAAGAAAAAGATGCTAAAAATCTCTTGAAAAACAGCAATCCAGAAACAGATTTAAAG 1140
QY 1141 CTGACATCAGAGAAAGATCACAAGAGTTCAAGAGCAGTGAATAATACCAGCCAGAGAA 1200
Db 1141 CTGACATCAGAGAAAGATCACAAGAGTTCAAGAGCAGTGAATAATACCAGCCAGAGAA 1200
QY 1201 ATGCTCTAAGAACAGAAATTAATTAAGATGTTGATAGAGGTTGAAGAAAGATGAG 1260
Db 1201 ATGCTCTAAGAACAGAAATTAATTAAGATGTTGATAGAGGTTGAAGAAAGATGAG 1260
QY 1261 AAGCATGAAGTATATATGTTGGGATTTACTAGAAAACCTGATATGTTGCTACGCTGCC 1320
Db 1261 AAGCATGAAGTATATATGTTGGGATTTACTAGAAAACCTGATATGTTGCTACGCTGCC 1320
QY 1321 AATGCTGATATGATTAATTTCTCTCAAGAGAAAGACAGAACACCTGAAATCAGCAATTT 1380
Db 1321 AATGCTGATATGATTAATTTCTCTCAAGAGAAAGACAGAACACCTGAAATCAGCAATTT 1380
QY 1381 CCTGACACAGAAAGTGAAGATATCACAGAAATTTGCAATTAAGTTTCTGACTACAAAGAA 1440
Db 1381 CCTGACACAGAAAGTGAAGATATCACAGAAATTTGCAATTAAGTTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCAAAATCTCTTGAAGAAACAGCAACCCAGAACAGCAAGCTTAAACCTACA 1500
Db 1441 AAACAGATGCAAAATCTCTTGAAGAAACAGCAACCCAGAACAGCAAGCTTAAACCTACA 1500
QY 1501 TCAGAGAGAAAGATCACAAGAGCTTGAGAGCAGTGAATGGCCAGCCAGAGAAAGATCT 1560
Db 1501 TCAGAGAGAAAGATCACAAGAGCTTGAGAGCAGTGAATGGCCAGCCAGAGAAAGATCT 1560
QY 1561 CAAGAACCAAGAAATTAATTAAGATGTTGATAGAGCTAGAAATTTTATGGCTATGAAA 1620
Db 1561 CAAGAACCAAGAAATTAATTAAGATGTTGATAGAGCTAGAAATTTTATGGCTATGAAA 1620
QY 1621 GAATGAAGAAAGCAGGAAGTACTATGCTGGATTTCCAGAAAACCTGACTAATGTTGCC 1680
Db 1621 GAATGAAGAAAGCAGGAAGTACTATGCTGGATTTCCAGAAAACCTGACTAATGTTGCC 1680

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QY 1681 ACTGCTGGCAATGGTGATGATGATTAATTCCTCAAGAGAGACAGACACCTGAAAGC 1740
Db 1681 ACTGCTGGCAATGGTGATGATGATTAATTCCTCAAGAGAGAGACAGACACCTGAAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGAAATGAAGAGATATACAGTACAGAAACAAATGATACCTAG 1800
Db 1741 CAGCAATTTCTGACACTGAGAAATGAAGAGATATACAGTACAGAAACAAATGATACCTAG 1800
QY 1801 AAGCAATTTTGTGAAGAACACAGACATGGAATTTTACACGATGATGATTCATGATA 1860
Db 1801 AAGCAATTTTGTGAAGAACACAGACATGGAATTTTACACGATGATGATTCATGATA 1860
QY 1861 GAAAGCAGATAGAAAGTGGTTGAAAAATGAATTTCTGAGCTTCTCTAGTTGTAAGAAA 1920
Db 1861 GAAAGCAGATAGAAAGTGGTTGAAAAATGAATTTCTGAGCTTCTCTAGTTGTAAGAAA 1920
QY 1921 GAAAAAGCATCTTGATGATAAATGATACGTTGGGGAGAAATTTGCCATGCTTAAGCTG 1980
Db 1921 GAAAAAGCATCTTGATGATAAATGATACGTTGGGGAGAAATTTGCCATGCTTAAGCTG 1980
QY 1981 GAGCTAGACACATGAATGAACATCAGAGCAGCTAAAAAAGAAAAAAGAAAAA 2040
Db 1981 GAGCTAGACACATGAATGAACATCAGAGCAGCTAAAAAAGAAAAAAGAAAAA 2040

RESULT 22
US-09-709-729-375
; Sequence 375, Application us/09709729
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Wang, Aljun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C22
; CURRENT APPLICATION NUMBER: US/09/709,729
; CURRENT FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 351
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-709-729-375

Query Match 100.0%; Score 2040; DB 28; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2,7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGTTGAGTGGATTCCATGCGCGCTGCTCTTCTGTGAAGAACCATTTGGTCTC 60
Db 1 ATGTGTTGAGTGGATTCCATGCGCGCTGCTCTTCTGTGAAGAACCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGCTTGTCCCTGCTGCTCAGAGAGGGAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGTGCTGCGCTTGTCCCTGCTGCTCAGAGAGGGAAG 120
QY 121 AGCAACGTGGCACTTCTGAGACACAGACACTCTCTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAACGTGGCACTTCTGAGACACAGACACTCTCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGCCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAACGTG 240

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Db 181 ATGGGCAAGTGTGTCCTCCCTGCTGAGGGGAGTGGCAAGCAACGTG 240
QY 241 GGGCTTGTGGAGACGAGAGCTGTGTGAAGACACTCAGAGCAATGGGCAAG 300
Db 241 GGGCTTGTGGAGACGAGAGCTGTGTGAAGACACTCAGAGCAATGGGCAAG 300
QY 301 TGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 301 TGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 361 GGAGACTACGATGACAGTGCCTTCATGAGGCCAGGTACCACTGCTGAGAAATGTG 420
Db 361 GGAGACTACGATGACAGTGCCTTCATGAGGCCAGGTACCACTGCTGAGAAATGTG 420
QY 421 GACAAAGTCCCAAGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421 GACAAAGTCCCAAGAGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 CTCAGGACACTGACGTGACAGCAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCA 540
Db 481 CTCAGGACACTGACGTGACAGCAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCA 540
QY 541 TCTGCCAATGGGAATTCAGAAATGTAAGAACTCTGCTGCTGCTGCTGCTGCTGCT 600
Db 541 TCTGCCAATGGGAATTCAGAAATGTAAGAACTCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 GTCTTTCACACAAACAAAGAGAGACAGCTCTGTAAAGCCGCTGCAATGCTGCAAGATTA 660
Db 601 GTCTTTCACACAAACAAAGAGAGACAGCTCTGTAAAGCCGCTGCAATGCTGCAAGATTA 660
QY 661 TGTGCTGTAATGTTGCTGTAAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 661 TGTGCTGTAATGTTGCTGTAAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 721 ACCACTGTGCACTACGTATCTATATGAAATGTAAGTAAATGCTGCTGCTGCTGCT 780
Db 721 ACCACTGTGCACTACGTATCTATATGAAATGTAAGTAAATGCTGCTGCTGCTGCT 780
QY 781 TATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
Db 781 TATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
QY 841 CATGAGCAAAACAGCAAGTGTGAATTTTAAATCAAGAAAGCAATTTAAATCA 900
Db 841 CATGAGCAAAACAGCAAGTGTGAATTTTAAATCAAGAAAGCAATTTAAATCA 900
QY 901 CTGATAGATATGAGAGAGTGTCTCATACCTGCTGATGCTGCTGATGCTGCTGCTG 960
Db 901 CTGATAGATATGAGAGAGTGTCTCATACCTGCTGATGCTGCTGATGCTGCTGCTG 960
QY 961 GTGAGCTTCTACTGAGCAAAATATGATATCTTCTCAAGATCTATCTGAGACAG 1020
Db 961 GTGAGCTTCTACTGAGCAAAATATGATATCTTCTCAAGATCTATCTGAGACAG 1020
QY 1021 GCCAGAGATGCTGCTTCTGATCATCATGTAATTTCCAGTTTCTTCTGACATAC 1080
Db 1021 GCCAGAGATGCTGCTTCTGATCATCATGTAATTTCCAGTTTCTTCTGACATAC 1080
QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAAAGACTTAAAG 1140
Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAAAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGTGTCAAAAGTTCAAAGGCAAGTGAATAGCCAGACAGAA 1200
Db 1141 CTGACATCAGAGAGAGTGTCAAAAGTTCAAAGGCAAGTGAATAGCCAGACAGAA 1200
QY 1201 ATGTCTCAGAGACAGAAATTAATAGAGTGTGATAGAGAGTGAAGAAAGAAATAGAG 1260
Db 1201 ATGTCTCAGAGACAGAAATTAATAGAGTGTGATAGAGAGTGAAGAAAGAAATAGAG 1260
QY 1261 AAGCATGAAGTAAATATGTTGATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1320
Db 1261 AAGCATGAAGTAAATATGTTGATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1320

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Db 1261 AAGCATGAAGTAAATATGTTGATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1320
QY 1321 AATGCTGATTAATGATTAATTCCTCAAGAGAGACAGACAGACAGACAGACAGACAGATTT 1380
Db 1321 AATGCTGATTAATGATTAATTCCTCAAGAGAGAGACAGACAGACAGACAGACAGATTT 1380
QY 1381 CCTGACACAGAAAGTGAAGAGTATCAGAAATTTTCCGATTAATGTTCTGACATCAAGAA 1440
Db 1381 CCTGACACAGAAAGTGAAGAGTATCAGAAATTTTCCGATTAATGTTCTGACATCAAGAA 1440
QY 1441 AAACAGATGCCAAATTAATCTTCTGAAAAACAGCAACCAAGAAACAGATTAAGTGA 1500
Db 1441 AAACAGATGCCAAATTAATCTTCTGAAAAACAGCAACCAAGAAACAGATTAAGTGA 1500
QY 1501 TCAGAGAGAGTGCACAAAGCTTGAGGCGCTGAAATTTGCGACCCAGAGAAAGATCT 1560
Db 1501 TCAGAGAGAGTGCACAAAGCTTGAGGCGCTGAAATTTGCGACCCAGAGAAAGATCT 1560
QY 1561 CAAGAACAGAAATTAATTAAGATGATGATAGAGAGTGAAGAAATTTATGCTATCGAA 1620
Db 1561 CAAGAACAGAAATTAATTAAGATGATGATAGAGAGTGAAGAAATTTATGCTATCGAA 1620
QY 1621 GAAATGAAGAGACAGAGATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
Db 1621 GAAATGAAGAGACAGAGATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
QY 1681 ACTGCTGCAATGCTGATGATGATGATTAATTCCTCCAAAGAGAGAGAGAGAGAGAGAG 1740
Db 1681 ACTGCTGCAATGCTGATGATGATGATTAATTCCTCCAAAGAGAGAGAGAGAGAGAGAG 1740
QY 1741 CAGCAATTTCTGACACTGAGATGAGATGATGATGATGATGATGATGATGATGATGATG 1800
Db 1741 CAGCAATTTCTGACACTGAGATGAGATGATGATGATGATGATGATGATGATGATGATG 1800
QY 1801 AAGCAATTTTGTGAAGAACAGAACAGTGAATTTTACAGATGATGATGATGATGATG 1860
Db 1801 AAGCAATTTTGTGAAGAACAGAACAGTGAATTTTACAGATGATGATGATGATGATG 1860
QY 1861 GAAAGCAGATGAGAGTGTGAAAGAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
Db 1861 GAAAGCAGATGAGAGTGTGAAAGAAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
QY 1921 GAAAGACATCTTGCATGAAATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
Db 1921 GAAAGACATCTTGCATGAAATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
QY 1981 GAGCTAGACACAAATGAATCAGAGCAGCTAAAAAGAGAGAGAGAGAGAGAGAGAGAG 2040
Db 1981 GAGCTAGACACAAATGAATCAGAGCAGCTAAAAAGAGAGAGAGAGAGAGAGAGAGAG 2040

```

RESULT 23
 US-09-759-143-375
 Sequence 375, Application US/09759143
 GENERAL INFORMATION:
 APPLICANT: Xu, Jiangshun
 APPLICANT: Dillon, Devin C.
 APPLICANT: Mitcham, Jennifer L.
 APPLICANT: Harlocker, Susan L.
 APPLICANT: Jjiang, Yuyu
 APPLICANT: Henderson, Robert A.
 APPLICANT: Kalos, Michael D.
 APPLICANT: Rafter, Gary R.
 APPLICANT: Rafter, Marc W.
 APPLICANT: Stolck, John A.
 APPLICANT: Day, Craig H.
 APPLICANT: Vedrick, Thomas S.
 APPLICANT: Carter, Derrick
 APPLICANT: Li, Samuel
 APPLICANT: Wang, Aljun
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Hepler, William
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

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; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-375

Query Match      100.0%; Score 2040; DB 29; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2,7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGCTGAGGTGATTCATGCGCGGCTCCCTCTTGTAAGAAAGCATTTGGCTTC 60
DB 1 ATGGTGCTGAGGTGATTCATGCGCGGCTCCCTCTTGTAAGAAAGCATTTGGCTTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTCCGTCCTCCCTGCTGAGGAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGCTCCGTCCTCCCTGCTGAGGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGACACGACGACTGTGTATGAAAGCACTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTGAGACACGACGACTGTGTATGAAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAATGGTGGCGGCACTGCTCCCTGCTGAGGAGGAGTGGCAAGACCAAG 240
DB 181 ATGGGCAATGGTGGCGGCACTGCTCCCTGCTGAGGAGGAGTGGCAAGACCAAG 240
QY 241 GCGGCTTCTGAGAGACCAAGCACTGCTATGAAAGCACTCAGAAAGATGGGCAAG 300
DB 241 GCGGCTTCTGAGAGACCAAGCACTGCTATGAAAGCACTCAGAAAGATGGGCAAG 300
QY 301 TGGTGCTGCACTGCTTCCCTGCTGAGGAGGAGCGGCAAGAGTGGGCTTGG 360
DB 301 TGGTGCTGCACTGCTTCCCTGCTGAGGAGGAGCGGCAAGAGTGGGCTTGG 360
QY 361 GGAGACTAGATGACGATGCTTCATGAGCCAGGTACCAAGTCCGTGGAGAAAGTTC 420
DB 361 GGAGACTAGATGACGATGCTTCATGAGCCAGGTACCAAGTCCGTGGAGAAAGTTC 420
QY 421 GACAAAGCTCCAGAGACCTGCTGTTGAGGAGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
DB 421 GACAAAGCTCCAGAGACCTGCTGTTGAGGAGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
QY 481 CTCAGGACACTGACCTGTAAGAAAGAAAGCAAGCAAGAGACTGCTTACATCTGGCC 540
DB 481 CTCAGGACACTGACCTGTAAGAAAGAAAGCAAGCAAGAGACTGCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAAATCAAGATGTAAGAAATCCTGCTGAGACGAGATGTCAACTTAAT 600
DB 541 TCTGCCAATGGGAAATCAAGATGTAAGAAATCCTGCTGAGACGAGATGTCAACTTAAT 600
QY 601 GTCTTTCAGCAACAAAAAGAGAGAGCTGTGATTAAGCCGTACAATGCCAGAAAGATGAA 660
DB 601 GTCTTTCAGCAACAAAAAGAGAGAGCTGTGATTAAGCCGTACAATGCCAGAAAGATGAA 660
QY 661 TGTGCTTAATGTGCTGGAACATGGCACTGATCCAAATATTCACAGATGATGGAAT 720
DB 661 TGTGCTTAATGTGCTGGAACATGGCACTGATCCAAATATTCACAGATGATGGAAT 720
QY 721 ACCACTCTGACCTAGCTTCTATATATGAAATTAATTAAGGCCAAGAGACTGCTTA 780
DB 721 ACCACTCTGACCTAGCTTCTATATATGAAATTAATTAAGGCCAAGAGACTGCTTA 780
QY 781 TATGCTGATATGCAATCAAAAAAAGCAAGATGGCTCAGACACACTGTACTTGGTGA 840
DB 781 TATGCTGATATGCAATCAAAAAAAGCAAGATGGCTCAGACACACTGTACTTGGTGA 840
QY 841 CATGAGCAAAAAACGCAAGTCTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
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DB 841 CATGAGCAAAAAACGCAAGTCTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATAGATATGAGAGAGAGCTGCTCATACCTGCTGATAGTGTGATCAGCAAGTATA 960
DB 901 CTGATAGATATGAGAGAGAGCTGCTCATACCTGCTGATAGTGTGATCAGCAAGTATA 960
QY 961 GTCAGCCTTCTACTGAGCAAAAAATATGATGATTCCTCAAGATCATCTGAGCAGAGC 1020
DB 961 GTCAGCCTTCTACTGAGCAAAAAATATGATGATTCCTCAAGATCATCTGAGCAGAGC 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCAATCATATGTAATTTGCCAGTTACTTCTGATC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCAATCATATGTAATTTGCCAGTTACTTCTGATC 1080
QY 1081 AAGAAAAACAGATGCTAAAAATCTCTGTAAGAACAGCAATCCAGAACAACTTAAG 1140
DB 1081 AAGAAAAACAGATGCTAAAAATCTCTGTAAGAACAGCAATCCAGAACAACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCCAAAGGTTCCAAAGGCAAGTAAATAGCCAGCCAGAAA 1200
DB 1141 CTGACATCAGAGAGAGAGTCCAAAGGTTCCAAAGGCAAGTAAATAGCCAGCCAGAAA 1200
QY 1201 ATGCTCAAGAACCAAAATTAATTAAGATGCTGATAGAGAGTGAAGAAATGAAG 1260
DB 1201 ATGCTCAAGAACCAAAATTAATTAAGATGCTGATAGAGAGTGAAGAAATGAAG 1260
QY 1261 AAGCTGAAGATATATGATGGGATTAAGTAAGAAACCTGCTAATGCTGCTGAGC 1320
DB 1261 AAGCTGAAGATATATGATGGGATTAAGTAAGAAACCTGCTAATGCTGCTGAGC 1320
QY 1321 AATGATGATTAATGATTAATTCCTCAAGAGAGAGCAAGAACCTGAAATGCAATTT 1380
DB 1321 AATGATGATTAATGATTAATTCCTCAAGAGAGAGCAAGAACCTGAAATGCAATTT 1380
QY 1381 CCTGACAAGAAAGTGAAGATTCACAGAAATTTGGGAATTAATTTCTGACTCAAGAA 1440
DB 1381 CCTGACAAGAAAGTGAAGATTCACAGAAATTTGGGAATTAATTTCTGACTCAAGAA 1440
QY 1441 AAGCAATGCAAAATACCTTCTGAAAACAGCAACCCAGAACAACTTAAGCTGACA 1500
DB 1441 AAGCAATGCAAAATACCTTCTGAAAACAGCAACCCAGAACAACTTAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGTCCAAAGGCTTGAAGGCGATGAATATGCTGAGCAAGAAAGATCT 1560
DB 1501 TCAGAGAGAGAGTCCAAAGGCTTGAAGGCGATGAATATGCTGAGCAAGAAAGATCT 1560
QY 1561 CAAGAAACCAAAATTAATTAAGATGCTGATAGAGACTGAAATTTTATGGCTATCGAA 1620
DB 1561 CAAGAAACCAAAATTAATTAAGATGCTGATAGAGACTGAAATTTTATGGCTATCGAA 1620
QY 1621 GAAATGAAGAGCAGGAAGTACTCATGTCGATTCCTCCAGAAAACCTGACTAATGGTGC 1680
DB 1621 GAAATGAAGAGCAGGAAGTACTCATGTCGATTCCTCCAGAAAACCTGACTAATGGTGC 1680
QY 1681 ACTGCTGCAATGATGATGATTAATTCCTCAAGAGAGAGCAAGAACCTGTAAGC 1740
DB 1681 ACTGCTGCAATGATGATGATTAATTCCTCAAGAGAGAGCAAGAACCTGTAAGC 1740
QY 1741 CAGCAATTTCTCAACACTGAGATGAAGATTAACAGATGAGATTCGATTCATGAA 1800
DB 1741 CAGCAATTTCTCAACACTGAGATGAAGATTAACAGATGAGATTCGATTCATGAA 1800
QY 1801 AAGCAATTTTGTGAAGAACAGACACTGGAATTTTACAGATGAGATTCGATTCATGAA 1860
DB 1801 AAGCAATTTTGTGAAGAACAGACACTGGAATTTTACAGATGAGATTCGATTCATGAA 1860
QY 1861 GAAAGCAGATAGAGTGTGTAAGAAATGAATTCAGCTTCTGATGTTGAAGAA 1920
DB 1861 GAAAGCAGATAGAGTGTGTAAGAAATGAATTCAGCTTCTGATGTTGAAGAA 1920
QY 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTGCGGGAAGAAATTCATGCTAAGAC 1980
```

Db 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTGCGGAGAAATTTGCCATGCTAAGACTG 1980
Oy 1981 GAGCTAGACACAATGAACATCATGAGCCAGCTAAATAAAAAATAAAAAATAAAAA 2040
Db 1981 GAGCTAGACACAATGAACATCATGAGCCAGCTAAATAAAAAATAAAAAATAAAAA 2040

RESULT 24

us-09-780-669-375
: Sequence 375, Application US/09780669

GENERAL INFORMATION:

: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yugu
: APPLICANT: Henderson, Robert A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darick
: APPLICANT: Li, Samuel
: APPLICANT: Wang, Aljun
: APPLICANT: Skelky, Yastir A.W.
: APPLICANT: Hepler, William
: APPLICANT: Hurst, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghton, Raymond L.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.427C24
: CURRENT APPLICATION NUMBER: US/09/780, 669
: NUMBER OF SEQ ID NOS: 943
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 375
: LENGTH: 2040
: TYPE: DNA
: ORGANISM: Homo sapien
us-09-780-669-375

Query Match 100.0% Score 2040: DB 30: Length 2040:
Best Local Similarity 100.0%: Pred. No. 2,7e-264: Mismatches 0: Indels 0: Gaps 0:
Matches 2040: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Oy 1 ATGCTGTTGAGTGTGATTCATGCGCGCTGCTTCTGTGAAGAGCCATTGGTCTC 60
Db 1 ATGCTGTTGAGTGTGATTCATGCGCGCTGCTTCTGTGAAGAGCCATTGGTCTC 60
Oy 61 AGGACCAAGATGGGCAAGTGTGTCGCTTCCCTGCTGAGGAGGAGCGCAAG 120
Db 61 AGGACCAAGATGGGCAAGTGTGTCGCTTCCCTGCTGAGGAGGAGCGCAAG 120
Oy 121 AGCAAGGCGGCACTTCTGGAGACAGACGACTCTGCTATGAAGACACTCAGAACTGAGCAAG 180
Db 121 AGCAAGGCGGCACTTCTGGAGACAGACGACTCTGCTATGAAGACACTCAGAACTGAGCAAG 180
Oy 181 ATGGCAAGTGTGCGGCACTGCTTCCCTGCTGAGGAGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGCAAGTGTGCGGCACTGCTTCCCTGCTGAGGAGGAGTGGCAAGCAAGCTG 240
Oy 241 GCGCTTCTGAGACACGACGACTCTGCTATGAAGACACTCAGAACTGAGCAAG 300
Db 241 GCGCTTCTGAGACACGACGACTCTGCTATGAAGACACTCAGAACTGAGCAAG 300
Oy 301 TGGTCTGCGCACTGCTTCCCTGCTGAGGAGGAGGAGGAGCAAGCAAGTGGCCCTTG 360
Db 301 TGGTCTGCGCACTGCTTCCCTGCTGAGGAGGAGGAGGAGCAAGCAAGTGGCCCTTG 360
Oy 361 GGAGACTACGATGACAGTGCCTTCATGAGCCAGGTAACGATCGCTCGTGAAGAATCTG 420

Db 361 GGAGACTACGATGACAGTGCCTTCATGAGCCAGGTAACGATCGCTCGTGAAGAATCTG 420
Oy 421 GACAAGCTTCCACAGAGCTGCTGCTGAGGTAAGTCCCAAGAAAGATCTCATCTGATG 480
Db 421 GACAAGCTTCCACAGAGCTGCTGCTGAGGTAAGTCCCAAGAAAGATCTCATCTGATG 480
Oy 481 CTCAGGACACTGAGTGAACAAAGAGCAAGCAAAAGAGAGCTGCTCATCTGAGCC 540
Db 481 CTCAGGACACTGAGTGAACAAAGAGCAAGCAAAAGAGAGCTGCTCATCTGAGCC 540
Oy 541 TCTGCCAATGGGAATTCAGAACTAGTAAATCTCTGCTGAGAGAGATGTCACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAACTAGTAAATCTCTGCTGAGAGAGATGTCACTTAAT 600
Oy 601 GTCTTGGACAAACAAAAGAGGACAGCTCTGATTAAGGCGCTACATGCTCAGAAATGA 660
Db 601 GTCTTGGACAAACAAAAGAGGACAGCTCTGATTAAGGCGCTACATGCTCAGAAATGA 660
Oy 661 TGTGGGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCCAGATAGTATGGAAT 720
Db 661 TGTGGGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCCAGATAGTATGGAAT 720
Oy 721 ACCACTCTGCACTAGGCTATCTATATGAAGATTAATATGAGCCAAAGCACTGCTTA 780
Db 721 ACCACTCTGCACTAGGCTATCTATATGAAGATTAATATGAGCCAAAGCACTGCTTA 780
Oy 781 TATGCTGCTGATATGATCAATCAAAAACAGCATGGCTCTACACCACTGTTACTGGTGA 840
Db 781 TATGCTGCTGATATGATCAATCAAAAACAGCATGGCTCTACACCACTGTTACTGGTGA 840
Oy 841 CATGAGCAAAAACAGCAATGCTGAATTTAATCAAAAAGCGAATTTAATATGA 900
Db 841 CATGAGCAAAAACAGCAATGCTGAATTTAATCAAAAAGCGAATTTAATATGA 900
Oy 901 CTGATATGATATGAAGAGCTGCTCATATCTGCTGATGTTGTTGATCAGCAAGTATA 960
Db 901 CTGATATGATATGAAGAGCTGCTCATATCTGCTGATGTTGTTGATCAGCAAGTATA 960
Oy 961 GTACAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAGC 1020
Db 961 GTACAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAGC 1020
Oy 1021 GCCAGAGTATGCTGTTCTATGATCATCATGATTAATTTGCAAGTATCTGCTGCTC 1080
Db 1021 GCCAGAGTATGCTGTTCTATGATCATCATGATTAATTTGCAAGTATCTGCTGCTC 1080
Oy 1081 AAAAGAAAACAGATGCTAAAAATCTTCTGAAAACAGCAATCCAGAACAGCTTAAG 1140
Db 1081 AAAAGAAAACAGATGCTAAAAATCTTCTGAAAACAGCAATCCAGAACAGCTTAAG 1140
Oy 1141 CTGACATCAGAGAAAGTCTCAAAAGTTCAAAGCAGTGAATAATGCCAGCAGAAA 1200
Db 1141 CTGACATCAGAGAAAGTCTCAAAAGTTCAAAGCAGTGAATAATGCCAGCAGAAA 1200
Oy 1201 ATGCTCAAGAACCAAAATTAATGAAGTGAAGAGAGTGAAGAGAAATGAAG 1260
Db 1201 ATGCTCAAGAACCAAAATTAATGAAGTGAAGAGAGTGAAGAGAAATGAAG 1260
Oy 1261 AAGCATGAAGTAAATATGAGTATGAGTATCTAGAAAACCTACTAATGCTGCTGCG 1320
Db 1261 AAGCATGAAGTAAATATGAGTATGAGTATCTAGAAAACCTACTAATGCTGCTGCG 1320
Oy 1321 AATGATATATGATTAATCTCTCAAAAGAGAGCAGAAACCTGAAAATCGCAATTT 1380
Db 1321 AATGATATATGATTAATCTCTCAAAAGAGAGCAGAAACCTGAAAATCGCAATTT 1380
Oy 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGATTTAGTTCTGACATCAAAAGA 1440
Db 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGATTTAGTTCTGACATCAAAAGA 1440
Oy 1441 AAACAGATCCAAAATACTCTCTGAAAACAGCAACCCAGAAACAGACTTAAGCTGACA 1500

Db	1441	AAACGATGCCAAATACTCTTCTGAAAACAGCAACCCAGAACCAAGACTTAAAGCTGACA	1500
Oy	1501	TCACAGCAGAGTCACACAAAGCTTTGAGGGCAGTGAATAATGCCACCGACAGAAAAAGATCT	1560
Db	1501	TCACAGGAGAGTCACCAAAAGCTTTGAGGGCAGTGAATAATGCCACCGACAGAAAAAGATCT	1560
Oy	1561	CAAGACCAGAAATTAATTAAGATGGTGATAGAGACTGAAAAATTTTATGGCTATCGAA	1620
Db	1561	CAAGACCAGAAATTAATTAAGATGGTGATAGAGACTGAAAAATTTTATGGCTATCGAA	1620
Oy	1621	GAATTCGAAGAAGCAGCGAGTACTCATGTGCGATTTCCAGAAAACCTGACTAATGGTCC	1680
Db	1621	GAATTCGAAGAAGCAGCGAGTACTCATGTGCGATTTCCAGAAAACCTGACTAATGGTCC	1680
Oy	1681	ACTGCTGGCAATGGTGATGATTTAATTTCCCTCCAAAGAGCAGAGAACACTGAAAGC	1740
Db	1681	ACTGCTGGCAATGGTGATGATTTAATTTCCCTCCAAAGAGCAGAGAACACTGAAAGC	1740
Oy	1741	CAGCAATTTCTGTCACTGGAATGGAAGATACACAGTGCAGCAACAAATGATACTCAG	1800
Db	1741	CAGCAATTTCTGTCACTGGAATGGAAGATACACAGTGCAGCAACAAATGATACTCAG	1800
Oy	1801	AAGCAATTTGTGAGAAACGAACACTGGAAATTTACAGATGAGATTTCTGATTTACAA	1860
Db	1801	AAGCAATTTGTGAGAAACGAACACTGGAAATTTACAGATGAGATTTCTGATTTACAA	1860
Oy	1861	GAAGAAGCAGATAGAAAGTGTGAAAAAATGAATTCGACCTTCTCTTAGTGTGAAGAA	1920
Db	1861	GAAGAAGCAGATAGAAAGTGTGAAAAAATGAATTCGACCTTCTCTTAGTGTGAAGAA	1920
Oy	1921	GAAAAAGCATTCTTGATGAAAATAGTACGTTGCGGGAAGAAATTTGCCATGCTAAGACTG	1980
Db	1921	GAAAAAGCATTCTTGATGAAAATAGTACGTTGCGGGAAGAAATTTGCCATGCTAAGACTG	1980
Oy	1981	GAGCTAGACCAATGAAGAAACATCGACCCAGCTTAAAAAATTTTTTTTTTTTTTTTTTTT	2040
Db	1981	GAGCTAGACCAATGAAGAAACATCGACCCAGCTTAAAAAATTTTTTTTTTTTTTTTTTTT	2040

```

RESULT 25
US-09-810-936-303
/ Sequence 303, Application US/09810936
/ GENERAL INFORMATION:
/ APPLICANT: Fridakis, Tony N.
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Smith, John M.
/ APPLICANT: Misher, Linda E.
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Harlocker, Susan L.
/ APPLICANT: Day, Craig H.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
/ TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
/ FILE REFERENCE: 210121.419C11
/ CURRENT APPLICATION NUMBER: US/09/810,936
/ CURRENT FILING DATE: 2001-03-16
/ NUMBER OF SEQ ID NOS: 334
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 303
/ LENGTH: 2040
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-810-936-303

```

Query Match	100.0%;	Score 2040;	DB 31;	Length 2040;
Best Local Similarity	100.0%;	Pred. No. 2.7e-264;		
Matches 2040;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	Db
1 ATGCGGTGAGGTTGATTCATGCCGGGCTCTTCTGTGAAGACCATTTGGTCTC 60	1 ATGCGGTGAGGTTGATTCATGCCGGGCTCTTCTGTGAAGACCATTTGGTCTC 60

OY	61	AGGAGCAAGATGGGCAAGTGGTGGCTGGCGTGGTCCCGCTGGCGGAGGAGGCGGCAAG	120
Db	61	AGGAGCAAGATGGGCAAGTGGTGGCTGGCGTGGTCCCGCTGGCGGAGGAGGCGGCAAG	120
OY	121	AGCAACGTGGGCACTTCTTGAGAACCAAGCAAGCACTCTGCTATGAAGCACTCAGAGCAAG	180
Db	121	AGCAACGTGGGCACTTCTTGAGAACCAAGCAAGCACTCTGCTATGAAGCACTCAGAGCAAG	180
OY	181	ATGGGCAAGTGGTGGCCGCACTGTTCCCTGCTGCAGGGGGAGTGGCAAGCAAGCTG	240
Db	181	ATGGGCAAGTGGTGGCCGCACTGTTCCCTGCTGCAGGGGGAGTGGCAAGCAAGCTG	240
OY	241	GGCCGTTCTGAGAGCCAGCAAGCACTGCTATGAACAACACTCAGAAACAAGTGGGCAAG	300
Db	241	GGCCGTTCTGAGAGCCAGCAAGCACTGCTATGAACAACACTCAGAAACAAGTGGGCAAG	300
OY	301	TGGTGTCCCACTCTCCCTGGTGGAGGGGAGGGGCAAGCAAGTGGGCGCTTGG	360
Db	301	TGGTGTCCCACTCTCCCTGGTGGAGGGGAGGGGCAAGCAAGTGGGCGCTTGG	360
OY	361	GGAGCACTAGTATGACAGTGGCTTCATGAGCCAGCCAGGACACGCTCCGTGAACAATCTG	420
Db	361	GGAGCACTAGTATGACAGTGGCTTCATGAGCCAGCCAGGACACGCTCCGTGAACAATCTG	420
OY	421	GACAACTCCACAGAGTGCCTGGTGGGTTAAAGTCCCAAGAAAGATCTCATGCTCATG	480
Db	421	GACAACTCCACAGAGTGCCTGGTGGGTTAAAGTCCCAAGAAAGATCTCATGCTCATG	480
OY	481	CTCAGGGGCACTGACGAGGAACAAGAAAGCAAAAGAGGAGCTGCTACATGTGGCC	540
Db	481	CTCAGGGGCACTGACGAGGAACAAGAAAGCAAAAGAGGAGCTGCTACATGTGGCC	540
OY	541	TCTGCAATGGGAATTGAGAAAGTAAACTCTCTGAGACAGAGATGTCACTTAAT	600
Db	541	TCTGCAATGGGAATTGAGAAAGTAAACTCTCTGAGACAGAGATGTCACTTAAT	600
OY	601	GTCCTTGACAAACAAAAGAGAGACAGCTGATAAAGCCGTACAAATGCCAGGAAGATGA	660
Db	601	GTCCTTGACAAACAAAAGAGAGACAGCTGATAAAGCCGTACAAATGCCAGGAAGATGA	660
OY	661	TGTGGCTTAATGTTGCTGAGAAACATGGGACATGATCCAAATATTCCAGATGATGGAAT	720
Db	661	TGTGGCTTAATGTTGCTGAGAAACATGGGACATGATCCAAATATTCCAGATGATGGAAT	720
OY	721	ACCACTGTGCACTACGCTATCTATATGAAGATTAATGAGCCAAACACTGCTCTTA	780
Db	721	ACCACTGTGCACTACGCTATCTATATGAAGATTAATGAGCCAAACACTGCTCTTA	780
OY	781	TATGGTGTGATATCGAATCAAAAACAAACATGAGGCTCAACACACTGTTACTTGGTGA	840
Db	781	TATGGTGTGATATCGAATCAAAAACAAACATGAGGCTCAACACACTGTTACTTGGTGA	840
OY	841	CATGAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAAGCAATTTAAATGCA	900
Db	841	CATGAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAAGCAATTTAAATGCA	900
OY	901	CTGATATGATATGGAAGAGCTGCTCATACTGCTGATATGTTGGATCAGCAAGTATA	960
Db	901	CTGATATGATATGGAAGAGCTGCTCATACTGCTGATATGTTGGATCAGCAAGTATA	960
OY	961	GTCAGCTTCTACTTGGAGCAAAATATTGATGTAATCTTCAAGATCTATCTGGACAGAG	1020
Db	961	GTCAGCTTCTACTTGGAGCAAAATATTGATGTAATCTTCAAGATCTATCTGGACAGAG	1020
OY	1021	GCCAGAGATATGCTGTTTCTAGTCATCATATGTAATTTGCCAGTACTTCTGATAC	1080
Db	1021	GCCAGAGATATGCTGTTTCTAGTCATCATATGTAATTTGCCAGTACTTCTGATAC	1080
OY	1081	AAAGAAAAACGATGCTAAAAATCTCTTGAAACACAGAAATCCAGAACAGACTTAAG	1140
Db	1081	AAAGAAAAACGATGCTAAAAATCTCTTGAAACACAGAAATCCAGAACAGACTTAAG	1140

QY	1141	CTGCATCAGAGGAAAGGTCACCAAGCTTCAAAAGCAGTGAATAATAGCCACGACGAGAA	1200
Db	1141	CTGCATCAGAGGAAAGGTCACCAAGCTTCAAAAGCAGTGAATAATAGCCACGACGAGAA	1200
QY	1201	ATGCTCTCAAGAACCCACAATAATTAATTAAGCATGTGTCATAGAGAGTGTGAAGAAAGAAATGAG	1260
Db	1201	ATGCTCTCAAGAACCCAGAATAATTAATTAAGCATGTGTCATAGAGAGTGTGAAGAAAGAAATGAG	1260
QY	1261	AAGCATGAAAGTAATTAATGTGGGATTACTAGAAAAA	1320
Db	1261	AAGCATGAAAGTAATTAATGTGGGATTACTAGAAAAA	1320
QY	1321	AATGGTGATTAATGATTTAATCTCTCAAGAGAGCAGACAACTCTGAAATTCAGCAATTT	1380
Db	1321	AATGGTGATTAATGATTTAATCTCTCAAGAGAGCAGACAACTCTGAAATTCAGCAATTT	1380
QY	1381	CCTGACCAACAAAGTGAAGATTCACAGAAATTTGGGAAATTCAGTCTGACTACACAAAGAA	1440
Db	1381	CCTGACCAACAAAGTGAAGATTCACAGAAATTTGGGAAATTCAGTCTGACTACACAAAGAA	1440
QY	1441	AAACAGATGCCAAAATACTCTTCTGAAAAACAGCAACCCAGAACCAAGACTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAAATACTCTTCTGAAAAACAGCAACCCAGAACCAAGACTTAAAGCTGACA	1500
QY	1501	TCAGAGAGAGATTCACAAAGGCTTGAGGCGAGTGAATAATGGCCAGCCAGAGAAAAAGATCT	1560
Db	1501	TCAGAGAGAGATTCACAAAGGCTTGAGGCGAGTGAATAATGGCCAGCCAGAGAAAAAGATCT	1560
QY	1561	CAGGAACCAAGAAATTAATTAAGATGGTGATPAGAGAGCTGAATAATTTATGGCTATGCAA	1620
Db	1561	CAGGAACCAAGAAATTAATTAAGATGGTGATPAGAGAGCTGAATAATTTATGGCTATGCAA	1620
QY	1621	GAATGAGAAGACGACGGAAGTACTCATCTGCGATTTCCAGAAAACTGACTAATGCTGCC	1680
Db	1621	GAATGAGAAGACGACGGAAGTACTCATCTGCGATTTCCAGAAAACTGACTAATGCTGCC	1680
QY	1681	ACTGCTGGCAATGGTGTATGTGATTAATTTCTCCAGGAGAAAGCAGAAACCTCTGAAAGC	1740
Db	1681	ACTGCTGGCAATGGTGTATGTGATTAATTTCTCCAGGAGAAAGCAGAAACCTCTGAAAGC	1740
QY	1741	CAGCAATTCCTGACACTGATGTAAGATPACACAGTACGAAACAAATGATCTCAG	1800
Db	1741	CAGCAATTCCTGACACTGATGTAAGATPACACAGTACGAAACAAATGATCTCAG	1800
QY	1801	AAGCAATTTTGTGAGAACACAGAACACTGGAATAATTAACAGATGAGATTTCTGATTCATGAA	1860
Db	1801	AAGCAATTTTGTGAGAACACAGAACACTGGAATAATTAACAGATGAGATTTCTGATTCATGAA	1860
QY	1861	GAAGACAGATAGAGTGTGTAATAAATGAATTCAGACTTCTCTTAGTTGAAGAA	1920
Db	1861	GAAGACAGATAGAGTGTGTAATAAATGAATTCAGACTTCTCTTAGTTGAAGAA	1920
QY	1921	GAAGAAACATCTTGCATGAAATTAATACGTGGCGGAGAAATTCGCAATGCTAAGACTG	1980
Db	1921	GAAGAAACATCTTGCATGAAATTAATACGTGGCGGAGAAATTCGCAATGCTAAGACTG	1980
QY	1981	GAGCTAGACAGATGAAACATCGAGCCAGCTRAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2040
Db	1981	GAGCTAGACAGATGAAACATCGAGCCAGCTRAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2040
RESULT 26			
US-09-822-827-375			
; Sequence 375, Application US/09822827			
; GENERAL INFORMATION:			
; APPLICANT: Xu, Jiangchun			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER			
; FILE REFERENCE: 210121.534c1			
; CURRENT APPLICATION NUMBER: US/09/822,827			
; CURRENT FILING DATE: 2001-03-28			
; NUMBER OF SEQ ID NOS: 982			
; SOFTWARE: fastSeq for Windows Version 3.0			

[illegible]


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Db 661 TGTGGTAAATGTTGTCGAAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
Oy 721 ACCACTGTCAGTACGATCTATATATGAGATTAATTAATGACCAAGCACTGCTTA 780
Db 721 ACCACTGTCAGTACGATCTATATATGAGATTAATTAATGACCAAGCACTGCTTA 780
Oy 781 TATGTCGTGATATGAAATCAAAAAAACAAGCATGGCTCACACACTGTTACTGCTGA 840
Db 781 TATGTCGTGATATGAAATCAAAAAAACAAGCATGGCTCACACACTGTTACTGCTGA 840
Oy 841 CATGAGCAAAAAACAGCAAGTCGTGAATTTTAAATCAAGAAAAAAGCAATTTAAATGA 900
Db 841 CATGAGCAAAAAACAGCAAGTCGTGAATTTTAAATCAAGAAAAAAGCAATTTAAATGA 900
Oy 901 CTGGATATATGAGAGAGCTGCTCATCTGCTGATATGTTGGATCAGCAAGTATA 960
Db 901 CTGGATATATGAGAGAGCTGCTCATCTGCTGATATGTTGGATCAGCAAGTATA 960
Oy 961 GTCAGCCCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAG 1020
Db 961 GTCAGCCCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGAGACAG 1020
Oy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Oy 1081 AAAGAAAAACAGATCTAAAAATCTCTCTGAAAAACAGCAATCCAGAACACTTAAAG 1140
Db 1081 AAAGAAAAACAGATCTAAAAATCTCTCTGAAAAACAGCAATCCAGAACACTTAAAG 1140
Oy 1141 CTGACATCAGAGAGAGATCTCAAAAGTTCAAGAGCAGTGAAGAAATAGCCAGCAGAAA 1200
Db 1141 CTGACATCAGAGAGAGATCTCAAAAGTTCAAGAGCAGTGAAGAAATAGCCAGCAGAAA 1200
Oy 1201 ATGTCCTCAAGAACCAAGAAATTAATTAAGATGTTAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGTCCTCAAGAACCAAGAAATTAATTAAGATGTTAGAGAGTTGAAGAAATGAAG 1260
Oy 1261 AAGCATGAAGATTAATTAATGTTGGATTTACTAGAAAACTGACTAAATGGTCTCCTGGC 1320
Db 1261 AAGCATGAAGATTAATTAATGTTGGATTTACTAGAAAACTGACTAAATGGTCTCCTGGC 1320
Oy 1321 AATGTCGATTAATGATTAATCTCTCAAGAGAGACAGAACCTGAAATACGAATTT 1380
Db 1321 AATGTCGATTAATGATTAATCTCTCAAGAGAGACAGAACCTGAAATACGAATTT 1380
Oy 1381 CCTGCAACGAAAGTGAAGAGTATCACAGAAATTTGCCAATTAATGTTCTGACTACAAAGAA 1440
Db 1381 CCTGCAACGAAAGTGAAGAGTATCACAGAAATTTGCCAATTAATGTTCTGACTACAAAGAA 1440
Oy 1441 AAACGATGCCAAATACTCTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db 1441 AAACGATGCCAAATACTCTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Oy 1501 TCAGAGAGAGAGTCAAAAGCTTGAGGGCAGTGAAGAAATGGCCAGCAGAGAAAGATCT 1560
Db 1501 TCAGAGAGAGAGTCAAAAGCTTGAGGGCAGTGAAGAAATGGCCAGCAGAGAAAGATCT 1560
Oy 1561 CAAGAACCAAGAAATTAATTAAGATGTTAGAGAGTGAAGAAATTTATGGCTATCGAA 1620
Db 1561 CAAGAACCAAGAAATTAATTAAGATGTTAGAGAGTGAAGAAATTTATGGCTATCGAA 1620
Oy 1621 GAAATGAAGAGAGAGAGAGTATCATGTCGATTCAGAGAAACCTGACTAATGTCGCC 1680
Db 1621 GAAATGAAGAGAGAGAGAGTATCATGTCGATTCAGAGAAACCTGACTAATGTCGCC 1680
Oy 1681 ACTGTCGCAATGATGATGATGATTAATCTCTCAAGAGAGAGAGAGACACTGAAAGC 1740
Db 1681 ACTGTCGCAATGATGATGATGATTAATCTCTCAAGAGAGAGAGAGACACTGAAAGC 1740
Oy 1741 CAGCAATTTCTGACACTGAGAAATGAAGTATCACAGTGAAGCAAAATGATACTGAG 1800
Db 1741 CAGCAATTTCTGACACTGAGAAATGAAGTATCACAGTGAAGCAAAATGATACTGAG 1800
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Db 1741 CAGCAATTTCTGACACTGAGAAATGAAGTATCACAGTGAAGCAAAATGATACTGAG 1800
Oy 1801 AAGCAATTTTGGAGAGACAGAACTGGAATATTAACAGATGATGATTCATGAA 1860
Db 1801 AAGCAATTTTGGAGAGACAGAACTGGAATATTAACAGATGATGATTCATGAA 1860
Oy 1861 GAAAGCAGATGAAGTGTGAAAAAATGAATTCGACCTTCTTCTGATGTAAGAA 1920
Db 1861 GAAAGCAGATGAAGTGTGAAAAAATGAATTCGACCTTCTTCTGATGTAAGAA 1920
Oy 1921 GAAAAAGACATCTTCATGAAAAATAGTACGTTGGGGAAGAAATTTGCCATGTAAGACTG 1980
Db 1921 GAAAAAGACATCTTCATGAAAAATAGTACGTTGGGGAAGAAATTTGCCATGTAAGACTG 1980
Oy 1981 GAGCTAGACACATGAATGACATGAGCCAGCTTAAAAAATGAAAAAATGAAAAA 2040
Db 1981 GAGCTAGACACATGAATGACATGAGCCAGCTTAAAAAATGAAAAAATGAAAAA 2040

RESULT 28
US-09-852-911-375
; Sequence 375, Application US/09852911
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jlang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedyck, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Hepler, Yasir A.W.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C25
; CURRENT APPLICATION NUMBER: US/09/852,911
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-852-911-375

Query Match 100.0%; Score 2040; DB 32; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2,7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGGTGGTTGAGTGGATTCATCGTCGCGGCTGCTCTTCTGTAAGAGCATTTGCTC 60
Db 1 ATGGTGGTTGAGTGGATTCATCGTCGCGGCTGCTCTTCTGTAAGAGCATTTGCTC 60
Oy 61 AGGACCAAGATGGGCAAGTGTGCTGCGTTCCTCCCTGCTGAGGAGAGCGGCAAG 120
Db 61 AGGACCAAGATGGGCAAGTGTGCTGCGTTCCTCCCTGCTGAGGAGAGCGGCAAG 120
Oy 121 AGCAACGTGGGACCTTCTGAGACACAGACACTGCTGATGAGACACTCAGAGCAAG 180
Db 121 AGCAACGTGGGACCTTCTGAGACACAGACACTGCTGATGAGACACTCAGAGCAAG 180
Oy 181 ATGGCAAGTGGTGGCGGCACTGCTCCCTGCTGACAGGGGAGTGGCAAGCAACTG 240
Db 181 ATGGCAAGTGGTGGCGGCACTGCTCCCTGCTGACAGGGGAGTGGCAAGCAACTG 240
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Db 181 ATGGGAAAGTGTGCGCCGCTCTCCCTGCTGAGGGGGAGTGGCAAGACACGCTG 240
QY 241 GGGCTTTGAGAGACGACGACGCTGCTATGAAAGACATCAGGAACAAGATGGGCAAG 300
Db 241 GGGCTTTGAGAGACGACGACGCTGCTATGAAAGACATCAGGAACAAGATGGGCAAG 300
QY 301 TGGTGTGACACTGCTTCCCTCTGACAGGGGGAGGGGCAAGAGCAAGTGGGCGCTGG 360
Db 301 TGGTGTGACACTGCTTCCCTCTGACAGGGGGAGGGGCAAGAGCAAGTGGGCGCTGG 360
QY 361 GGAAGACTAGATGACAGTGGCTTCATGAGAGCCAGGTACCAGCTCCGTGAGAAAGTCTG 420
Db 361 GGAAGACTAGATGACAGTGGCTTCATGAGAGCCAGGTACCAGCTCCGTGAGAAAGTCTG 420
QY 421 GAAAGCTCCACAGAGTGGCTGGGGGTAAGTCCCGAAGAAAGATGTCATGCTATG 480
Db 421 GAAAGCTCCACAGAGTGGCTGGGGGTAAGTCCCGAAGAAAGATGTCATGCTATG 480
QY 481 CTCAGGAGACATGACGTGAACAAGAGACAAAGAGAGACTGCTTACATCTGGCC 540
Db 481 CTCAGGAGACATGACGTGAACAAGAGAGACAAAGAGAGACTGCTTACATCTGGCC 540
QY 541 TCTGCCAATGGAATTCAGAAAGTAAACCTCCTGCTGACAGACAGTCAACTTAAT 600
Db 541 TCTGCCAATGGAATTCAGAAAGTAAACCTCCTGCTGACAGACAGTCAACTTAAT 600
QY 601 GTCTTGACAAACAAAAGAGAGACGCTGATAAAGGCGGTACAAATCCCGAAGAAAGTAA 660
Db 601 GTCTTGACAAACAAAAGAGAGACGCTGATAAAGGCGGTACAAATCCCGAAGAAAGTAA 660
QY 661 TGTGCGTAAATGTTGCTGGAACATGGGACATGATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGCGTAAATGTTGCTGGAACATGGGACATGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTCTGACACTACCTATCTATTAATGAAGATTAATTAATGGCCAAAGACATGCTT 780
Db 721 ACCACTCTGACACTACCTATCTATTAATGAAGATTAATTAATGGCCAAAGACATGCTT 780
QY 781 TATGAGCTGATATGCAATGCAAAAACAGCATGGGCTCACACACATGTTACTTGGTGA 840
Db 781 TATGAGCTGATATGCAATGCAAAAACAGCATGGGCTCACACACATGTTACTTGGTGA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATATGATATGGAAGGACTGCTCTCATCTGCTGATGTTGTGATGACAGATATA 960
Db 901 CTGATATGATATGGAAGGACTGCTCTCATCTGCTGATGTTGTGATGACAGATATA 960
QY 961 GTGAGCCTTCTACTGAGCAAAATATGATGATATCTCAAGATCATATGAGCAGAC 1020
Db 961 GTGAGCCTTCTACTGAGCAAAATATGATGATATCTCTCAAGATCATATGAGCAGAC 1020
QY 1021 GCCAGAGAGTATCTGTTTCTAGTCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
Db 1021 GCCAGAGAGTATCTGTTTCTAGTCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
QY 1081 AAAAGAAAAACAGATGCTAAAAATCTCTTGAAGAACGCAATCCAGCAAGACTTAAG 1140
Db 1081 AAAAGAAAAACAGATGCTAAAAATCTCTTGAAGAACGCAATCCAGCAAGACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGTGAACAAGGTTCAAGGCGAGTAAATATGAGCCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGTGAACAAGGTTCAAGGCGAGTAAATATGAGCCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGTGATAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGTGATAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTAAATTAATGTTGAGTAACTGAAACCTGACTAATGTTGCTGCTGC 1320
Db 1261 AAGCATGAAAGTAAATTAATGTTGAGTAACTGAAACCTGACTAATGTTGCTGCTGC 1320

Db 1261 AAGCATGAAAGTAAATTAATGTTGAGTAACTGAAACCTGACTAATGTTGCTGCTGC 1320
QY 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGAGAAACACCTGAAATACGAATTT 1380
Db 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGAGAAACACCTGAAATACGAATTT 1380
QY 1381 CCTGACAAAGAAAGTGAAGATATCACAGAAATTTGGAAATTAATTTCTGACTCAAGAA 1440
Db 1381 CCTGACAAAGAAAGTGAAGATATCACAGAAATTTGGAAATTAATTTCTGACTCAAGAA 1440
QY 1441 AAACAGATGCAAAATTTCTTCTGAAACAGCAACCCAGAACAAAGACTTAAGCTGACA 1500
Db 1441 AAACAGATGCAAAATTTCTTCTGAAACAGCAACCCAGAACAAAGACTTAAGCTGACA 1500
QY 1501 TCAGAGAAAGATTCACAAAGGCTTGAAGGCGATGAAATTTGGCCAGAGAAAGATCT 1560
Db 1501 TCAGAGAAAGATTCACAAAGGCTTGAAGGCGATGAAATTTGGCCAGAGAAAGATCT 1560
QY 1561 CAAGAACCCAGAAATTAATTAAGATGTTGATAGAGAGCTAGAAATTTATGCTATCGAA 1620
Db 1561 CAAGAACCCAGAAATTAATTAAGATGTTGATAGAGAGCTAGAAATTTATGCTATCGAA 1620
QY 1621 GAATGAAAGAGACGAGAAATCTCATGCTGGGATTTCCCAAGAAACCTGACTAATGGTCC 1680
Db 1621 GAATGAAAGAGACGAGAAATCTCATGCTGGGATTTCCCAAGAAACCTGACTAATGGTCC 1680
QY 1681 ACTGCTGCAATGATGATGATGATTAATTTCTCAAGAAAGAGACAGAACCTGGAAGC 1740
Db 1681 ACTGCTGCAATGATGATGATGATTAATTTCTCAAGAAAGAGACAGAACCTGGAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCACAGTACGACAAACAAATGATCTCAG 1800
Db 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCACAGTACGACAAACAAATGATCTCAG 1800
QY 1801 AAGCAATTTGTAAGAGACAGAACTGGAATTTACACATGATGATGATTTCAATGAA 1860
Db 1801 AAGCAATTTGTAAGAGACAGAACTGGAATTTACACATGATGATGATTTCAATGAA 1860
QY 1861 GAAAGAGAGATGAAGGTTGAAAAATGAAATTTGAGCTTCTGTAATGTAAGAA 1920
Db 1861 GAAAGAGAGATGAAGGTTGAAAAATGAAATTTGAGCTTCTGTAATGTAAGAA 1920
QY 1921 GAAAAAGACATCTTGCATGAAATTAAGTACGTTCCGGAGAGAAATGGCATGTAAGACTG 1980
Db 1921 GAAAAAGACATCTTGCATGAAATTAAGTACGTTCCGGAGAGAAATGGCATGTAAGACTG 1980
QY 1981 GAGCTAGACACAAATGAAACATCAAGCCAGCTAAAAAAGAAAAAAGAAAAA 2040
Db 1981 GAGCTAGACACAAATGAAACATCAAGCCAGCTAAAAAAGAAAAAAGAAAAA 2040

RESULT 29
; Sequence 375, Application US/09895793
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
```

APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-895-793-375

Query Match 100.0%; Score 2040; DB 33; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2.7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGTGGTGGAGTGGATTCATGCCGGCTGCTTCTGTGTGAAGAGCCATTGGTCTC 60
DB 1 AAGGTGGTGGAGTGGATTCATGCCGGCTGCTTCTGTGTGAAGAGCCATTGGTCTC 60
QY 61 AAGAGCAAGATGGGCAAGTGTGTGCTGCTGCTTCCCTGCTGAGGGAGAGCGGCAAG 120
DB 61 AAGAGCAAGATGGGCAAGTGTGTGCTGCTGCTTCCCTGCTGAGGGAGAGCGGCAAG 120
QY 121 AAGCAAGCTGGGCACTTCTGGAGACGACGACGACTGTGTATGAAGCACTCAGAGCAAG 180
DB 121 AAGCAAGCTGGGCACTTCTGGAGACGACGACGACTGTGTATGAAGCACTCAGAGCAAG 180
QY 181 AAGGGCAATGGTGGCCGACACCTGCTTCCCTGCTGAGGGAGAGTGGCAAGCAACGTG 240
DB 181 AAGGGCAATGGTGGCCGACACCTGCTTCCCTGCTGAGGGAGAGTGGCAAGCAACGTG 240
QY 241 GAGCGTCTGGAGACGACGACGACTGTGTATGAAGCACTCAGAGCAAGTGGGCAAG 300
DB 241 GAGCGTCTGGAGACGACGACGACTGTGTATGAAGCACTCAGAGCAAGTGGGCAAG 300
QY 301 TGGTGTGCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 301 TGGTGTGCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 361 GGAGACTAGAGTACAGTCTTCTGATGAGCCAGGTACACGCTCGTGGAGAGATCTG 420
DB 361 GGAGACTAGAGTACAGTCTTCTGATGAGCCAGGTACACGCTCGTGGAGAGATCTG 420
QY 421 GACAAGCTCAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 421 GACAAGCTCAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 CTCAGGAGACCTGAGCTGAACAAGAGCAAGCAAGAGAGAGCTCTACATCTGGCC 540
DB 481 CTCAGGAGACCTGAGCTGAACAAGAGCAAGCAAGAGAGAGCTCTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAGTAACTCTGCTGAGACAGAGATGCACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAGTAACTCTGCTGAGACAGAGATGCACTTAAT 600
QY 601 GTCTCTGACAACAAAAGAGAGAGCTGTATGAAGCGGTACAAATGCCAGAGAGTGA 660
DB 601 GTCTCTGACAACAAAAGAGAGAGCTGTATGAAGCGGTACAAATGCCAGAGAGTGA 660
QY 661 TGTGGCTTAATGTGTGTGAGACATGGCAATATTTCCAGATAGTATGAAT 720
DB 661 TGTGGCTTAATGTGTGTGAGACATGGCAATATTTCCAGATAGTATGAAT 720
QY 721 ACCAGCTCTGACCTATCTATATGAAGATAAATTAATGGCCAAAGCACTGCTTA 780
DB 721 ACCAGCTCTGACCTATCTATATGAAGATAAATTAATGGCCAAAGCACTGCTTA 780

QY 781 TATGTGCTGATATTCGAATCAAAAAAAGACATGGCTCACAACACTGTTACTGGTGA 840
DB 781 TATGTGCTGATATTCGAATCAAAAAAAGACATGGCTCACAACACTGTTACTGGTGA 840
QY 841 CATGACCAAAAACAGCAAGTCTGAAATTTTAAATCAGAAAAAAGCAATTTAAATGCA 900
DB 841 CATGACCAAAAACAGCAAGTCTGAAATTTTAAATCAGAAAAAAGCAATTTAAATGCA 900
QY 901 CTGGATAGATATGGAAGAGAGCTGCTCATACTGCTGATGTTGTGGATCAGAACTATA 960
DB 901 CTGGATAGATATGGAAGAGAGCTGCTCATACTGCTGATGTTGTGGATCAGAACTATA 960
QY 961 GTGAGCTTCTACTTATGAGCAAAATATTGATGTATCTTCAAGATATATCTGGACGAG 1020
DB 961 GTGAGCTTCTACTTATGAGCAAAATATTGATGTATCTTCAAGATATATCTGGACGAG 1020
QY 1021 GCCAGAGATATGCTGTTCTATGCTATCATCATATTAATTTGCCAGTTACTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTCTATGCTATCATCATATTAATTTGCCAGTTACTTCTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATTCAGAACAGCTTAAG 1140
DB 1081 AAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATTCAGAACAGCTTAAG 1140
QY 1141 CTGACATCAGAGAGAGTCAACAAGGTTCAAAAGCAGTGAATAATAGCCAGAGAGAA 1200
DB 1141 CTGACATCAGAGAGAGTCAACAAGGTTCAAAAGCAGTGAATAATAGCCAGAGAGAA 1200
QY 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGTGATAGAGAGTTGAAGAATAATGAAG 1260
DB 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGTGATAGAGAGTTGAAGAATAATGAAG 1260
QY 1261 AAGCATGAAGATTAATTAATGTGGATTAATTAAGAAACCTGACTAATGTGCTGCTGGC 1320
DB 1261 AAGCATGAAGATTAATTAATGTGGATTAATTAAGAAACCTGACTAATGTGCTGCTGGC 1320
QY 1321 AATGCTGATTAATGATTAATTCCTCAAGAGAGAGAGCAACCTGAAATAGCAATTT 1380
DB 1321 AATGCTGATTAATGATTAATTCCTCAAGAGAGAGAGCAACCTGAAATAGCAATTT 1380
QY 1381 CCGTGAACAGAAAGTGAAGATATCAAGAAATTTGCGAATTAATTTCTGACTCAAGAA 1440
DB 1381 CCGTGAACAGAAAGTGAAGATATCAAGAAATTTGCGAATTAATTTCTGACTCAAGAA 1440
QY 1441 AAACAGATGCCAAATATCTTCTGAAAGACAGAACCCAGAAACCTTAAGAGTGACA 1500
DB 1441 AAACAGATGCCAAATATCTTCTGAAAGACAGAACCCAGAAACCTTAAGAGTGACA 1500
QY 1501 TCAGAGGAAGAGTCAACAAGGCTTGAAGGCAAGTGAAGAGAGAGAGAGAGAGATCT 1560
DB 1501 TCAGAGGAAGAGTCAACAAGGCTTGAAGGCAAGTGAAGAGAGAGAGAGAGAGATCT 1560
QY 1561 CAAGAACAGAAATTAATTAAGATGTGATAGAGAGCTGAGAAATTTATGCTATCGAA 1620
DB 1561 CAAGAACAGAAATTAATTAAGATGTGATAGAGAGCTGAGAAATTTATGCTATCGAA 1620
QY 1621 GAAATGAAGAGACGGAAGTACTCATGTGCGATTTCCAGAAAACTGTAAATGTGTGCC 1680
DB 1621 GAAATGAAGAGACGGAAGTACTCATGTGCGATTTCCAGAAAACTGTAAATGTGTGCC 1680
QY 1681 ACTGTGGCAATGTGATGATGATTAATTTCCCAAGGAAGAGCAAGCACTGGAAGC 1740
DB 1681 ACTGTGGCAATGTGATGATGATTAATTTCCCAAGGAAGAGCAAGCACTGGAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGAAATGAAGATACAGAGTACAGCAACAAATGATACTCAG 1800
DB 1741 CAGCAATTTCTGACACTGAGAAATGAAGATACAGAGTACAGCAACAAATGATACTCAG 1800
QY 1801 AAGCAATTTTGTGAGAGACAGAACTGGAATTTACAGAGTGAATTTGATTCATGA 1860
DB 1801 AAGCAATTTTGTGAGAGACAGAACTGGAATTTACAGAGTGAATTTGATTCATGA 1860
QY 1861 GAAAGCAGATGAAGTGTGTAAGAAAAATGAATTTGAGAGCTTCTGATGTTGAAGAA 1920

```
Db 1861 GAAAGACGATAGAGTGTGAAAAATGAATCTGAGCTTCTTACTGTGAAGAAA 1920
Qy 1921 GAAAAACATCTTGCATGAAAAATAGTGTGGGAGAGAAATTTGCCATGCTAGACTG 1980
Db 1921 GAAAAACATCTTGCATGAAAAATAGTGTGGGAGAGAAATTTGCCATGCTAGACTG 1980
Qy 1981 GAGCTAGACACAATGAAACATCAGAGCCAGCTAAAAA 2040
Db 1981 GAGCTAGACACAATGAAACATCAGAGCCAGCTAAAAA 2040

RESULT 30
US-09-895-814-375
; Sequence 375, Application us/09895814
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; NUMBER OF FILING DATE: 2001-06-29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-895-814-375

Query Match 100.0%; Score 2040; DB 33; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2,7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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Db 241 GCGGCTTCTGAGACACAGACGACTGTGTATGAGACACTCAGAGAAACAATGGCGAAG 300
Qy 301 TGGTGTGCCACTGCTTCCCTGCTGACAGGGGAGCGGCAAGAGCAAGTGGCGCTTGG 360
Db 301 TGGTGTGCCACTGCTTCCCTGCTGACAGGGGAGCGGCAAGAGCAAGTGGCGCTTGG 360
Qy 361 GGAGACTAGCATGACAGTGCCTTCATGAGCCAGGATACAGCTCCGTGGAGAAAGTCTG 420
Db 361 GGAGACTAGCATGACAGTGCCTTCATGAGCCAGGATACAGCTCCGTGGAGAAAGTCTG 420
Qy 421 GACAGCTCCACAGAGTGTGCTGGGTTAAAGTCCCGAAGAAAGATCTCATGCTCATG 480
Db 421 GACAGCTCCACAGAGTGTGCTGGGTTAAAGTCCCGAAGAAAGATCTCATGCTCATG 480
Qy 481 CTCAGGGACACTGACGTGACAAAGAAAGACAGCAAGAAAGAGACTGCTTACATCTGGCC 540
Db 481 CTCAGGGACACTGACGTGACAAAGAAAGACAGCAAGAAAGAGACTGCTTACATCTGGCC 540
Qy 541 TCTGCCAATGGGAATTCAGAAATAGTAAACCTCTGCTGACAGAGAGTCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATAGTAAACCTCTGCTGACAGAGAGTCAACTTAAT 600
Qy 601 GTCTTTACACAAACAAAAGAGACAGCTGTATAAAGCCGTACAAATGCCAGAAAGTAA 660
Db 601 GTCTTTACACAAACAAAAGAGACAGCTGTATAAAGCCGTACAAATGCCAGAAAGTAA 660
Qy 661 TGTGCGTTAATGTGTGCTGAACATGGCAGTATCCAAATATTCAGATGATATGAAAT 720
Db 661 TGTGCGTTAATGTGTGCTGAACATGGCAGTATCCAAATATTCAGATGATATGAAAT 720
Qy 721 ACCACTGTGACATGCTATATATGAAATTAATGACCAAGCAAGCTGCTTGA 780
Db 721 ACCACTGTGACATGCTATATATGAAATTAATGACCAAGCAAGCTGCTTGA 780
Qy 781 TATGCTGCTATATATGAAATTAATGAAACAGATGAGCTGACACACTGCTTACTTGGTGA 840
Db 781 TATGCTGCTATATGAAATTAATGAAACAGATGAGCTGACACACTGCTTACTTGGTGA 840
Qy 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTATATCAAGAAAAAGCAATTTAAATGA 900
Db 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTATATCAAGAAAAAGCAATTTAAATGA 900
Qy 901 CTGGATGATATGAGAGAGACTGCTCATACCTGCTATGTTGTGATACAGCAAGTATA 960
Db 901 CTGGATGATATGAGAGAGACTGCTCATACCTGCTATGTTGTGATACAGCAAGTATA 960
Qy 961 GTGAGCTTCTACTGTGAGCAAAATATGATGATCTCTCAAGATCATGTGAGCAGACAG 1020
Db 961 GTGAGCTTCTACTGTGAGCAAAATATGATGATCTCTCTCAAGATCATGTGAGCAGACAG 1020
Qy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
Qy 1081 AAAGAAAAACAGATGTAAAAATCTCTTCTGAAACAGCAATCCAGAAAGACTTAAAG 1140
Db 1081 AAAGAAAAACAGATGTAAAAATCTCTTCTGAAACAGCAATCCAGAAAGACTTAAAG 1140
Qy 1141 CTGACATCAAGAGAGAGTGTACAAAGGTTCAAGAGGCTGAAATATGCCAGCCAGAGAA 1200
Db 1141 CTGACATCAAGAGAGAGTGTACAAAGGTTCAAGAGGCTGAAATATGCCAGCCAGAGAA 1200
Qy 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
Db 1261 AAGCATGAAAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
Qy 1321 AATGCTATATATGATTAATTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1380
Db 1321 AATGCTATATATGATTAATTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1380
```

```
QY 1381 CCTGACAAAGAAAGTGAAGATATACAGAAATTTGCGAATTAGTTTCTGACTACAAAGAA 1440
|||
Db 1381 CCTGACAAAGAAAGTGAAGATATACAGAAATTTGCGAATTAGTTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAAATACTCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
|||
Db 1441 AAACAGATGCCAAAATACTCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
QY 1501 TCACAGAGAAAGTGCACAAAGGCTTGAGGGCAGTGAATAATGGCCAGACCCAGAGAAAAGATCT 1560
|||
Db 1501 TCACAGAGAAAGTGCACAAAGGCTTGAGGGCAGTGAATAATGGCCAGACCCAGAGAAAAGATCT 1560
QY 1561 CAAGAACACAGAAATTAATTAAGATGATGATAGAGACTAGAAAATTTATGGCTATGCAA 1620
|||
Db 1561 CAAGAACACAGAAATTAATTAAGATGATGATAGAGACTAGAAAATTTATGGCTATGCAA 1620
QY 1621 GAAATGAAGAAGACAGGAAGTACTCATGTCCGATTTCCAGAAAACCTGACTAATGGTCC 1680
|||
Db 1621 GAAATGAAGAAGACAGGAAGTACTCATGTCCGATTTCCAGAAAACCTGACTAATGGTCC 1680
QY 1681 ACTCTGGCATGTGTGATGATGATATATCTCTCCAGAGAGACAGAACCTGTAAGC 1740
|||
Db 1681 ACTCTGGCATGTGTGATGATGATATATCTCTCCAGAGAGACAGAACCTGTAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGAAATGAAAGTATCAGACTGAGAACCAAAATGATCTCAG 1800
|||
Db 1741 CAGCAATTTCTGACACTGAGAAATGAAAGTATCAGACTGAGAACCAAAATGATCTCAG 1800
QY 1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATATTACAGATGAGATTCTGATTCATGAA 1860
|||
Db 1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATATTACAGATGAGATTCTGATTCATGAA 1860
QY 1861 GAAAGCAGATAGAAAGTGTGAAAAATGAAATTCAGCTTCTCTTATGTTAAGAA 1920
|||
Db 1861 GAAAGCAGATAGAAAGTGTGAAAAATGAAATTCAGCTTCTCTTATGTTAAGAA 1920
QY 1921 GAAAAAGCATCTTGCATGAAATAGTACGTTGGGGGAAAGAAATTCATGCTAAGACTG 1980
|||
Db 1921 GAAAAAGCATCTTGCATGAAATAGTACGTTGGGGGAAAGAAATTCATGCTAAGACTG 1980
QY 1981 GAGCTAGACACAAATGAAACATCAGAGCCAGCTAAATAAAAAAAAAAAAAAAAAAAAAA 2040
|||
Db 1981 GAGCTAGACACAAATGAAACATCAGAGCCAGCTAAATAAAAAAAAAAAAAAAAAAAAAA 2040

RESULT 31
US-09-924-400-303
: Sequence 303, Application US/09924400
: GENERAL INFORMATION:
: APPLICANT: Fridakis, Tony N.
: APPLICANT: Reed, Steven G.
: APPLICANT: Smith, John M.
: APPLICANT: Misner, Lynda E.
: APPLICANT: Dillon, Davin C.
: APPLICANT: Retter, Marc W.
: APPLICANT: Wang, Ajjun
: APPLICANT: Skeiky, Yasir A. W.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Day, Craig H.
: APPLICANT: Li, Samuel X.
: APPLICANT: Deng, Ta
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
: FILE REFERENCE: 210121.419C12
: CURRENT APPLICATION NUMBER: US/09/924,400
: NUMBER OF SEQ ID NOS: 340
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 303
: LENGTH: 2040
: TYPE: DNA
: ORGANISM: Homo sapiens
```

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US-09-924-400-303
Query Match 100.0%; Score 2040; DB 34; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2,7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGTGGATTCATGCGCGGCTGCTCTTCTGTGTAAGAACCAATTTGGTCTC 60
|||
Db 1 ATGGTGGTTGAGTGGATTCATGCGCGGCTGCTCTTCTGTGTAAGAACCAATTTGGTCTC 60
QY 61 AGAGCAAGATGGCGCAAGTGTGCTGCGTTCCTCCCTGCGAGGAGAGCGGCAAG 120
|||
Db 61 AGAGCAAGATGGCGCAAGTGTGCTGCGTTCCTCCCTGCGAGGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACCTTCTGAGAGACCACAGCACTCTGCTATGAAACACTCAGAGCAAG 180
|||
Db 121 AGCAACGTGGGCACCTTCTGAGAGACCACAGCACTCTGCTATGAAACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGGCTGCTCTTCCCTGCTGAGGGGAGTGGCAAGACGTCG 240
|||
Db 181 ATGGGCAAGTGGTGGCGGCTGCTCTTCCCTGCTGAGGGGAGTGGCAAGACGTCG 240
QY 241 GGGCGCTTGGAGACACGACGACTCTGCTATGAAACACTCAGAGCAAGTGGGCAAG 300
|||
Db 241 GGGCGCTTGGAGACACGACGACTCTGCTATGAAACACTCAGAGCAAGTGGGCAAG 300
QY 301 TGTGCTGCTGCTGCTTCCCTGCTGCTGAGGGGAGCGGCAAGAGTGGGCTTGG 360
|||
Db 301 TGTGCTGCTGCTGCTTCCCTGCTGCTGAGGGGAGCGGCAAGAGTGGGCTTGG 360
QY 361 GGAGACTGAGTGAACAGTGGCTCTCATGAGGCCAGGTCACAGTCGCTGGAGAAATCTG 420
|||
Db 361 GGAGACTGAGTGAACAGTGGCTCTCATGAGGCCAGGTCACAGTCGCTGGAGAAATCTG 420
QY 421 GACAACTCCACAGAGCTGCTGCTGAGGGAAGTCCCGAGAAAGATCTCATCTCATG 480
|||
Db 421 GACAACTCCACAGAGCTGCTGCTGAGGGAAGTCCCGAGAAAGATCTCATCTCATG 480
QY 481 CTCAGGGACACTGACGTGAACAGAGCAAGCAAAAGAGAGCTCTTACATCTGGCC 540
|||
Db 481 CTCAGGGACACTGACGTGAACAGAGCAAGCAAAAGAGAGCTCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTATGAAACCTCGCTGAGAGAGTGCATCTAAT 600
|||
Db 541 TCTGCCAATGGGAATTCAGAAAGTATGAAACCTCGCTGAGAGAGTGCATCTAAT 600
QY 601 GTCTTTGACAAACAAAAGAGGACAGCTCTGATTAAGGCGGTACATGCGCAGAGATGAA 660
|||
Db 601 GTCTTTGACAAACAAAAGAGGACAGCTCTGATTAAGGCGGTACATGCGCAGAGATGAA 660
QY 661 TGTGCGTTAATGTTCTGGAACATGGCACATGATCCAAATATTCCAGATGATGGAAT 720
|||
Db 661 TGTGCGTTAATGTTCTGGAACATGGCACATGATCCAAATATTCCAGATGATGGAAT 720
QY 721 ACCACTGTGCACTAGCTATCTATATGAAGTAATTAATGAGGCAAGCACTGCTCTTA 780
|||
Db 721 ACCACTGTGCACTAGCTATCTATATGAAGTAATTAATGAGGCAAGCACTGCTCTTA 780
QY 781 TATGCTGCTGATATGCAATCAAAAACAAAGATGGCTCACACCACTGTACTTGGTGA 840
|||
Db 781 TATGCTGCTGATATGCAATCAAAAACAAAGATGGCTCACACCACTGTACTTGGTGA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCAATTTAATGCA 900
|||
Db 841 CATGAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCAATTTAATGCA 900
QY 901 CTGATATATATGGAAGAGCTGCTCAGTCTGCTGATGATGTTGATGAGCAAGTATA 960
|||
Db 901 CTGATATATATGGAAGAGCTGCTCAGTCTGCTGATGATGTTGATGAGCAAGTATA 960
QY 961 GTCAAGCTTCTACTTGACCAAAATATTGATGATCTTCTCAAGATCTATCTGGACAGC 1020
|||
Db 961 GTCAAGCTTCTACTTGACCAAAATATTGATGATCTTCTCAAGATCTATCTGGACAGC 1020
```


Oy	1021	GCACAGAGATAGTGGCTTTCTTACGACATCATCATGTAAATTTGGCAGTATCTTTCAGACAC	1089
Oy	1021	GCACAGAGATAGTGGCTTTCTTACGACATCATCATGTAAATTTGGCAGTATCTTTCAGACAC	1089
Db	1021	GCACAGAGATAGTGGCTTTCTTACGACATCATCATGTAAATTTGGCAGTATCTTTCAGACAC	1089
Oy	1081	AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAACAGCAATCCAGAACAGACTTAAAG	1140
Db	1081	AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAACAGCAATCCAGAACAGACTTAAAG	1140
Oy	1141	CTGACATCAGAGGAAAGTGCACAAAGGTTCAAAGGACAGTGAATAATAGCCAGCCAGAGAA	1200
Db	1141	CTGACATCAGAGGAAAGTGCACAAAGGTTCAAAGGACAGTGAATAATAGCCAGCCAGAGAA	1200
Oy	1201	ATGTCTCAAGAACACAGAAATTAATTAAGAGTGGTATGATAGAGAGTGGTAAGAAACAAATGAAG	1260
Db	1201	ATGTCTCAAGAACACAGAAATTAATTAAGAGTGGTATGATAGAGAGTGGTAAGAAACAAATGAAG	1260
Oy	1261	AAGCATGAAAGTAATTAATGTGGGATTACTAGAAAACCTGACTAATGTGTCTACTGTGGC	1320
Db	1261	AAGCATGAAAGTAATTAATGTGGGATTACTAGAAAACCTGACTAATGTGTCTACTGTGGC	1320
Oy	1321	AATGGTGATATGATTAATTTCTCTCAAGGAGACAGAACCTGACTAATGTGTCTACTGTGGC	1380
Db	1321	AATGGTGATATGATTAATTTCTCTCAAGGAGACAGAACCTGACTAATGTGTCTACTGTGGC	1380
Oy	1381	CCTGCACACGAAAGTGAAGATATCACAGAAATTTGGCAATTAGTTTCTGACTACACAAAGAA	1440
Db	1381	CCTGCACACGAAAGTGAAGATATCACAGAAATTTGGCAATTAGTTTCTGACTACACAAAGAA	1440
Oy	1441	AAACAGATGCCAAATATCTTCTTGAAAACAGCACACCCAGAACAAAGACTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAATATCTTCTTGAAAACAGCACACCCAGAACAAAGACTTAAAGCTGACA	1500
Oy	1501	TCAGAGGAAGAGTGCACAAAGGCTTTGAGGGCAGTGAATAATGGCCAGCAGAGAAAAGACT	1560
Db	1501	TCAGAGGAAGAGTGCACAAAGGCTTTGAGGGCAGTGAATAATGGCCAGCAGAGAAAAGACT	1560
Oy	1561	CAAGAACCCAGAAATTAATTAAGATGGTGAATAGAGACTGAAAATTTTATGGCTATGCAA	1620
Db	1561	CAAGAACCCAGAAATTAATTAAGATGGTGAATAGAGACTGAAAATTTTATGGCTATGCAA	1620
Oy	1621	GAATGGAAGAAAGCAGGGAATCTCATGTTCGGATTTCCCGAATAACCTGACTAATGTGTCC	1680
Db	1621	GAATGGAAGAAAGCAGGGAATCTCATGTTCGGATTTCCCGAATAACCTGACTAATGTGTCC	1680
Oy	1681	ACTGCTGGCATGTGTGATGATGATTAAATTCCTCCAAAGGAAAGACAGAAACCTGACTAATGTGTCC	1740
Db	1681	ACTGCTGGCATGTGTGATGATGATTAAATTCCTCCAAAGGAAAGACAGAAACCTGACTAATGTGTCC	1740
Oy	1741	CAGCAATTTCTGCACTGAGAAATGGAAGATACACAGTGACGAAACAAATGATACTCAG	1800
Db	1741	CAGCAATTTCTGCACTGAGAAATGGAAGATACACAGTGACGAAACAAATGATACTCAG	1800
Oy	1801	AAGCAATTTTGTGAAGAACAGAACTGTGAATTAACAGAGATATCTGATTCATCAGAA	1860
Db	1801	AAGCAATTTTGTGAAGAACAGAACTGTGAATTAACAGAGATATCTGATTCATCAGAA	1860
Oy	1861	GAAGAACAGATAGAAAGTGTGTGAATAAATGAATTTGAGACCTTCTCTTATGTTGTAAGAAA	1920
Db	1861	GAAGAACAGATAGAAAGTGTGTGAATAAATGAATTTGAGACCTTCTCTTATGTTGTAAGAAA	1920
Oy	1921	GAAGAACAGATAGAAAGTGTGTGAATAAATGAATTTGAGACCTTCTCTTATGTTGTAAGAAA	1980
Db	1921	GAAGAACAGATAGAAAGTGTGTGAATAAATGAATTTGAGACCTTCTCTTATGTTGTAAGAAA	1980
Oy	1981	GAGCTAGACACATGAAACATTCAGACCCAGCTGAAAAAATTTGCAATGCTAAGACTG	2040
Db	1981	GAGCTAGACACATGAAACATTCAGACCCAGCTGAAAAAATTTGCAATGCTAAGACTG	2040

RESULT 32
US-10-006-920-375
; Sequence 375, Application US/10006920

```

; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/006,920
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-006-920-375

```

Query Match Similarity	100.0%	Score 2040;	DB 38;	Length 2040;
Best Local Similarity	100.0%	Pred. No. 2,7e-264;		
Matches 2040;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
QY	1	ATGCGTTGAGGTTGATTCATGCGCGCTGCGCTCTTCTGTGAGAGAGCCATTGGTCTC	60	
Db	1	ATGGTGTTGAGAGTTGATTCATGCGCGCTGCGCTCTTCTGTGAGAGAGCCATTGGTCTC	60	
QY	61	AGGACCAAGATGGGCAAGGAGTGCGCCGTTCCCTCGCTGGAGGGAGCGGCAG	120	
Db	61	AGGACCAAGATGGGCAAGGAGTGCGCCGTTCCCTCGCTGGAGGGAGCGGCAG	120	
QY	121	AGCAACGTGGGCACTTCTGGAGACCAGCAGCACTCTGCTATGAAAGACATCTGAGAGCAG	180	
Db	121	AGCAACGTGGGCACTTCTGGAGACCAGCAGCACTCTGCTATGAAAGACATCTGAGAGCAG	180	
QY	181	ATGGGCAAGTGGTGCGCGCACATGCTTCCCTGCTGCAGAGGGGAGTGGCAAGAGCAACG	240	
Db	181	ATGGGCAAGTGGTGCGCGCACATGCTTCCCTGCTGCAGAGGGGAGTGGCAAGAGCAACG	240	
QY	241	GGCGCTTCTGGAGACACGACGACCTCTATGAAAGACACTGAGAACAAATGGGCAG	300	
Db	241	GGCGCTTCTGGAGACACGACGACCTCTATGAAAGACACTGAGAACAAATGGGCAG	300	
QY	301	TGCTGCTCCACACTGCTTCCCTGCTGTCAGGGGAGACGGCAGAGCAAGTGGGCCCTGG	360	
Db	301	TGCTGCTCCACACTGCTTCCCTGCTGTCAGGGGAGACGGCAGAGCAAGTGGGCCCTGG	360	
QY	361	GGAGACTAGATGAGACAGTGCCTTCATGAGAGCCAGGATACAGTCCGTGAGAAATCTG	420	
Db	361	GGAGACTAGATGAGACAGTGCCTTCATGAGAGCCAGGATACAGTCCGTGAGAAATCTG	420	
QY	421	GACAAAGCTCCACAGAGCTGCTGGTGGGGTAAAGTCCCAAGAAAGATCTATCGTCAAG	480	
Db	421	GACAAAGCTCCACAGAGCTGCTGGTGGGGTAAAGTCCCAAGAAAGATCTATCGTCAAG	480	

QY 121 AGCAAGTGGGACCTTCTGAGACACGACGACTGCTATGAAAGCACTCAGAGCAAG 180
 |||||
 Db 121 AGCAAGTGGGACCTTCTGAGACACGACGACTGCTATGAAAGCACTCAGAGCAAG 180
 QY 181 ATGGGAAATGGTGGCCGACCTGCTTCCCTGCTGAGAGGGGAGTGGCAAGACAACTG 240
 |||||
 Db 181 ATGGGAAATGGTGGCCGACCTGCTTCCCTGCTGAGAGGGGAGTGGCAAGACAACTG 240
 QY 241 GGGGCTTCTGAGAGACGACGACTGCTGATGAAACACTCAGAAACAGATGGGCAAG 300
 |||||
 Db 241 GGGGCTTCTGAGAGACGACGACTGCTGATGAAACACTCAGAAACAGATGGGCAAG 300
 QY 301 TGGTGTGCACTGCTTCCCTGCTGAGAGGGGAGGCGCAAGAGCAAGTGGGCGCTGG 360
 |||||
 Db 301 TGGTGTGCACTGCTTCCCTGCTGAGAGGGGAGGCGCAAGAGCAAGTGGGCGCTGG 360
 QY 361 GAGAGATAGAGTAGAGTGGCTTCTGATGAGGCCAGGTACCAGTCCGCTGGAAGAGTCTG 420
 |||||
 Db 361 GAGAGATAGAGTAGAGTGGCTTCTGATGAGGCCAGGTACCAGTCCGCTGGAAGAGTCTG 420
 QY 421 GACAACTCCACAGACGCTGCTGGGGTAAAGTCCCGCAAGAGATCTCATGCTCATG 480
 |||||
 Db 421 GACAACTCCACAGACGCTGCTGGGGTAAAGTCCCGCAAGAGATCTCATGCTCATG 480
 QY 481 CTCAGGACACTGACGCTGAACAAGAGACAAAGCAAGAGACTGCTCATCTGCGCC 540
 |||||
 Db 481 CTCAGGACACTGACGCTGAACAAGAGACAAAGCAAGAGACTGCTCATCTGCGCC 540
 QY 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGAGACAGAGATGCTCAACTTAAT 600
 |||||
 Db 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGAGACAGAGATGCTCAACTTAAT 600
 QY 601 GTCTTGAACAACAAAAGAGAGACGCTGATTAAGGCCCTACATGCGCAAGAGATGA 660
 |||||
 Db 601 GTCTTGAACAACAAAAGAGAGACGCTGATTAAGGCCCTACATGCGCAAGAGATGA 660
 QY 661 TGTGCGTAAATGTTGCTGGAACATGGCACTGATCAAAATATTCAGATGATGGAAT 720
 |||||
 Db 661 TGTGCGTAAATGTTGCTGGAACATGGCACTGATCAAAATATTCAGATGATGGAAT 720
 QY 721 ACCACTCTGCACCTACCTATCTATTAATGAAGATTAATTAATGSCCAAGACCTGCTTA 780
 |||||
 Db 721 ACCACTCTGCACCTACCTATCTATTAATGAAGATTAATTAATGSCCAAGACCTGCTTA 780
 QY 781 TATGCTGCTGATATCGAATCAAAAACAAAGCATGGCCCTCACACACTGTTACTTGCTGA 840
 |||||
 Db 781 TATGCTGCTGATATCGAATCAAAAACAAAGCATGGCCCTCACACACTGTTACTTGCTGA 840
 QY 841 CATGAGCAAAAACAGCAAGTCTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
 |||||
 Db 841 CATGAGCAAAAACAGCAAGTCTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
 QY 901 CTGGATAGATATGGAAGGACTGCTCTCATCTGCTGATGTTGTGATAGCAAGTATA 960
 |||||
 Db 901 CTGGATAGATATGGAAGGACTGCTCTCATCTGCTGATGTTGTGATAGCAAGTATA 960
 QY 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGCAGAG 1020
 |||||
 Db 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGCAGAG 1020
 QY 1021 GCCAGAGATATGCTTCTTACTGATCATCATGATTAATTTGCGAGTTACTTCTGACTAC 1080
 |||||
 Db 1021 GCCAGAGATATGCTTCTTACTGATCATCATGATTAATTTGCGAGTTACTTCTGACTAC 1080
 QY 1081 AAGAGAAAAAGATGCTTAAAAATCTCTTCTGAAAAACAGCAATCAGAAACAGCTTAAG 1140
 |||||
 Db 1081 AAGAGAAAAAGATGCTTAAAAATCTCTTCTGAAAAACAGCAATCAGAAACAGCTTAAG 1140
 QY 1141 CTGACATCAGAGAGAGTACAAAGTTTCAAGGCGAGTGAATATGCGCCAGAGAA 1200
 |||||
 Db 1141 CTGACATCAGAGAGAGTACAAAGTTTCAAGGCGAGTGAATATGCGCCAGAGAA 1200
 QY 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGCTGATGAGAGGTTGAAGAAATGTAAG 1260

Db 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGCTGATGAGAGGTTGAAGAAATGAAG 1260
 |||||
 QY 1261 AAGCATGAAGATATATATGATGGATTAATGAGAAACCTGACTAATGCTGACTGCTGGC 1320
 |||||
 Db 1261 AAGCATGAAGATATATATGATGGATTAATGAGAAACCTGACTAATGCTGACTGCTGGC 1320
 QY 1321 AATGCTGATTAATGATTAATTTCTCAAGAGAGAGCAAGAACCTGATAATGCAATTT 1380
 |||||
 Db 1321 AATGCTGATTAATGATTAATTTCTCAAGAGAGAGCAAGAACCTGATAATGCAATTT 1380
 QY 1381 CCTGACAAACGAAAGTGAAGATATCACAGAAATTTGGGAATTAATTTCTGACTCAAGAA 1440
 |||||
 Db 1381 CCTGACAAACGAAAGTGAAGATATCACAGAAATTTGGGAATTAATTTCTGACTCAAGAA 1440
 QY 1441 AATGATGCTCAAAATATCTTCTGAAAAACAGCAACCCAGCAAGACTTAAAGCTGACA 1500
 |||||
 Db 1441 AATGATGCTCAAAATATCTTCTGAAAAACAGCAACCCAGCAAGACTTAAAGCTGACA 1500
 QY 1501 TCAGAGGAAGAGTTCACAAAGGCTTGAAGGCGAGTGAATAATGGCCAGAGAAAGATCT 1560
 |||||
 Db 1501 TCAGAGGAAGAGTTCACAAAGGCTTGAAGGCGAGTGAATAATGGCCAGAGAAAGATCT 1560
 QY 1561 CAAGAACACAGAAATTAATTAAGATGCTGATAGAGCTGAGAAATTTTATGCTATCGAA 1620
 |||||
 Db 1561 CAAGAACACAGAAATTAATTAAGATGCTGATAGAGCTGAGAAATTTTATGCTATCGAA 1620
 QY 1621 GAAATGAGAGAGCAGGAAGTACTCATGCTGAGTTCCCAAGAAACCTGACTAATGGTCC 1680
 |||||
 Db 1621 GAAATGAGAGAGCAGGAAGTACTCATGCTGAGTTCCCAAGAAACCTGACTAATGGTCC 1680
 QY 1681 ACTGCTGGCAATGCTGATGATGATTAATTTCTCAAGAGAGAGCAAGAACCTGAAAGC 1740
 |||||
 Db 1681 ACTGCTGGCAATGCTGATGATGATTAATTTCTCAAGAGAGAGCAAGAACCTGAAAGC 1740
 QY 1741 CAGCAATTTCTCTACACTGGAATGAAGATATACAGAGTACAGAAACAAATGATCTCAG 1800
 |||||
 Db 1741 CAGCAATTTCTCTACACTGGAATGAAGATATACAGAGTACAGAAACAAATGATCTCAG 1800
 QY 1801 AAGCAATTTTGTGAGAGACGAAACCTGGAATTTACAGATGAGATTTGATTTCATGA 1860
 |||||
 Db 1801 AAGCAATTTTGTGAGAGACGAAACCTGGAATTTACAGATGAGATTTGATTTCATGA 1860
 QY 1861 GAAAGCAGATAGAGGTTGTAAGAAATGAAATTTCTGAGCTTCTCTTACTGTAAGAA 1920
 |||||
 Db 1861 GAAAGCAGATAGAGGTTGTAAGAAATGAAATTTCTGAGCTTCTCTTACTGTAAGAA 1920
 QY 1921 GAAAAAGACATCTTGATGAAATTAATGATGCTTCCGGAGAGAAATTTGCCATGTAAGCTG 1980
 |||||
 Db 1921 GAAAAAGACATCTTGATGAAATTAATGATGCTTCCGGAGAGAAATTTGCCATGTAAGCTG 1980
 QY 1981 GAGCTGACACATGAAACATCAGAGCCACTGAAAAAATTTTTTTTTTTTTTTTTTTT 2040
 |||||
 Db 1981 GAGCTGACACATGAAACATCAGAGCCACTGAAAAAATTTTTTTTTTTTTTTTTTTT 2040

RESULT 34
 US-10-012-896-375

; Sequence 375, Application US/10012896
 ; GENERAL INFORMATION:

; APPLICANT: Xu, JIANGCHUN
 ; APPLICANT: Dillon, David C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aijun

Db 1741 CAGCAATTCCTGACACTGGAATGAAAGACTATCAGATGACGACAAACAAATGATCTACAG 1800
QY 1801 AAGCAATTTGTGAGAGACGACACTGGAATTTACAGATGAGATTCGATTCATGAA 1860
Db 1801 AAGCAATTTGTGAGAGACGACACTGGAATTTACAGATGAGATTCGATTCATGAA 1860
QY 1861 GAAAGCAGATAGAGTGTGAAAAAATGAAATTCGAGCTTCTCTTACTTGTAGAAA 1920
Db 1861 GAAAGCAGATAGAGTGTGAAAAAATGAAATTCGAGCTTCTCTTACTTGTAGAAA 1920
QY 1921 GAAAAAGACATCTTGCACTGAAAAATGACTGTCGGGAGAAAAATTCGATCTAGACTG 1980
Db 1921 GAAAAAGACATCTTGCACTGAAAAATGACTGTCGGGAGAAAAATTCGATCTAGACTG 1980
QY 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAA 2040
Db 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAA 2040

RESULT 35
US-10-079-137B-303
; Sequence 303, Application US/10079137B
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Lynda E.
; APPLICANT: Dillon, Davlin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A. W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; APPLICANT: Li, Samuel X.
; APPLICANT: Deng, Fa
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.419C13
; CURRENT APPLICATION NUMBER: US/10/079,137B
; CURRENT FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-079-137B-303

Query Match 100.0%; Score 2040; DB 39; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2,7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGTTGAGGTGATTCATGCGCGCTCTTCTGTGAAGAACCATTTGGCTC 60
Db 1 ATGCTGTTGAGGTGATTCATGCGCGCTCTTCTGTGAAGAACCATTTGGCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTCCCGTGTGAGAGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTCCCGTGTGAGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGACACGACGACTGTCTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTGAGACACGACGACTGTCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGCGCACTGCTCCCTGCTGCAAGGGGAGTGGCAAGACACGTG 240
Db 181 ATGGGCAAGTGTGCGCGCACTGCTCCCTGCTGCAAGGGGAGTGGCAAGACACGTG 240
QY 241 GGGCTTTCTGAGACGACGACGACTGTCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
Db 241 GGGCTTTCTGAGACGACGACGACTGTCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
QY 301 TGGTGTGCGCACATGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGGTGGCGCTTGG 360

Db 301 TGGTGTGCGCACATGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGGTGGCGCTTGG 360
QY 361 GGAGACTACGATACAGTGTGCTTCATGAGACCCAGGATACAGACCTCCGTGGAGAAAGATCTG 420
Db 361 GGAGACTACGATACAGTGTGCTTCATGAGACCCAGGATACAGACCTCCGTGGAGAAAGATCTG 420
QY 421 GACAACTCCACAGAGCTGCTGTGGGATTAAGTCCCGGAAAGATCTCATCTGCATG 480
Db 421 GACAACTCCACAGAGCTGCTGTGGGATTAAGTCCCGGAAAGATCTCATCTGCATG 480
QY 481 CTCAGGACACTGACGTGAACAAGAGACAAACAAAGAGACTGCTTACATCTGCGC 540
Db 481 CTCAGGACACTGACGTGAACAAGAGACAAACAAAGAGACTGCTTACATCTGCGC 540
QY 541 TCTGCCAATGGGAATTCAGAAATGATTAACCTCTGCTGACAGACGATCTCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATGATTAACCTCTGCTGACAGACGATCTCAACTTAAT 600
QY 601 GTCCCTTGACAAACAAAAAGAGACGCTGTGATTAAGCCCTACAAATGCGAGAAAGATGAA 660
Db 601 GTCCCTTGACAAACAAAAAGAGACGCTGTGATTAAGCCCTACAAATGCGAGAAAGATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGCGACTGATCCAATATTCAGATGATGGAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGCGACTGATCCAATATTCAGATGATGGAAT 720
QY 721 ACCACTGTGACATACGCTATCTAATGATTAATGATTAATGATGATGATGATGATGATGAT 780
Db 721 ACCACTGTGACATACGCTATCTAATGATTAATGATTAATGATGATGATGATGATGATGAT 780
QY 781 TATGCTGCTATATGCAATCAAAAAACAAAGATGCGCTCACACAGCTTACTTGGTGA 840
Db 781 TATGCTGCTATATGCAATCAAAAAACAAAGATGCGCTCACACAGCTTACTTGGTGA 840
QY 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATATGATATGAAAGAGATGCTGCTCATCTGCTGATGATGATGATGATGATGATGAT 960
Db 901 CTGATATGATATGAAAGAGATGCTGCTCATCTGCTGATGATGATGATGATGATGATGAT 960
QY 961 GTGAGCTTCTACTTGTGCAAAATATGATGATCTTCTCAAGATCATCTGAGACAGC 1020
Db 961 GTGAGCTTCTACTTGTGCAAAATATGATGATCTTCTCAAGATCATCTGAGACAGC 1020
QY 1021 GCCAGAGATGCTGTTCTAGTCATCATGATTAATTTGCCAGTACTTCTGACTAC 1080
Db 1021 GCCAGAGATGATGCTGTTCTAGTCATCATGATTAATTTGCCAGTACTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAAAATCTCTTGAAGAACGCAATCCAGAACAGACTTAAG 1140
Db 1081 AAGAAAAACAGATGCTAAAAATCTCTTGAAGAACGCAATCCAGAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCCAAAGGTTTCAAGGCAAGTGAATATGAGCCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGAGTCCAAAGGTTTCAAGGCAAGTGAATATGAGCCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACAGAAAAATTAAGATGATGATGAGAGGTTGAAGAAATGAAAG 1260
Db 1201 ATGTCTCAAGAACAGAAAAATTAAGATGATGATGAGAGGTTGAAGAAATGAAAG 1260
QY 1261 AAGCATGAAGATTAATATGTTGGGATTAATGATTAATGATTAATGATTAATGATTAAT 1320
Db 1261 AAGCATGAAGATTAATATGTTGGGATTAATGATTAATGATTAATGATTAATGATTAAT 1320
QY 1321 AATGATGATTAATGATTAATTTCTCAAGAGAGAGAGCAACACTGATTAATGATTAAT 1380
Db 1321 AATGATGATTAATGATTAATTTCTCAAGAGAGAGAGCAACACTGATTAATGATTAAT 1380
QY 1381 CTTGACAAACGAAAGTGAAGATATCAGAAATTTGGCAATTTTCTGACTCAAGAA 1440
Db 1381 CTTGACAAACGAAAGTGAAGATATCAGAAATTTGGCAATTTTCTGACTCAAGAA 1440

Db 1381 COTGACAAAGAAAGTGAAGAGTATCATCAGAAATTTGCGAATTTAGTTCTTGACTACAAAGAA 1440
QY 1441 AAAGAGATGCCAAATACCTCTTGAAAAACAGAACCCAGAACAGACTTAAGCTGANA 1500
Db 1441 AAACAGATGCCAAATACCTCTTGAAAAACAGAACCCAGAACAGACTTAAGCTGANA 1500
QY 1501 TCAGAGAAAGTGCACAAAGGCTTGAGGGCAGTGAATAATGCGCAGCAGAGAAAGATCT 1560
Db 1501 TCAGAGAAAGTGCACAAAGGCTTGAGGGCAGTGAATAATGCGCAGCAGAGAAAGATCT 1560
QY 1561 CAGACACAGAAATTAATTAAGAGTGTGATAGAGACTAGAAATTTATGCTATCGAA 1620
Db 1561 CAGACACAGAAATTAATTAAGAGTGTGATAGAGACTAGAAATTTATGCTATCGAA 1620
QY 1621 GAAATGAAGAAGCAGGAAAGTCTCATGCGGATTCGCCGAAACCTGACTAATGCTGCC 1680
Db 1621 GAAATGAAGAAGCAGGAAAGTCTCATGCGGATTCGCCGAAACCTGACTAATGCTGCC 1680
QY 1681 ACTGCTGGCAATGTGATGATGATTAATCTCCAGAGAGCAGACACCTGAAAGC 1740
Db 1681 ACTGCTGGCAATGTGATGATGATTAATCTCCAGAGAGACAGAACACCTGAAAGC 1740
QY 1741 CAGCAATTTCTTGACACTGAGAAATGAGATATCACAGTGAACCAAAATGATACTCAG 1800
Db 1741 CAGCAATTTCTTGACACTGAGAAATGAGATATCACAGTGAACCAAAATGATACTCAG 1800
QY 1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATTTACAGAGATGCTGTGATTCAGAA 1860
Db 1801 AAGCAATTTTGTGAAGAACAGAACACTGGAATTTACAGAGATGCTGTGATTCAGAA 1860
QY 1861 GAAAGACAGATAGATGCTGTGAAAAAATGAATTCGACCTTCTTGTAGTGAAGAA 1920
Db 1861 GAAAGACAGATAGATGCTGTGAAAAAATGAATTCGACCTTCTTGTAGTGAAGAA 1920
QY 1921 GAAAAAGACATTTCTTCAGTGAATAATAGTACGTTCCGGGAGAAATTCGCTAAGACTG 1980
Db 1921 GAAAAAGACATTTCTTCAGTGAATAATAGTACGTTCCGGGAGAAATTCGCTAAGACTG 1980
QY 1981 GAGCTAGACACATGAATCAATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAA 2040
Db 1981 GAGCTAGACACATGAATCAATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAA 2040

RESULT 36
US-10-144-678A-375
; Sequence 375, Application US/10144678A
; GENERAL INFORMATION:
; APPLICANT: Xu, JIANGCHUN
; APPLICANT: DILLON, Davin C.
; APPLICANT: MITCHEAM, Jennifer L.
; APPLICANT: HARLOCKER, Susan L.
; APPLICANT: JIANG, YUJUN
; APPLICANT: HENDERSON, Robert A.
; APPLICANT: KALOS, Michael D.
; APPLICANT: FANGER, Gary R.
; APPLICANT: RETTER, Marc W.
; APPLICANT: STOLK, John A.
; APPLICANT: DAY, Craig H.
; APPLICANT: VEDVICK, Thomas S.
; APPLICANT: CARTER, Darriick
; APPLICANT: LI, Samuel X.
; APPLICANT: WANG, Aijun
; APPLICANT: SKEIKY, Yasir A. W.
; APPLICANT: HEPLER, William T.
; APPLICANT: HURAL, John
; APPLICANT: MCNEILL, Patricia D.
; APPLICANT: HOUGHTON, Raymond L.
; APPLICANT: VINALS Y de Bassols, Carlota
; APPLICANT: FOY, Teresa M.
; APPLICANT: WATANABE, Yoshihiro
; APPLICANT: DENG, Ya
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C28
; CURRENT APPLICATION NUMBER: US/10/144,678A
; CURRENT FILING DATE: 2002-08-12
; NUMBER OF SEQ ID NOS: 1033
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-144-678A-375

Query Match 100.0%; Score 2040; DB 40; Length 2040;
Best Local Similarity 100.0%; Pred. No. 2.7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTGTTGAGTGTGATTCATATGCCGCTGCTCTTCTGTGAAGACCATTTGGTCTC 60
Db 1 ATGTGTGTTGAGTGTGATTCATATGCCGCTGCTCTTCTGTGAAGACCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGTGTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGTGCTGCGTGTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTTGAGACACAGACGACTCTGTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTTGAGACACAGACGACTCTGTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGCCGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGTGCGCCGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAAGCTG 240
QY 241 GGGGCTTGTGAGACACAGACGACTCTGTATGAAGACACTCAGAGCAAGTGGGCAAG 300
Db 241 GGGGCTTGTGAGACACAGACGACTCTGTATGAAGACACTCAGAGCAAGTGGGCAAG 300
QY 301 TGTGTGCTGCACTGCTTCCCTGCTGCTGAGGGGAGCGCAAGCAAGTGGGCGCTTG 360
Db 301 TGTGTGCTGCACTGCTTCCCTGCTGCTGAGGGGAGCGCAAGCAAGTGGGCGCTTG 360
QY 361 GGAAGCTACAGTACAGTCTCTCATGAGCCAGGTACACGCTCCGTGGAGAAATCTG 420
Db 361 GGAAGCTACAGTACAGTCTCTCATGAGCCAGGTACACGCTCCGTGGAGAAATCTG 420
QY 421 GACAAAGCTCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCATCGCATG 480
Db 421 GACAAAGCTCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCATCGCATG 480
QY 481 CTCAGGACACTGACGTGAACAAAGAGACAAAGAGCAAGGACTCTTACATCTGGCC 540
Db 481 CTCAGGACACTGACGTGAACAAAGAGACAAAGAGCAAGGACTCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAATGATAAATCTCTCTGAGACAGAGATGTCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATGATAAATCTCTCTGAGACAGAGATGTCAACTTAAT 600
QY 601 GTTCCTTGACAAACAAAAGAGGAGACGCTGTGATTAAGGCGGTACAAATGCCAGAAATGAA 660
Db 601 GTTCCTTGACAAACAAAAGAGGAGACGCTGTGATTAAGGCGGTACAAATGCCAGAAATGAA 660
QY 661 TGTGCTTAATGTTGTGGAACATGACACTGATCAAAATATTCAGATGAGTGAAT 720
Db 661 TGTGCTTAATGTTGTGGAACATGACACTGATCAAAATATTCAGATGAGTGAAT 720
QY 721 ACCACTCTGACACTAGCTATCTATAATGAAGATTAATTAAGGCCAAAGCACTGCTTA 780
Db 721 ACCACTCTGACACTAGCTATCTATAATGAAGATTAATTAAGGCCAAAGCACTGCTTA 780
QY 781 TATGTGCTGATATGCAATCAAAAGCAAGCATGGCTCAGACACATGTTACTTGGTGA 840
Db 781 TATGTGCTGATATGCAATCAAAAGCAAGCATGGCTCAGACACATGTTACTTGGTGA 840
QY 841 CATGACAAAGACAGAGTGTGAATTTTAATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGACAAAGACAGAGTGTGAATTTTAATCAAGAAAAAGCAATTTAAATGCA 900

Db 841 CATGACAAAAACGCAAGTCGTAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATAGATATGAGAGAGACTCTCTCATCTTGTATGTTGGATCAGCAATATA 960
|||
Db 901 CTGATAGATATGAGAGAGACTCTCTCATCTTGTATGTTGGATCAGCAATATA 960
QY 961 GTGACCTTCTACTTGGACAAATATTTGATGATCTTCTCAAGATCTATCTGACAGC 1020
|||
Db 961 GTGACCTTCTACTTGGACAAATATTTGATGATCTTCTCAAGATCTATCTGACAGC 1020
QY 1021 GCCAGAGATATGCTTTTCTAGTCATCATCATTAATTTTCCGCTACTTCTGACTAC 1080
|||
Db 1021 GCCAGAGATATGCTTTTCTAGTCATCATCATTAATTTTCCGCTACTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAAAATCTCTTGAAGAACAGCAATCCAGAAACAGACTTAAG 1140
|||
Db 1081 AAGAAAAACAGATGCTAAAAATCTCTTGAAGAACAGCAATCCAGAAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGTCAAAAGTTCAAGGCAAGTGAATTAAGCCAGAGAAA 1200
|||
Db 1141 CTGACATCAGAGAGAGTCAAAAGTTCAAGGCAAGTGAATTAAGCCAGAGAAA 1200
QY 1201 ATGCTCAGAGACGAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAAAGAAATGAG 1260
|||
Db 1201 ATGCTCAGAGACGAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAAAGAAATGAG 1260
QY 1261 AAGCATGAAGATTAATTAATGATGAGTACTAGAAAACCTGACTAATGCTGCTGCG 1320
|||
Db 1261 AAGCATGAAGATTAATTAATGATGAGTACTAGAAAACCTGACTAATGCTGCTGCG 1320
QY 1321 AATGCTATATGATTAATTTCTCAAGAGAGAGCAAGAACCTGAAATCAGCAATTT 1380
|||
Db 1321 AATGCTATATGATTAATTTCTCAAGAGAGAGCAAGAACCTGAAATCAGCAATTT 1380
QY 1381 CCTGACAGCAAGATGTAAGAGTATCAGAGATTTGCAATTAATTTGCTGACTAAGAA 1440
|||
Db 1381 CCTGACAGCAAGATGTAAGAGTATCAGAGATTTGCAATTAATTTGCTGACTAAGAA 1440
QY 1441 AAGCAGATGCCAAATACTCTTGTGAAGAACAGCAACCAGAACAGACTTAAGCTGACA 1500
|||
Db 1441 AAGCAGATGCCAAATACTCTTGTGAAGAACAGCAACCAGAACAGACTTAAGCTGACA 1500
QY 1501 TCAGAGAGAGTATCAAAAGCTTGAAGGCAAGTGAATTTGCGCCAGAGAGAAAAGTCT 1560
|||
Db 1501 TCAGAGAGAGTATCAAAAGCTTGAAGGCAAGTGAATTTGCGCCAGAGAGAAAAGTCT 1560
QY 1561 CAAGAACAGCAATTAATTAAGATGATGATGAGAGTTCAGAGAAACCTGACTAATGCTGCC 1620
|||
Db 1561 CAAGAACAGCAATTAATTAAGATGATGATGAGAGTTCAGAGAAACCTGACTAATGCTGCC 1620
QY 1621 GAAATGAAGAGACGGAAGTACTCATGTCGATTCAGAGAAACCTGACTAATGCTGCC 1680
|||
Db 1621 GAAATGAAGAGACGGAAGTACTCATGTCGATTCAGAGAAACCTGACTAATGCTGCC 1680
QY 1681 ACTGCTGGCAATGGTATGATGATTAATTTCTTCAAGAGAGAGCAACACTGAAAAGC 1740
|||
Db 1681 ACTGCTGGCAATGGTATGATGATTAATTTCTTCAAGAGAGAGCAACACTGAAAAGC 1740
QY 1741 CAGCAATTTCTGACTGAGATGAGAGTATCAGAGTGAAGAAATTAATGATGATGAG 1800
|||
Db 1741 CAGCAATTTCTGACTGAGATGAGAGTATCAGAGTGAAGAAATTAATGATGATGAG 1800
QY 1801 AAGCAATTTTGTGAAGAACAGAACTGGAATATTACAGAGTGAATTTGATTCATGAA 1860
|||
Db 1801 AAGCAATTTTGTGAAGAACAGAACTGGAATATTACAGAGTGAATTTGATTCATGAA 1860
QY 1861 GAAAAAGCAGATAGAGTGGTTGAAAAATGAATTTCTGAGCTTTCTTAACTGTAAGAAA 1920
|||
Db 1861 GAAAAAGCAGATAGAGTGGTTGAAAAATGAATTTCTGAGCTTTCTTAACTGTAAGAAA 1920
QY 1921 GAAAAAGCAGATTTGCAATGAATTAAGTAACTTGGGGGAGAAAGAAATTTGCCATGCTAAGACTG 1980
|||
Db 1921 GAAAAAGCAGATTTGCAATGAATTAAGTAACTTGGGGGAGAAAGAAATTTGCCATGCTAAGACTG 1980

QY 1981 GAGCTAGACACAAATGAACATCAGAGCCAGCTAATAAAAAAAAAAAAAAAAAAAAAA 2040
|||
Db 1981 GAGCTAGACACAAATGAACATCAGAGCCAGCTAATAAAAAAAAAAAAAAAAAAAAAA 2040
RESULT 37
US-10-212-679-303
; Sequence 303, Application us/10212679
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, Davin
; APPLICANT: Foy, Teresa
; APPLICANT: Houghton, Ray
; APPLICANT: Persing, David
; APPLICANT: Kalos, Michael
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.419C14
; CURRENT APPLICATION NUMBER: US/10/212,679
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ. ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-212-679-303
Query Match 100.0%; Score 2040; DB 42; Length 2040;
Best Local Similarly 100.0%; Pred. No. 2,7e-264;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTGTTGAGTGGTGAATTCATATGCGCGCTCCCTCTGTAAGAAAGCATTTGCTC 60
|||
Db 1 ATGCTGTTGAGTGGTGAATTCATATGCGCGCTCCCTCTGTAAGAAAGCATTTGCTC 60
QY 61 AGAGCAAGATGAGCAAGTGGTGGCTGCTTCCCTGCTGCTCAGAGAGCGGCAAG 120
|||
Db 61 AGAGCAAGATGAGCAAGTGGTGGCTGCTTCCCTGCTGCTCAGAGAGCGGCAAG 120
QY 121 AGCAAGCTGGGCACTTGTGAGACACAGACACTCTCTATGAAGACACTCAGAGCAAG 180
|||
Db 121 AGCAAGCTGGGCACTTGTGAGACACAGACACTCTCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGACGTG 240
|||
Db 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGACGTG 240
QY 241 GGCCTTCTGGAGACAGCAAGTCTGATGAAGACACTCAGAGAAAGATGGCAAG 300
|||
Db 241 GGCCTTCTGGAGACAGCAAGTCTGATGAAGACACTCAGAGAAAGATGGCAAG 300
QY 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGTGGCGCTTGG 360
|||
Db 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGTGGCGCTTGG 360
QY 361 GGAAGACTGAGTGAAGTGGCTTCCCTGATGAGAGCCAGAGTACAGCTGGGAGAACTG 420
|||
Db 361 GGAAGACTGAGTGAAGTGGCTTCCCTGATGAGAGCCAGAGTACAGCTGGGAGAACTG 420
QY 421 GACAAAGCTCCAGAGAGTGGCTGGTGGGTTAAAGTCCCAAGAAAGATCTCATGTCATG 480
|||
Db 421 GACAAAGCTCCAGAGAGTGGCTGGTGGGTTAAAGTCCCAAGAAAGATCTCATGTCATG 480
QY 481 CTCAGGAGCACTGACGTGAACAAGAAAGACAAGCAAGAAAAAGAGACTGCTTACATCGCC 540
|||
Db 481 CTCAGGAGCACTGACGTGAACAAGAAAGACAAGCAAGAAAAAGAGACTGCTTACATCGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGAGACAGAGATGCTCAACTTAAT 600
|||
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGAGACAGAGATGCTCAACTTAAT 600

Qy	601	GTGTTTGACACAAACAAAAGAGGAGACGCTGCTGATRAAGGCCGTRACATGCGCAGGAAGATGAA	660
Db	601	GTGCTTGACACAAACAAAAGAGGAGACGCTGATRAAAGGCCGTRACATGCGCAGGAAGATGAA	660
Qy	661	TGTGCGTATATGTTGCTGGCAACATGGCCACTGATGCCAAATATATCCAGATATGGAAT	720
Db	661	TGTGCGTATATGTTGCTGGCAACATGGCCACTGATGCCAAATATATCCAGATATGGAAT	720
Qy	721	ACCACTGTGCATACGCTATCTATATAATGAAGATAAATATATGGCCAAAGCACTGCTCTTA	780
Db	721	ACCACTGTGCATACGCTATCTATATAATGAAGATAAATATATGGCCAAAGCACTGCTCTTA	780
Qy	781	TATGGTGTCTATATTCGAATCAACAAAACAAGCATGGCCCTCACACACTGTACTGGTGTA	840
Db	781	TATGGTGTCTATATTCGAATCAACAAAACAAGCATGGCCCTCACACACTGTACTGGTGTA	840
Qy	841	CATGAGCAAAAACAGCAAGCGTGAAATTTTATATCAGAAAAAGCAATTAATAATGCA	900
Db	841	CATGAGCAAAAACAGCAAGCGTGAAATTTTATATCAGAAAAAGCAATTAATAATGCA	900
Qy	901	CTGGATATGATATGAAGAGCACTGCTCATACTTGGTATGTTGGATCCAGCAAGTATA	960
Db	901	CTGGATATGATATGAAGAGCACTGCTCATACTTGGTATGTTGGATCCAGCAAGTATA	960
Qy	961	GTCAGCCTTACTTACTGAGCAAAAATATTTGATATCTCTCAAGATCTATCTGAGACAGC	1020
Db	961	GTCAGCCTTACTTACTGAGCAAAAATATTTGATATCTCTCAAGATCTATCTGAGACAGC	1020
Qy	1021	GCCAGNAGATATCTGTTCTTCTAGTCATCATGTAATTTGGCAGTTACTTCTGACTAC	1080
Db	1021	GCCAGNAGATATCTGTTCTTCTAGTCATCATGTAATTTGGCAGTTACTTCTGACTAC	1080
Qy	1081	AAAGAAAAACAGATGCTAAAAAATCTCTTGTGAAAACAGCAATCCAGAACAGACTTAAG	1140
Db	1081	AAAGAAAAACAGATGCTAAAAAATCTCTTGTGAAAACAGCAATCCAGAACAGACTTAAG	1140
Qy	1141	CTGACATCAGAGGAGAAGAGTCACAAAGGTTCAAAAGCAGTGAATAATAGCCAGCCAGAGAA	1200
Db	1141	CTGACATCAGAGGAGAAGAGTCACAAAGGTTCAAAAGCAGTGAATAATAGCCAGCCAGAGAA	1200
Qy	1201	ATGTCCTAAGAACCCAGAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAATAGAG	1260
Db	1201	ATGTCCTAAGAACCCAGAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAATAGAG	1260
Qy	1261	AAGCATGAAGTATATATGTTGGGATATCTAGAAAACCTGACATAATGAGTGTACATGCTGCC	1320
Db	1261	AAGCATGAAGTATATATGTTGGGATATCTAGAAAACCTGACATAATGAGTGTACATGCTGCC	1320
Qy	1321	AATGCTATATATGATTAATTCCTCAAGAGAGACACAGAACCTCGAATAATCACAATTT	1380
Db	1321	AATGCTATATATGATTAATTCCTCAAGAGAGACACAGAACCTCGAATAATCACAATTT	1380
Qy	1381	CTGTACACAGAAAGTGAAGATATCAACAATAATTCGAATTTAGTTTCTGACTACAAAGAA	1440
Db	1381	CTGTACACAGAAAGTGAAGATATCAACAATAATTCGAATTTAGTTTCTGACTACAAAGAA	1440
Qy	1441	AAAAGATGGCAAAATATCTTCTGTGAAAACACCAACCCAGAACCAAGACTTAAAGCTGCA	1500
Db	1441	AAAAGATGGCAAAATATCTTCTGTGAAAACACCAACCCAGAACCAAGACTTAAAGCTGCA	1500
Qy	1501	TCAGAGCAAGAGTCACAAAGGCTTTGAGGGCAGTGAATAATGGCCAGCCAGACAAAAGATCT	1560
Db	1501	TCAGAGCAAGAGTCACAAAGGCTTTGAGGGCAGTGAATAATGGCCAGCCAGACAAAAGATCT	1560
Qy	1561	CAGAGACCAAGAAATTAATAAGATGCTGATAGAGACTAGAAAATTTTATGGCTATCGAA	1620
Db	1561	CAGAGACCAAGAAATTAATAAGATGCTGATAGAGACTAGAAAATTTTATGGCTATCGAA	1620
Qy	1621	GAATATGAAGAAGCAGGAAGTACTCATGTGCGGATTCACAGAAAACCTACTATATGTGTCC	1680
Db	1621	GAATATGAAGAAGCAGGAAGTACTCATGTGCGGATTCACAGAAAACCTACTATATGTGTCC	1680

Qy	1681	ACGCGTGGCAATGGTGAATGATGGATTATTTCTCCAAAGAAAGACAGAAACCTGAAAGC	1740
Db	1681	ACTGCTGGCAATGGTGAATGATGGATTATTTCTCCAAAGAAAGACAGAAACCTGAAAGC	1740
Qy	1741	CAGCAATTTCCCTGCACACTGAGAAATGAAGATGCACAGTGCAGAAACAAATGATACCTAG	1800
Db	1741	CAGCAATTTCCCTGCACACTGAGAAATGAAGATGCACAGTGCAGAAACAAATGATACCTAG	1800
Qy	1801	AAGCAATTTTGTGAAGAAGACAGAACCTGGAATATTACAGATGAGATTCGTATTCATGAA	1860
Db	1801	AAGCAATTTTGTGAAGAAGACAGAACCTGGAATATTACAGATGAGATTCGTATTCATGAA	1860
Qy	1861	GAAAAAGCAGATAGAAAGTGCTTGAAAAAATGAATTCGTGAGCTTCTCTTATGTTGTAAGAAA	1920
Db	1861	GAAAAAGCAGATAGAAAGTGCTTGAAAAAATGAATTCGTGAGCTTCTCTTATGTTGTAAGAAA	1920
Qy	1921	GAAAAAGACATCTTGCATGAAAAATGTAAGTCGTTGGCGGGAAGAAATTCGCATGCTAAGACTG	1980
Db	1921	GAAAAAGACATCTTGCATGAAAAATGTAAGTCGTTGGCGGGAAGAAATTCGCATGCTAAGACTG	1980
Qy	1981	GAGCTAGACACAAATGAACATCAGAGCCAGCTAAAAAATTTTTTTTTTTTTTTTTTTTTTTT	2040
Db	1981	GAGCTAGACACATATAACATCAGAGCCAGCTAAAAAATTTTTTTTTTTTTTTTTTTTTTTT	2040

```

RESULT 38
PCT-US02-24917-302
; Sequence 302, Application PC/TUS0224917
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, Davin C.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.41931PC
; CURRENT APPLICATION NUMBER: PCT/US02/24917
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-24917-302

Query Match          76.0%; Score 1551; DB 1; Length 2000;
Best Local Similarity 100.0%; Pred. No. 5e-199;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ATGGTGATTGGAGTGTGATTCATGCCGGCTGCCCTTCTGTGAAAGAACCATTTGGTCTC 60
DB      1  ATGGGTGTTGAGGTTTGATTCATGCCGGCTGCCCTTCTGTGAAAGAACCATTTGGTCTC 60

QY      61  AGGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTTCCCTGCTGCAGGAGAGCGGCAG 120
DB      61  AGGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTTCCCTGCTGCAGGAGAGCGGCAG 120

QY      121  AGCAACGTGGGCACTCTGTGGAGACCAAGAGACACTCTGTGAAAGCACTCAGAGCAG 180
DB      121  AGCAACGTGGGCACTCTGTGGAGACCAAGAGACACTCTGTGAAAGCACTCAGAGCAG 180

QY      181  ATGGCAGATGGTGCCTGGCACTGCTTCCCTGCTGCAGGGGGAGATGGCAAGACAACTG 240
DB      181  ATGGCAGATGGTGCCTGGCACTGCTTCCCTGCTGCAGGGGGAGATGGCAAGACAACTG 240

QY      241  GGCCTTCTGAGAGACCAAGACGACTGTGTTATGAGACACTCAGAAACAAGATGGCCAG 300
DB      241  GGCCTTCTGAGAGACCAAGACGACTGTGTTATGAGACACTCAGAAACAAGATGGCCAG 300

```


QY 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCTGCTGAGACAGATGTCACACTTAAT 600
|||||
Db 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCTGCTGAGACAGATGTCACACTTAAT 600
QY 601 GTCTTGCACAAACAAAAGAGAGACGCTGTGATAAAGCCGTCACATGCGCAGAGATGAA 660
|||||
Db 601 GTCTTGCACAAACAAAAGAGAGACGCTGTGATAAAGCCGTCACATGCGCAGAGATGAA 660
QY 661 TGTGGTAAATGTGCTGAGACATGCGCAGCTATCCAAATATTCAGATGATGTAAT 720
|||||
Db 661 TGTGGTAAATGTGCTGAGACATGCGCAGCTATCCAAATATTCAGATGATGTAAT 720
QY 721 ACCACTGCTGACACTAGCTATCTATATGAAATATTAATGAGCAAGCACTGCTCTTA 780
|||||
Db 721 ACCACTGCTGACACTAGCTATCTATATGAAATATTAATGAGCAAGCACTGCTCTTA 780
QY 781 TATGCTGCTGATTCGAAATCAAAAAACAAGATGCGCTCACACCACTGTACTGTGTA 840
|||||
Db 781 TATGCTGCTGATTCGAAATCAAAAAACAAGATGCGCTCACACCACTGTACTGTGTA 840
QY 841 CATGAGCAAAAACAGCAATGCTGAAATTTTAAATCAAGAAAAAAGCAATTTAAATGCA 900
|||||
Db 841 CATGAGCAAAAACAGCAATGCTGAAATTTTAAATCAAGAAAAAAGCAATTTAAATGCA 900
QY 901 CTGATATGATATGAGAGAGCTGCTCTCATCTGCTGATGTTGATGTCAGCAAGTATA 960
|||||
Db 901 CTGATATGATATGAGAGAGCTGCTCTCATCTGCTGATGTTGATGTCAGCAAGTATA 960
QY 961 CTCAGCCTTCTACTGAGCAAAATATGATGATCTCTCAAGATCTATCTGAGACAGAG 1020
|||||
Db 961 CTCAGCCTTCTACTGAGCAAAATATGATGATCTCTCAAGATCTATCTGAGACAGAG 1020
QY 1021 GCCAGAGAGTATGCTGTTCTAGTCATCATCATGTAATTTGCGCACTTACTTCTGACAC 1080
|||||
Db 1021 GCCAGAGAGTATGCTGTTCTAGTCATCATCATGTAATTTGCGCACTTACTTCTGACAC 1080
QY 1081 AAAGAAAACAGATGCTTAAATATCTCTCTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
|||||
Db 1081 AAAGAAAACAGATGCTTAAATATCTCTCTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGTCTACAAAGGTTCAAAGGAGTGAATATAGCCAGCAGAGAAA 1200
|||||
Db 1141 CTGACATCAGAGAGAGTCTACAAAGGTTCAAAGGAGTGAATATAGCCAGCAGAGAAA 1200
QY 1201 ATGCTCTAAGAGAGAGAGTAAATTAAGATGCTGATAGAGAGTGAAGAGAAATGAG 1260
|||||
Db 1201 ATGCTCTAAGAGAGAGAGTAAATTAAGATGCTGATAGAGAGTGAAGAGAAATGAG 1260
QY 1261 AAGCATGAAATGTAATATGTGGATTTACTAGAAAACCTGACTAATGTGTCTCTGCTG 1320
|||||
Db 1261 AAGCATGAAATGTAATATGTGGATTTACTAGAAAACCTGACTAATGTGTCTCTGCTG 1320
QY 1321 AATGCTGTAATGTAATTTCTCAAGAGAGAGACAGACCTGAAATATCAGCAATTT 1380
|||||
Db 1321 AATGCTGTAATGTAATTTCTCAAGAGAGAGACAGACCTGAAATATCAGCAATTT 1380
QY 1381 CCTGACAAAGAGAGAGAGTATCAGAAATTTGCGAATTAAGTTCTGACACTACAAAGAA 1440
|||||
Db 1381 CCTGACAAAGAGAGAGAGTATCAGAAATTTGCGAATTAAGTTCTGACACTACAAAGAA 1440
QY 1441 AAACAGATGCAAAATACTCTTCTGAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
|||||
Db 1441 AAACAGATGCAAAATACTCTTCTGAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGCAAGTGAATATGCGCAGCAGAG 1551
|||||
Db 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGCAAGTGAATATGCGCAGCAGAG 1551

RESULT 40
US-09-289-198-302
; Sequence 302, Application us/09289198
; GENERAL INFORMATION:

APPLICANT: Fridakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE REFERENCE: 210121.419C5
CURRENT APPLICATION NUMBER: US/09/289.198
EARLIER FILING DATE: 1998-04-09
EARLIER APPLICATION NUMBER: US 09/062.451
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: US 08/991.789
EARLIER FILING DATE: 1997-12-11
EARLIER APPLICATION NUMBER: US 08/838.762
EARLIER FILING DATE: 1997-04-09
EARLIER APPLICATION NUMBER: PCT/US97/00485
EARLIER FILING DATE: 1997-01-10
EARLIER APPLICATION NUMBER: US 08/700.014
EARLIER FILING DATE: 1996-08-20
EARLIER APPLICATION NUMBER: US 08/585.392
EARLIER FILING DATE: 1996-01-01
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 302
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-289-198-302

Query Match 76.0%; Score 1551; DB 16; Length 2000;
Best Local Similarity 100.0%; Pred. No. 5e-199;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTGTTGAGCTTGATTCATGCGCGCTGCTTCTGTGAGAACCATTTGCTC 60
Db 1 ATGTGTGTTGAGCTTGATTCATGCGCGCTGCTTCTGTGAGAACCATTTGCTC 60
QY 61 AGGACAGATGAGGAGAGGAGGCGGCTGCTCCCTGCTGAGGAGAGGCGCAAG 120
Db 61 AGGACAGATGAGGAGAGGAGGCGGCTGCTCCCTGCTGAGGAGAGGCGCAAG 120
QY 121 AGCAAGCTGGGCACTTCTGAGACACGACGACTGCTGATGAGACACTCAGAGCAAG 180
Db 121 AGCAAGCTGGGCACTTCTGAGACACGACGACTGCTGATGAGACACTCAGAGCAAG 180
QY 181 ATGGCAAGTGTGCGCGCAGCTGCTCCCTGCTCAGGGGAGTGGCAAGCAAGTG 240
Db 181 ATGGCAAGTGTGCGCGCAGCTGCTCCCTGCTCAGGGGAGTGGCAAGCAAGTG 240
QY 241 GGGCGTTTGGAGACAGAGACGACTGCTATGAGACACTCAGAGCAAGTGGGCAAG 300
Db 241 GGGCGTTTGGAGACAGAGACGACTGCTATGAGACACTCAGAGCAAGTGGGCAAG 300
QY 301 TGTGCTGCTGCACTGCTCCCTGCTGACAGGGGAGCGCAAGAGTGGCGCTGG 360
Db 301 TGTGCTGCTGCACTGCTCCCTGCTGACAGGGGAGCGCAAGAGTGGCGCTGG 360
QY 361 GGAGACTACGATGACAGTGTCTTCAATGAGCCAGGTACACGTCCTGAGAGATCTG 420
Db 361 GGAGACTACGATGACAGTGTCTTCAATGAGCCAGGTACACGTCCTGAGAGATCTG 420
QY 421 GACAGCTCCACAGAGCTGCTGAGGGGTAAGTCCCAAGAAAGATCTCATGCTCATG 480
Db 421 GACAGCTCCACAGAGCTGCTGAGGGGTAAGTCCCAAGAAAGATCTCATGCTCATG 480
QY 481 CTCAGGACACTGACGTACAGCAAGAGGAGCAAGCAAAAGAGAGTCTTACATCTGGCC 540
Db 481 CTCAGGACACTGACGTACAGCAAGAGGAGCAAGCAAAAGAGAGTCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCTGCTGAGACAGATGTCACACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCTGCTGAGACAGATGTCACACTTAAT 600

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QY 601 GTCTTGACACAAAAAGGAGACGCTGTGATTAAGGCGCTACAAATGCCGGAAGATGAA 660
DB GTCTTGACACAAAAAGGAGACGCTGTGATTAAGGCGCTACAAATGCCGGAAGATGAA 660
QY 661 TGTGCGTTAATGTTGGTGGAAATGGACGATGCAAAATTTCCAGATGATGTAAT 720
DB TGTGCGTTAATGTTGGTGGAAATGGACGATGCAAAATTTCCAGATGATGTAAT 720
QY 721 ACCACTCTGCACATACGCTATCTAATTAAGATTAATTAAGGCAAAAGCAGCTCTT 780
DB ACCACTCTGCACATACGCTATCTAATTAAGATTAATTAAGGCAAAAGCAGCTCTT 780
QY 781 TATGTCGTATATCCAAATAAAAAAGACATGCGCTCACACCACTGTTACTTGCTGA 840
DB TATGTCGTATATCCAAATAAAAAAGACATGCGCTCACACCACTGTTACTTGCTGA 840
QY 841 CATGAGCAAAAACAGCAAGCTGTAATTTTATCAAGAAAAAGGATTTAAATGCA 900
DB CATGAGCAAAAACAGCAAGCTGTAATTTTATCAAGAAAAAGGATTTAAATGCA 900
QY 901 CTGATATAGATATGAAGAGACGCTCTCATCTGATGTTGATGATGAGCAAGTATA 960
DB CTGATATAGATATGAAGAGACGCTCTCATCTGATGTTGATGATGAGCAAGTATA 960
QY 961 GTGACGCTTCTACTTGACAAAAATATTGATGTAATCTTCAAGATCTATGACAGAG 1020
DB GTGACGCTTCTACTTGACAAAAATATTGATGTAATCTTCAAGATCTATGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTTACTGATCATCATGATTAATTTGCGAGTTACTTGTGATAC 1080
DB GCCAGAGATATGCTGTTTACTGATCATCATGATTAATTTGCGAGTTACTTGTGATAC 1080
QY 1081 AAGAAAAACAGATGCTTAAATAATCTCTTCTGAAAAACAGCAATCCAGAACAGATTAAAG 1140
DB AAGAAAAACAGATGCTTAAATAATCTCTTCTGAAAAACAGCAATCCAGAACAGATTAAAG 1140
QY 1141 CTGACATCTAGAGAGAGATCACAAGGTTCAAGGCAAGTAAATAGCCAGCCAGAGAAA 1200
DB CTGACATCTAGAGAGAGATCACAAGGTTCAAGGCAAGTAAATAGCCAGCCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGATAGAGAGTTGAAGAAATGAAG 1260
DB ATGTCTCAAGAACAGAAATTAATTAAGATGATAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGAATTAATGATGAGATTACTAGAAACCTGACTAATGCTGCTGCTGCG 1320
DB AAGCATGAAGAATTAATGATGAGATTACTAGAAACCTGACTAATGCTGCTGCTGCG 1320
QY 1321 AATGTCGATTAATGATTAATCTCTCAAGAGAGAGACAGAACCTGAAATTCAGCAATTT 1380
DB AATGTCGATTAATGATTAATCTCTCTCAAGAGAGAGACAGAACCTGAAATTCAGCAATTT 1380
QY 1381 CCGTACAGCAAGAAATGAAGATATCAAGAAATTTGGAATTTAGTTCTGCTCAAAAGAA 1440
DB CCGTACAGCAAGAAATGAAGATATCAAGAAATTTGGAATTTAGTTCTGCTCAAAAGAA 1440
QY 1441 AAACAGATGCAAAATATCTTCTGAAAAAGCAGACCCAGAACAGACTTAAAGCTGACA 1500
DB AAACAGATGCAAAATATCTTCTGAAAAAGCAGACCCAGAACAGACTTAAAGCTGACA 1500
QY 1501 TCGAGAGAGAGATCACAAGGCTTGAGGCGAGTGAATAATGGCCAGCCAGAG 1551
DB TCGAGAGAGAGATCACAAGGCTTGAGGCGAGTGAATAATGGCCAGCCAGAG 1551

```

RESULT 41
US-09-429-755-302
Sequence 302, Application US/09429755A

GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda

```

; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-302

Query Match      76.0%; Score 1551; DB 18; Length 2000;
Best Local Similarity 100.0%; Pred No. 5e-199;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTTGAGGTTGATTCATATGCGGCTGCTCTTCTGGAAGAGCCATTGCTTC 60
DB 1 ATGTGTTGAGGTTGATTCATATGCGGCTGCTCTTCTGGAAGAGCCATTGCTTC 60
QY 61 AGAGCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGTCAGGAGAGCGGCAAG 120
DB 61 AGAGCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGTCAGGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACACAGACGACTGCTTGAAGACATCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACACAGACGACTGCTTGAAGACATCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGTCAGGAGGAGTGGCAAGCAAG 240
DB 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGTCAGGAGGAGTGGCAAGCAAG 240
QY 241 GGGCTTCTGGAACACACAGCACTGCTATTAAGACATCAGGAACAGATGGGCAAG 300
DB 241 GGGCTTCTGGAACACACAGCACTGCTATTAAGACATCAGGAACAGATGGGCAAG 300
QY 301 TGGTGTGCGCCACTGCTTCCCTGCTGTCAGGAGGAGGCAAGGATGGGCGCTTG 360
DB 301 TGGTGTGCGCCACTGCTTCCCTGCTGTCAGGAGGAGGCAAGGATGGGCGCTTG 360
QY 361 GGAGACTACGATGACAGTGTGCTTCAATGAGGCCAGGATACACGCTCGTGAGAGATCTG 420
DB 361 GGAGACTACGATGACAGTGTGCTTCAATGAGGCCAGGATACACGCTCGTGAGAGATCTG 420
QY 421 GACAAAGTCCACAGAGCTGCTGCTGTTAAAGTCCCGAAGAGATCTCATGCTCATG 480
DB 421 GACAAAGTCCACAGAGCTGCTGCTGTTAAAGTCCCGAAGAGATCTCATGCTCATG 480
QY 481 CTCAGGACATGACGCTGAGCAAGAAAGAGACAAAGAGAGCTGCTACATCTGCGC 540
DB 481 CTCAGGACATGACGCTGAGCAAGAAAGAGAGACAAAGAGAGCTGCTACATCTGCGC 540
QY 541 TCTGCAATGGAATTCAGAAATAGTAAATCTCTGCTGAGACAGAGATGCAACTTAAT 600
DB 541 TCTGCAATGGAATTCAGAAATAGTAAATCTCTGCTGAGACAGAGATGCAACTTAAT 600
QY 601 GTCTTGACACAAAAAGGAGACGCTGTGATTAAGGCGCTACAAATGCCGGAAGATGAA 660
DB 601 GTCTTGACACAAAAAGGAGACGCTGTGATTAAGGCGCTACAAATGCCGGAAGATGAA 660
QY 661 TGTGCGTTAATGTTGGTGGAAATGGACGATGCAAAATTTCCAGATGATGTAAT 720
DB 661 TGTGCGTTAATGTTGGTGGAAATGGACGATGCAAAATTTCCAGATGATGTAAT 720
QY 721 ACCACTCTGCACATACGCTATCTAATTAAGATTAATTAAGGCAAAAGCAGCTCTT 780
DB 721 ACCACTCTGCACATACGCTATCTAATTAAGATTAATTAAGGCAAAAGCAGCTCTT 780
QY 781 TATGTCGTATATCCAAATAAAAAAGACATGCGCTCACACCACTGTTACTTGCTGA 840
DB 781 TATGTCGTATATCCAAATAAAAAAGACATGCGCTCACACCACTGTTACTTGCTGA 840

```

Db 781 TATGTCGTGATATGCAATCAAAAAACAAGATGGCTCACACACTGTACTGTGTGA 840
Qy 841 CATGAGCAAAAAACAGACAGTCGTGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGACAGTCGTGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
Qy 901 CTGATAGATATGGAAGAGCTGCTCATACTTGTGTATGTGTGATGATGACAGATATA 960
Db 901 CTGATAGATATGGAAGAGCTGCTCATACTTGTGTATGTGTGATGATGACAGATATA 960
Qy 961 CTCAGCCTTCTACTTGACCAAAATTTGATGATCTTCTCAAGATCTATCTGGACAGAG 1020
Db 961 CTCAGCCTTCTACTTGACCAAAATTTGATGATCTTCTCAAGATCTATCTGGACAGAG 1020
Qy 1021 GCCAGAGATATGCTGTTCTAGTCATCATCTAATTTGGCCATTTCTTCTGACATC 1080
Db 1021 GCCAGAGATATGCTGTTCTAGTCATCATCTAATTTGGCCATTTCTTCTGACATC 1080
Qy 1081 AAAAGAAAAACAGATCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
Db 1081 AAAAGAAAAACAGATCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
Qy 1141 CTGACATCAGAGGAAGAGTCCACAAAGTTCAAGGCGAGTGAATAATGCCAGCAGAGAAA 1200
Db 1141 CTGACATCAGAGGAAGAGTCCACAAAGTTCAAGGCGAGTGAATAATGCCAGCAGAGAAA 1200
Qy 1201 ATGTCCTAAGAACCAAGATTAATTAAGAGTGGTGTATAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGTCCTAAGAACCAAGATTAATTAAGAGTGGTGTATAGAGGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAGATTAATTAATGAGGATTTACTAGAAAACTGACTAATGTTCTACTGCTGCG 1320
Db 1261 AAGCATGAAGATTAATTAATGAGGATTTACTAGAAAACTGACTAATGTTCTACTGCTGCG 1320
Qy 1321 AATGTTGATTAATGATTAATTTCTTCTCAAGAGGAGCAGACACCTGAAATATGCAATTT 1380
Db 1321 AATGTTGATTAATGATTAATTTCTTCTCAAGAGGAGCAGACACCTGAAATATGCAATTT 1380
Qy 1381 CCTGACACGAAGAGAGATGATCAGAAATTTGGAATTTGTTCTGATCTACCAAGAA 1440
Db 1381 CCTGACACGAAGAGAGATGATCAGAAATTTGGAATTTGTTCTGATCTACCAAGAA 1440
Qy 1441 AAACGATGCCAAATACTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db 1441 AAACGATGCCAAATACTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Qy 1501 TCAGAGGAAGAGTCCAAAGGCTTGAGGGCAGTGAATGGCCAGCCAGAG 1551
Db 1501 TCAGAGGAAGAGTCCAAAGGCTTGAGGGCAGTGAATGGCCAGCCAGAG 1551

RESULT 42
US-09-443-686-374
; Sequence 374, Application US/09443686
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jlang Yungui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solik, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 21021.427C9A
; CURRENT APPLICATION NUMBER: US/09/443,686
; CURRENT FILING DATE: 1999-11-18
; NUMBER OF SEQ ID NOS: 351
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-443-686-374

Query Match 76.0%; Score 1551; DB 18; Length 2000;
Best Local Similarity 100.0%; Pred. No. 5e-199;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGTGTTGAGCTGATTCATGCCGGCTGCTCTTCTGTGAAGAGCAATTTGGTCTC 60
Db 1 ATGTGTGTTGAGCTGATTCATGCCGGCTGCTCTTCTGTGAAGAGCAATTTGGTCTC 60
Qy 61 AGGACCAAGATGGGAAGGAGTGGCGGTGCTTCCCTGCTGAGGAGGAGCGGCAAG 120
Db 61 AGGACCAAGATGGGAAGGAGTGGCGGTGCTTCCCTGCTGAGGAGGAGCGGCAAG 120
Qy 121 AGCAACGTGGGCACTTCTTGAGACACGACGACTCTGTATGAAAGCACTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTTGAGACACGACGACTCTGTATGAAAGCACTCAGAGCAAG 180
Qy 181 ATGGCCAAAGTGGTCCCGCCTGCTTCCCTCTGCGAGGGGAGTGGCAAGCAACTG 240
Db 181 ATGGCCAAAGTGGTCCCGCCTGCTTCCCTCTGCGAGGGGAGTGGCAAGCAACTG 240
Qy 241 GGGCGTTCTGAGACACGACGACTCTGTATGAAAGCACTCAGAGCAAGATGGGCAAG 300
Db 241 GGGCGTTCTGAGACACGACGACTCTGTATGAAAGCACTCAGAGCAAGATGGGCAAG 300
Qy 301 TGGTCTGTCACACTGCTTCCCTGCTGACAGGGGAGCGCAAGAGTGGGCGCTTGG 360
Db 301 TGGTCTGTCACACTGCTTCCCTGCTGACAGGGGAGCGCAAGAGTGGGCGCTTGG 360
Qy 361 GGAGACTACGATGACAGTCCCTTCAATGAGCCAGTACAGTCCCTGGAAGATCTG 420
Db 361 GGAGACTACGATGACAGTCCCTTCAATGAGCCAGTACAGTCCCTGGAAGATCTG 420
Qy 421 GACAAGCTCCACAGAGCTGCTGAGGGGTAAAGTCCCGAAGAGATCTCATGCTGATG 480
Db 421 GACAAGCTCCACAGAGCTGCTGAGGGGTAAAGTCCCGAAGAGATCTCATGCTGATG 480
Qy 481 CTCAGGAGACACTGAGTGAACAAAGAGCAAGAAAGAGCACTGCTTACATCTGGCC 540
Db 481 CTCAGGAGACACTGAGTGAACAAAGAGCAAGAAAGAGCACTGCTTACATCTGGCC 540
Qy 541 TCTGCCAATGGGAATTCAGAGTAAATCTCTGCTGACAGAGATGTCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAGTAAATCTCTGCTGACAGAGATGTCAACTTAAT 600
Qy 601 GTCCCTTGCAAAAAAGAGACAGCTCTGATTAAGGCGGTCAATGCCAGAAAGATGAA 660
Db 601 GTCCCTTGCAAAAAAGAGAGACAGCTCTGATTAAGGCGGTCAATGCCAGAAAGATGAA 660
Qy 661 TGTGCTTAATGTTCTGGAACATGGCACTGATCCAAATATTCAGATAGTAAAT 720
Db 661 TGTGCTTAATGTTCTGGAACATGGCACTGATCCAAATATTCAGATAGTAAAT 720
Qy 721 ACCACTCTGCACTACGCTATCTAATGAAGATTAATTAATGAGCCAAAGCACTGCTT 780
Db 721 ACCACTCTGCACTACGCTATCTAATGAAGATTAATTAATGAGCCAAAGCACTGCTT 780
Qy 781 TATGTCGTGATATGCAATCAAAAAACAAGCAATGGCTCACACACTGTACTGTGTGA 840
Db 781 TATGTCGTGATATGCAATCAAAAAACAAGCAATGGCTCACACACTGTACTGTGTGA 840
Qy 841 CATGAGCAAAAAACAGACAGTCGTGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGACAGTCGTGAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
Qy 901 CTGATAGATATGGAAGAGCTGCTCATACTTGTGTATGTGTGATGATGACAGATATA 960
Db 901 CTGATAGATATGGAAGAGCTGCTCATACTTGTGTATGTGTGATGATGACAGATATA 960

|||||
Db 1021 GCCAAGAGTATGCTGTTCTAGTCATCATGTAAATTCGCACTACTTCTGACTAC 1080
Qy 1081 AAGAAAAACAGATGCTAAAAATCTCTCTGAAAACAGCAATCCCAACACTTAAAG 1140
Db 1081 AAGAAAAACAGATGCTAAAAATCTCTCTGAAAACAGCAATCCCAACACTTAAAG 1140
Qy 1141 CTGACATCAGAGAGAGTCTCAAAAGTTCAAAAGCAGTGAATAATAGCCAGCAGANA 1200
Db 1141 CTGACATCAGAGAGAGTCTCAAAAGTTCAAAAGCAGTGAATAATAGCCAGCAGANA 1200
Qy 1201 ATGTCCTCAAGAACAGAAATAAATAAGAGTGTATAGAGAGTTGAAGAATAAGAA 1260
Db 1201 ATGTCCTCAAGAACAGAAATAAATAAGAGTGTATAGAGAGTTGAAGAATAAGAA 1260
Qy 1261 AAGCATGAAGTAAATATGTTGGATTAATAGAAAACCTGACTAAATGTCCTCTGGC 1320
Db 1261 AAGCATGAAGTAAATATGTTGGATTAATAGAAAACCTGACTAAATGTCCTCTGGC 1320
Qy 1321 AATGCTGATTAATGATTAATTCCTCAAAAGAGACAGAACACTGAAAATCAGCAATT 1380
Db 1321 AATGCTGATTAATGATTAATTCCTCAAAAGAGACAGAACACTGAAAATCAGCAATT 1380
Qy 1381 CCTGACAAAGAAAGTGAAGATATCACAGAAATTCGCAATTAGTTCTGACTACAAAGAA 1440
Db 1381 CCTGACAAAGAAAGTGAAGATATCACAGAAATTCGCAATTAGTTCTGACTACAAAGAA 1440
Qy 1441 AAACGATGCCAAATTAATCTCTCTCAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db 1441 AAACGATGCCAAATTAATCTCTCTCAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Qy 1501 TCAGAGAGAGTCAAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551
Db 1501 TCAGAGAGAGTCAAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551

RESULT 44
US-09-534-825A-302

; Sequence 302, Application US/09534825A
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, David C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C7
; CURRENT APPLICATION NUMBER: US/09/534.825A
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 317
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-534-825A-302

Query Match 76.0%; Score 1551; DB 20; Length 2000;
Best Local Similarity 100.0%; Pred. No. 5e-199;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGCTTGAAGTTCATTCATGCGGCTGCTCTTCTGTGAAGAGCATTGTGCTC 60
Db 1 ATGCTGCTTGAAGTTCATTCATGCGGCTGCTCTTCTGTGAAGAGCATTGTGCTC 60
Qy 61 AGAGCAAGATGAGCAAGTGTGCTGCTGCTTCCCTGCTGAGGAGAGCGGCAAG 120
Db 61 AGAGCAAGATGAGCAAGTGTGCTGCTGCTTCCCTGCTGAGGAGAGCGGCAAG 120
Qy 121 AGCAAGCTGGGCACTTCTGAGACACAGACGACTGCTATGAAGACACTCGAGCAAG 180
Db 121 AGCAAGCTGGGCACTTCTGAGACACAGACGACTGCTATGAAGACACTCGAGCAAG 180

Db 121 AGCAAGCTGGGCACTTCTGAGACACAGACGACTGCTATGAAGACACTCGAGCAAG 180
Qy 181 ATGGGCAAGTGGTGGCGCCACAGTCTCCCTCTGAGGGGAGTGGCAAGCAACGCG 240
Db 181 ATGGGCAAGTGGTGGCGCCACAGTCTCCCTCTGAGGGGAGTGGCAAGCAACGCG 240
Qy 241 GCGGCTTCTGAGAGACACAGACACTCTGCTATGAAGACACTGAGAACAGATGGGCAAG 300
Db 241 GCGGCTTCTGAGAGACACAGACACTCTGCTATGAAGACACTGAGAACAGATGGGCAAG 300
Qy 301 TGGTCTGCTGCTCTCCCTCTGCTGACAGGGGAGCGGCAAGAGCAAGTGGGCGCTGG 360
Db 301 TGGTCTGCTGCTCTCCCTCTGCTGACAGGGGAGCGGCAAGAGCAAGTGGGCGCTGG 360
Qy 361 GGAGACTACGATGACAGTCCCTTCATGGAGCCAGGTACCAGTCCCTGAGCAAAATCTG 420
Db 361 GGAGACTACGATGACAGTCCCTTCATGGAGCCAGGTACCAGTCCCTGAGCAAAATCTG 420
Qy 421 GACAAAGCTCCACAGAGCTCTGCTGGGGTAAAGTCCCGAAGAGATCTCATGCTCATG 480
Db 421 GACAAAGCTCCACAGAGCTCTGCTGGGGTAAAGTCCCGAAGAGATCTCATGCTCATG 480
Qy 481 CTCAGGGACACTGACGTGAACAAGAACAAAGAGAGAGACTGCTTACATCTGGCC 540
Db 481 CTCAGGGACACTGACGTGAACAAGAACAAAGAGAGAGACTGCTTACATCTGGCC 540
Qy 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCTCTGACAGACAGATGCTCAACTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCTCTGACAGAGATGCTCAACTAAT 600
Qy 601 GTCTTTGACAAACAAAAGAGACAGCTCTGATTAAGGGCGTCAATGCCAGAGATGAA 660
Db 601 GTCTTTGACAAACAAAAGAGACAGCTCTGATTAAGGGCGTCAATGCCAGAGATGAA 660
Qy 661 TGTGCGTTAATGTGCTGAGACATGGCAGTATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGCGTTAATGTGCTGAGACATGGCAGTATCCAAATATTCAGATGATGGAAT 720
Qy 721 ACCACTCTGCACTAGCTATCTATATGAAGTAAATTAATGGCCAAACACTGCTCTTA 780
Db 721 ACCACTCTGCACTAGCTATCTATATGAAGTAAATTAATGGCCAAACACTGCTCTTA 780
Qy 781 TATGCTGCTGATATGAAATCAAAAAACAAGCATGGGCTCACACACTGTTACTGGTGA 840
Db 781 TATGCTGCTGATATGAAATCAAAAAACAAGCATGGGCTCACACACTGTTACTGGTGA 840
Qy 841 CATGAGCAAAAAACAGCAAGTCTGAATTTTAATCAGAAAAAAGCGAATTTAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTCTGAATTTTAATCAGAAAAAAGCGAATTTAATGCA 900
Qy 901 CTGATAGATATGGAAGACCTGCTCATACTTGTCTGTATGTTGGATCAGCAAGTATA 960
Db 901 CTGATAGATATGGAAGACCTGCTCATACTTGTCTGTATGTTGGATCAGCAAGTATA 960
Qy 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCCAGATCTATCTGGACAGAG 1020
Db 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCCAGATCTATCTGGACAGAG 1020
Qy 1021 GCCAGAGATATGCTTTCTAGTCATCATGTAAATTCGCACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTTTCTAGTCATCATGTAAATTCGCACTTCTGACTAC 1080
Qy 1081 AAGAAAAACAGATGCTAAAAATCTCTCTGAAAACAGCAATCCCAACACTTAAAG 1140
Db 1081 AAGAAAAACAGATGCTAAAAATCTCTCTGAAAACAGCAATCCCAACACTTAAAG 1140
Qy 1141 CTGACATCAGAGAGAGTCTCAAAAGTTCAAAAGCAGTGAATAATAGCCAGCAGANA 1200
Db 1141 CTGACATCAGAGAGAGTCTCAAAAGTTCAAAAGCAGTGAATAATAGCCAGCAGANA 1200
Qy 1201 ATGTCCTCAAGAACAGAAATAAATAAGAGTGTATAGAGAGTTGAAGAATAAGAA 1260
Db 1201 ATGTCCTCAAGAACAGAAATAAATAAGAGTGTATAGAGAGTTGAAGAATAAGAA 1260

Qy	1261	AAGATGAAGTATATATGCGGGATCTACTAGAAACCTGACTAAATGGTGTCACGTGGC	1320
Db	1261	AAGATGAAGTATATATGCGGGATCTACTAGAAACCTGACTAAATGGTGTCACGTGGC	1320
Qy	1321	AATGGTATATATGATTAATTTCTCCAAGGAAGCAGAAACCTGAAATCAGCAATTT	1380
Db	1321	AATGGTATATGATTAATTTCTCCAAGGAAGCAGAAACCTGAAATCAGCAATTT	1380
Qy	1381	CCTACACCAAGAAAGTGAAGGATTCACACAAATTTGGCATTTAGTTCTGCATCAACAATAA	1440
Db	1381	CCTACACCAAGAAAGTGAAGGATTCACACAAATTTGGCATTTAGTTCTGCATCAACAATAA	1440
Qy	1441	AAACAGATGCCAAATATCTTCTTCGAAAAACAGCAACCCGAACAAGACTTAAAGCTGCACA	1500
Db	1441	AAACAGATGCCAAATATCTTCTTCGAAAAACAGCAACCCGAACAAGACTTAAAGCTGCACA	1500
Qy	1501	TCAAGGAAGATGCACAAAGGCTTGAGGGCAGTGAATAATGGCCACGACGAG	1551
Db	1501	TCAAGGAAGATGCACAAAGGCTTGAGGGCAGTGAATAATGGCCACGACGAG	1551

RESULT 45
US-09-536-857-374

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; Sequence 374, Application US/09536857
; GENERAL INFORMATION:

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1  APPLICANT: Xu, Jiangchun
2  APPLICANT: Dillon, Davin C.
3  APPLICANT: Mitcham, Jennifer L.
4  APPLICANT: Harlocker, Susan L.
5  APPLICANT: JIANG, YUQU
6  APPLICANT: Reed, Steven G.
7  APPLICANT: Kalos, Michael D.
8  APPLICANT: Fanger, Gary R.
9  APPLICANT: Retter, Marc W.
10 APPLICANT: Stolk, John A.
11 APPLICANT: Day, Craig H.
12
13 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
14 FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
15 FILE REFERENCE: 2101.1.4271C12
16 CURRENT APPLICATION NUMBER: US/09/536,857
17 CURRENT FILING DATE: 2000-03-27
18 NUMBER OF SEQ ID NOS: 592
19 SOFTWARE: FastSeq for Windows Version 3.0
20 SEQ ID NO 374
21
22 LENGTH: 2000
23
24 TYPE: DNA
25 ORGANISM: Homo sapien
26
27 US-09-536-857-374

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Query Match	76.0%;	Score 1551;	DB 20;	Length 2000;
Best Local Similarity	100.0%;	Pred. No. 5e-199;		
Matches 1551;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0

Oy	1	ATGGGGTTGAGAGTTGATTCATCGCCGGCTCCCTCTTGTGAAGAAACATTTGGCTC	60
Db	1	ATGGGGTTGAGAGTTGATTCATCGCCGGCTCCCTCTTGTGAAGAAACCATTTGGCTC	60
Oy	61	AGGACCAAGATGGGCAAGTGTGCTGCCGTGCTTCCCTCTCTGACAGGAGAGCGGCAG	120
Db	61	AGGACCAAGATGGGCAAGTGTGCTGCCGTGCTTCCCTCTCTGACAGGAGAGCGGCAG	120
Oy	121	AGCAACGATGGGCACTTCTGGAGACACGAGACACTCTGTATGAAGACACTCAGGAGCAG	180
Db	121	AGCAACGATGGGCACTTCTGGAGACACGAGACACTCTGTATGAAGACACTCAGGAGCAG	180
Oy	181	ATGGGCAAGTGGTGCCTGCTTCCCTCCCTGTCAGGGGGAATGGCAAGAGCAACGTG	240
Db	181	ATGGGCAAGTGGTGCCTGCTTCCCTCCCTGTCAGGGGGAATGGCAAGAGCAACGTG	240
Oy	241	GGCGTTTGGAGACACAGACGACTCTGTATGAAGACACTCAGGAACCAAGTGGGCAAG	300
Db	241	GGCGTTTGGAGACACAGACGACTCTGTATGAAGACACTCAGGAACCAAGTGGGCAAG	300

QY	301	TGAGGTGGCCACCTGCTTCCCTGCTGGAGGGGAGCGGCAAGAGCAAGTGGGCGCTTG	360
Db	301	TGGTGTCTCCACTCTTCCCTGCTGTCGAGGGGAGCGGCAAGACAAAGTGGGCGCTTG	360
QY	361	GGAGACTACGATGACAGTGCCTTCATGAGAGCCCGATACCAAGTCCGTGGAGAGATCTG	420
Db	361	GGAGACTACGATGACAGTGCCTTCATGAGAGCCCGATACCAAGTCCGTGGAGAGATCTG	420
QY	421	GACAAAGCTCCACAGAGTGCCTGGTGGGGTAAAGTCCCCGAAAGAGATCTCATCGATG	480
Db	421	GACAAAGCTCCACAGAGTGCCTGGTGGGGTAAAGTCCCCGAAAGAGATCTCATCGATG	480
QY	481	CTCAGGGCACTGACGTGAACAAAGAGAGCAAGCAAAAGAGGAGCTGCTTACATCTGGCC	540
Db	481	CTCAGGGCACTGACGTGAACAAAGAGAGCAAGCAAAAGAGGAGCTGCTTACATCTGGCC	540
QY	541	TCTGCCAAATGGGAATTCAGAAAGTGTAAACTCTGCTGGACAGAGATGTCAACTTAAT	600
Db	541	TCTGCCAAATGGGAATTCAGAAAGTGTAAACTCTGCTGGACAGAGATGTCAACTTAAT	600

QY	601	GTCCCTGACAAACAAAAGAGACAGCTCGATTAAGGCGGTCAAAATGCGACGAAATATGA	660
Db	601	GTCCCTGACAAACAAAAGAGAGACGCTCTGATTAAGGCGGTCAAAATGCGACGAAATATGA	660
QY	661	TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGAGTGAAT	720
Db	661	TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGAGTGAAT	720
QY	721	ACCACTCTGCACATACGCTATCTTAATGAAGATAAATTATGGCCAAAGCACTGCTTTA	780
Db	721	ACCACTCTGCACATACGCTATCTTAATGAAGATAAATTATGGCCAAAGCACTGCTTTA	780
QY	781	TATGTCGTGATATGCAATCAAAAAACAAGCATGGGCTCACACCACTGTTACTGTGTA	840
Db	781	TATGTCGTGATATGCAATCAAAAAACAAGCATGGGCTCACACCACTGTTACTGTGTA	840
QY	841	CATGAGCAAAAAACAGCAAGCTGTGAATTTTTATCAAGAAAAAAGCGAATTTAAATGA	900
Db	841	CATGAGCAAAAAACAGCAAGCTGTGAATTTTTATCAAGAAAAAAGCGAATTTAAATGA	900
QY	901	CTGATAGATATGGAAGAGACTGCTCTCATCTTGCTGATGTTGTGATCAGCAAGTATA	960
Db	901	CTGATAGATATGGAAGAGACTGCTCTCATCTTGCTGATGTTGTGATCAGCAAGTATA	960
QY	961	GTCAGCCTTCTACTTGAGCAAAATATTGATGTAATCTTCTCAAGATCTATCTGGACAGAG	1020
Db	961	GTCAGCCTTCTACTTGAGCAAAATATTGATGTAATCTTCTCAAGATCTATCTGGACAGAG	1020
QY	1021	GCCAGAGATAGCGTGGTTCTAGCATCATCATGTAATTTGGCAGTTACTTCTCTACTAC	1080
Db	1021	GCCAGAGATAGCGTGGTTCTAGCATCATCATGTAATTTGGCAGTTACTTCTCTACTAC	1080
QY	1081	AAAGAAAAACGATGCTTAAAAATCTCTTCTGAAAACAGCAATCCAGAACCAAGACTTAAAG	1140
Db	1081	AAAGAAAAACGATGCTTAAAAATCTCTTCTGAAAACAGCAATCCAGAACCAAGACTTAAAG	1140
QY	1141	CTGACATCAGAGGAGATGCACAAAGGTTCAAGGCACTGAAATAATGCCAGCCAGAGAAA	1200
Db	1141	CTGACATCAGAGGAGATGCACAAAGGTTCAAGGCACTGAAATAATGCCAGCCAGAGAAA	1200
QY	1201	ATGTCCTCAAGAACCCAGAAAATTAATTAAGAGATGGTGAATGAGAGGTTGAAMAATAATGAAG	1260
Db	1201	ATGTCCTCAAGAACCCAGAAAATTAATTAAGAGATGGTGAATGAGAGGTTGAAMAATAATGAAG	1260
QY	1261	AAGCATGAAAGTATATATGGGGATTACTAGAAAACCTCACTAATAGGTTGCTCACTGCGC	1320
Db	1261	AAGCATGAAAGTATATATGGGGATTACTAGAAAACCTCACTAATAGGTTGCTCACTGCGC	1320
QY	1321	AATGCTATATGATTAATTTCTCTCAAGAGAGCAGACAACCTGAAAATCAGCAATTT	1380
Db	1321	AATGCTATATGATTAATTTCTCTCAAGAGAGCAGACAACCTGAAAATCAGCAATTT	1380

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Oy 1381 CCTGACAAAGAGAGATGATCAGAAATTTGCAATTAGTTCTGACTACAAAGNA 1440
    |||
Db 1381 CCTGACAAAGAGAGATGATCAGAAATTTGCAATTAGTTCTGACTACAAAGNA 1440
    |||
Oy 1441 AACGATGCCAAATCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
    |||
Db 1441 AACGATGCCAAATCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
    |||
Oy 1501 TCAGAGAAAGATCACAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551
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Db 1501 TCAGAGAAAGATCACAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551
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 Job time : 4035.93 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2002, 09:20:29 : Search time 61.604 Seconds
(without alignments)
5201.412 Million cell updates/sec

Title: US-09-924-400-303
Perfect score: 2040
Sequence: 1 atgtgtgttgatgttgc.....aaaaaaaaaaaaaaaaa 2040

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 205966 seqs, 78536166 residues

Word size : 15

Total number of hits satisfying chosen parameters: 10880

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_NA_New:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	2.5	298	5	US-09-513-999C-3605
2	32	1.6	2331	6	US-10-125-923A-59
3	31	1.5	114	6	US-10-240-425-582
4	31	1.5	931	6	US-10-264-237-1316
5	31	1.5	1522	6	US-10-258-105-12
6	31	1.5	1966	6	US-10-264-237-1274
7	31	1.5	8238	6	US-10-240-454-43
8	31	1.5	11735	6	US-10-240-453-42
9	30	1.5	330	5	US-09-728-552-24
10	30	1.5	452	6	US-10-240-425-442
11	30	1.5	563	6	US-10-266-829-12
12	30	1.5	776	6	US-10-266-829-26
13	30	1.5	876	6	US-10-264-237-1227
14	30	1.5	983	6	US-10-230-437-47
15	30	1.5	1018	5	US-09-699-266A-1
16	30	1.5	1081	6	US-10-264-237-1295
17	30	1.5	1228	6	US-10-240-425-1474
18	30	1.5	1275	6	US-10-264-237-1171
19	30	1.5	1292	6	US-10-264-237-234
20	30	1.5	1380	5	US-09-543-293C-21
21	30	1.5	1459	6	US-10-264-237-744
22	30	1.5	1726	5	US-09-674-988A-9
23	30	1.5	1968	6	US-10-131-813A-163
24	30	1.5	1968	6	US-10-131-819A-163
25	30	1.5	1968	6	US-10-131-823A-163
26	30	1.5	1968	6	US-10-131-824A-163

27	30	1.5	1968	6	US-10-131-826A-163	Sequence 163, App
28	30	1.5	1968	6	US-10-131-829A-163	Sequence 163, App
29	30	1.5	1968	6	US-10-125-976A-163	Sequence 163, App
30	30	1.5	1968	6	US-10-127-829A-163	Sequence 163, App
31	30	1.5	1968	6	US-10-127-831A-163	Sequence 163, App
32	30	1.5	1968	6	US-10-127-835A-163	Sequence 163, App
33	30	1.5	1968	6	US-10-127-837A-163	Sequence 163, App
34	30	1.5	1968	6	US-10-127-842A-163	Sequence 163, App
35	30	1.5	1968	6	US-10-127-850A-163	Sequence 163, App
36	30	1.5	1968	6	US-10-127-901A-163	Sequence 163, App
37	30	1.5	1968	6	US-10-128-689A-163	Sequence 163, App
38	30	1.5	1968	6	US-10-131-830A-163	Sequence 163, App
39	30	1.5	1968	6	US-10-131-833A-163	Sequence 163, App
40	30	1.5	1968	6	US-10-131-837A-163	Sequence 163, App
41	30	1.5	1968	6	US-10-125-930A-163	Sequence 163, App
42	30	1.5	1968	6	US-10-127-825A-163	Sequence 163, App
43	30	1.5	1968	6	US-10-127-838B-163	Sequence 163, App
44	30	1.5	1968	6	US-10-127-843A-163	Sequence 163, App
45	30	1.5	1968	6	US-10-127-849A-163	Sequence 163, App

ALIGNMENTS

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RESULT 1
US-09-513-999C-3605
Sequence 3605, Application US/09513999C
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclet, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513, 999C
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 3605
LENGTH: 298
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 77..298
US-09-513-999C-3605

Query Match          2.5%; Score 50; DB 5; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      811 CATGCCCTCACACACTGTTACTGTGTGATGAGCAAAACAGCAAGT 860
DB      83 CATGCCCTCACACACTGTTACTGTGTGATGAGCAAAACAGCAAGT 132

RESULT 2
US-10-125-923A-59
Sequence 59, Application US/10125923A
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pau, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
```

```

; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430RIC79
; CURRENT APPLICATION NUMBER: US/10/125,923A
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 59
; LENGTH: 2331
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-125-923A-59

```

```

Query Match
Best Local Similarity 100.0%; Score 32; DB 6; Length 2331;
Pred. No. 1.6e-05;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2009 AGCTAAAAAAAAAAAAAAAAAAAAAAAAA 2040
Db 2273 AGCTAAAAAAAAAAAAAAAAAAAAAAAAA 2304

```

```

RESULT 3
; Sequence 582, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 582
; LENGTH: 114
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AI349119
; US-10-240-425-582

```

```

Query Match
Best Local Similarity 100.0%; Score 31; DB 6; Length 114;
Pred. No. 5e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2010 GCTAAAAAAAAAAAAAAAAAAAAAAAAA 2040
Db 70 GCTAAAAAAAAAAAAAAAAAAAAAAAAA 100

```

```

RESULT 4
; Sequence 1316, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131PI
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1316
; LENGTH: 931
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-264-237-1316

```

```

Query Match
Best Local Similarity 100.0%; Score 31; DB 6; Length 931;
Pred. No. 4.8e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2010 GCTAAAAAAAAAAAAAAAAAAAAAAAAA 2040
Db 876 GCTAAAAAAAAAAAAAAAAAAAAAAAAA 906

```

```

RESULT 5
; Sequence 12, Application US/10258105
; GENERAL INFORMATION:
; APPLICANT: Wakamiya et al.
; TITLE OF INVENTION: Novel Collectin
; FILE REFERENCE: 19036/38785
; CURRENT APPLICATION NUMBER: US/10/258,105
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: PCT/JP01/03468
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: JP 2000-120358
; PRIOR FILING DATE: 2000-04-21
; NUMBER OF SEQ ID NOS: 61
; SEQ ID NO 12
; LENGTH: 1522
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (157)..(969)
; US-10-258-105-12

```

```

Query Match
Best Local Similarity 100.0%; Score 31; DB 6; Length 1522;
Pred. No. 4.7e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2010 GCTAAAAAAAAAAAAAAAAAAAAAAAAA 2040
Db 1454 GCTAAAAAAAAAAAAAAAAAAAAAAAAA 1484

```

```

RESULT 6
; Sequence 1274, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; US-10-264-237-1274

```

```

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131p1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1274
; LENGTH: 1996
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1975)..(1975)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1980)..(1980)
; OTHER INFORMATION: n equals a,t,g, or c
; US-10-264-237-1274

```

```

Query Match          1.5%; Score 31; DB 6; Length 1996;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2010 GCTAATAAAAAAAAAAAAAAAAAAAAAA 2040
    |||||||
Db 1917 GCTAATAAAAAAAAAAAAAAAAAAAAAA 1947

```

```

RESULT 7
US-10-240-454-43/c
; Sequence 43, Application US/10240454
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with Metabolism
; FILE REFERENCE: 5013.1010
; CURRENT APPLICATION NUMBER: US/10/240,454
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/04016
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 43
; LENGTH: 8238
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; US-10-240-454-43

```

```

Query Match          1.5%; Score 31; DB 6; Length 8238;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2010 GCTAATAAAAAAAAAAAAAAAAAAAAAA 2040
    |||||||
Db 2119 GCTAATAAAAAAAAAAAAAAAAAAAAAA 2089

```

RESULT 8

```

US-10-240-453-42/c
; Sequence 42, Application US/10240453
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
; TITLE OF INVENTION: Transcription
; TITLE OF INVENTION: by Means of Assessing the Methylation Status of Genes Associa
; TITLE OF INVENTION: With DNA Transcription
; FILE REFERENCE: 5013.1009
; CURRENT APPLICATION NUMBER: US/10/240,453
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/03973
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 350
; SEQ ID NO 42
; LENGTH: 11735
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; US-10-240-453-42

```

```

Query Match          1.5%; Score 31; DB 6; Length 11735;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2010 GCTAATAAAAAAAAAAAAAAAAAAAAAA 2040
    |||||||
Db 6782 GCTAATAAAAAAAAAAAAAAAAAAAAAA 6752

```

```

RESULT 9
US-09-728-552-24
; Sequence 24, Application US/09728552
; GENERAL INFORMATION:
; APPLICANT: Cho, Kong-Hong Andy
; APPLICANT: Du Sart, Desiree
; APPLICANT: Cancilla, Michael R.
; TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
; FILE REFERENCE: Davies Col
; CURRENT APPLICATION NUMBER: US/09/728,552
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: 09/078,294
; PRIOR FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 330
; TYPE: DNA
; ORGANISM: BAC-F2 contig 47 fragment 4
; US-09-728-552-24

```

```

Query Match          1.5%; Score 30; DB 5; Length 330;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2011 CTTAATAAAAAAAAAAAAAAAAAAAAAA 2040
    |||||||
Db 144 CTTAATAAAAAAAAAAAAAAAAAAAAAA 173

```

RESULT 10
US-10-240-425-442/c

```
; Sequence 442, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Metzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 442
; LENGTH: 452
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AI052543
US-10-240-425-442
```

```
Query Match 1.5%; Score 30; DB 6; Length 452;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
Db 31 CTAACAAAAAAAAAAAAAAAAAAAAA 2
```

```
RESULT 11
US-10-266-829-12
; Sequence 12, Application US/10266829
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 29 Human secreted proteins
; FILE REFERENCE: P2041P1
; CURRENT APPLICATION NUMBER: US/10/266,829
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 09/756,168
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: PCT/US00/19735
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/145,220
; PRIOR FILING DATE: 1999-07-23
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-266-829-12
```

```
Query Match 1.5%; Score 30; DB 6; Length 563;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
Db 514 CTAACAAAAAAAAAAAAAAAAAAAAA 543
```

```
RESULT 12
US-10-266-829-26
; Sequence 26, Application US/10266829
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
```

```
; TITLE OF INVENTION: 29 Human secreted proteins
; FILE REFERENCE: P2041P1
; CURRENT APPLICATION NUMBER: US/10/266,829
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 09/756,168
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: PCT/US00/19735
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/145,220
; PRIOR FILING DATE: 1999-07-23
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 776
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-266-829-26
```

```
Query Match 1.5%; Score 30; DB 6; Length 776;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
Db 744 CTAACAAAAAAAAAAAAAAAAAAAAA 773
```

```
RESULT 13
US-10-264-237-1227/C
; Sequence 1227, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1227
; LENGTH: 876
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-264-237-1227
```

```
Query Match 1.5%; Score 30; DB 6; Length 876;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
Db 30 CTAACAAAAAAAAAAAAAAAAAAAAA 1
```

```
RESULT 14
US-10-230-437-47
; Sequence 47, Application US/10230437
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerltsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
```

```

; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C94
; CURRENT APPLICATION NUMBER: US/10/230,437
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 47
; LENGTH: 983
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-230-437-47

```

```

Query Match          1.5%; Score 30; DB 6; Length 983;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
Db 940 CTAACAAAAAAAAAAAAAAAAAAAAA 969

```

```

RESULT 15
US-09-699-266A-1
; Sequence 1, Application US/09699266A
; GENERAL INFORMATION:
; APPLICANT: Ma, Hongchang
; APPLICANT: Morakinyo, Layo O.
; APPLICANT: Odell, Joan T.
; APPLICANT: Orozco Jr., Emil M.
; APPLICANT: Rafalek, J. Antoni
; TITLE OF INVENTION: TRANSCRIPTION AND GENE EXPRESSION REGULATORS
; FILE REFERENCE: B1164 US NA
; CURRENT APPLICATION NUMBER: US/09/699,266A
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: PCT/US99/08385
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/083,212
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 1018
; TYPE: DNA
; ORGANISM: Zea mays
US-09-699-266A-1

```

```

Query Match          1.5%; Score 30; DB 5; Length 1018;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
Db 972 CTAACAAAAAAAAAAAAAAAAAAAAA 1001

```

```

RESULT 16
US-10-264-237-1295
; Sequence 1295, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1295
; LENGTH: 1081
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1076)..(1076)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1078)..(1078)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-1295

```

```

Query Match          1.5%; Score 30; DB 6; Length 1081;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
Db 1023 CTAACAAAAAAAAAAAAAAAAAAAAA 1052

```

```

RESULT 17
US-10-240-425-1474
; Sequence 1474, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1474
; LENGTH: 1228
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. U92315
US-10-240-425-1474

```

```

Query Match          1.5%; Score 30; DB 6; Length 1228;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
|
Db 1198 CTAACAAAAAAAAAAAAAAAAAAAAA 1227

RESULT 18
US-10-264-237-1171/c
; Sequence 1171, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1171
; LENGTH: 1275
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-264-237-1171

Query Match 1.5%; Score 30; DB 6; Length 1275;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
|
Db 39 CTAACAAAAAAAAAAAAAAAAAAAAA 10

RESULT 19
US-10-264-237-234
; Sequence 234, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 234
; LENGTH: 1292
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (507)..(507)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-234

Query Match 1.5%; Score 30; DB 6; Length 1292;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
|
Db 1262 CTAACAAAAAAAAAAAAAAAAAAAAA 1291

RESULT 20
US-09-543-293C-21
; Sequence 21, Application US/09543293C
; GENERAL INFORMATION:

; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Meyer, David J.
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Sakai, Hajime
; APPLICANT: Tingey, Scott V.
; TITLE OF INVENTION: Secretory Pathway Proteins
; FILE REFERENCE: B1351 US NA
; CURRENT APPLICATION NUMBER: US/09/543,293C
; CURRENT FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,191
; PRIOR FILING DATE: 1999-04-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 21
; LENGTH: 1380
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1370)
; OTHER INFORMATION: n = a, c, g or t
US-09-543-293C-21

Query Match 1.5%; Score 30; DB 5; Length 1380;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
|
Db 1285 CTAACAAAAAAAAAAAAAAAAAAAAA 1314

RESULT 21
US-10-264-237-744
; Sequence 744, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 744
; LENGTH: 1459
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (25)..(25)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-744

Query Match 1.5%; Score 30; DB 6; Length 1459;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
|
Db 1394 CTAACAAAAAAAAAAAAAAAAAAAAA 1423

RESULT 22
US-09-674-988A-9
; Sequence 9, Application US/09674988A
; GENERAL INFORMATION:
; APPLICANT: McEliver, John A.
; APPLICANT: Zhao, Suling
; APPLICANT: Bowen, Benjamin A.

```

; TITLE OF INVENTION: Zea Mays Phosphate Transporter Genes
; FILE REFERENCE: 0859-PCT-US
; CURRENT APPLICATION NUMBER: US/09/674,988A
; CURRENT FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/085,292
; PRIOR FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1726
; TYPE: DNA
; ORGANISM: Zea mays
; US-09-674-988A-9

Query Match          1.5%: Score 30; DB 5; Length 1726;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
    |||
Db   1687 CTAACAAAAAAAAAAAAAAAAAAAAA 1716

RESULT 23
US-10-131-813A-163
; Sequence 163, Application US/10131813A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Laureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C139
; CURRENT APPLICATION NUMBER: US/10/131,813A
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
```

```

; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-131-813A-163

Query Match          1.5%: Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
    |||
Db   1923 CTAACAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 24
US-10-131-819A-163
; Sequence 163, Application US/10131819A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Laureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C134
; CURRENT APPLICATION NUMBER: US/10/131,819A
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-131-819A-163

Query Match          1.5%: Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
    |||
```

Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 25

US-10-131-823A-163

; Sequence 163, Application US/10131823A

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: Deforge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3330R1C143

; CURRENT APPLICATION NUMBER: US/10/131, 823A

; CURRENT FILING DATE: 2002-04-24

; PRIOR APPLICATION NUMBER: 60/049911

; PRIOR FILING DATE: 1997-06-18

; PRIOR APPLICATION NUMBER: 60/056974

; PRIOR FILING DATE: 1997-08-26

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059115

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059117

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059122

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059184

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059352

; PRIOR FILING DATE: 1997-09-19

; PRIOR APPLICATION NUMBER: 60/059588

; PRIOR FILING DATE: 1997-09-19

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 163

; LENGTH: 1968

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-131-823A-163

Query Match 1.5%; Score 30; DB 6; Length 1968;

Best Local Similarity 100.0%; Pred. No. 0.00013;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040

Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 26

US-10-131-824A-163

; Sequence 163, Application US/10131824A

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: Deforge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3330R1C126

; CURRENT APPLICATION NUMBER: US/10/131, 824A

; CURRENT FILING DATE: 2002-04-24

; PRIOR APPLICATION NUMBER: 60/049911

; PRIOR FILING DATE: 1997-06-18

; PRIOR APPLICATION NUMBER: 60/056974

; PRIOR FILING DATE: 1997-08-26

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059115

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059117

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059122

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059184

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059352

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059588

; PRIOR FILING DATE: 1997-09-19

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 163

; LENGTH: 1968

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-131-824A-163

Query Match 1.5%; Score 30; DB 6; Length 1968;

Best Local Similarity 100.0%; Pred. No. 0.00013;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040

Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 27

US-10-131-826A-163

; Sequence 163, Application US/10131826A

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: Deforge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.


```

; APPLICANT: Tumas,Daniel
; APPLICANT: Matanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-131-826A-163

Query Match          1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
    ||||||||||||||||||||||||||||
Db  1923 CTAACAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 28
; Sequence 163, Application US/10131829A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C138
; CURRENT APPLICATION NUMBER: US/10/131,829A
; CURRENT FILING DATE: 2002-04-27
; PRIOR APPLICATION NUMBER: 60/049911
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; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-131-829A-163

Query Match          1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
    ||||||||||||||||||||||||||||
Db  1923 CTAACAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 29
; Sequence 163, Application US/10125926A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C80
; CURRENT APPLICATION NUMBER: US/10/125,926A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
```

```
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-125-926A-163

Query Match          1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTRAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040
Db 1923 CTRAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 30
US-10-127-829A-163
; Sequence 163, Application US/10127829A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C85
; CURRENT APPLICATION NUMBER: US/10/127, 829A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-829A-163
```

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; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-829A-163

Query Match          1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTRAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040
Db 1923 CTRAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 31
US-10-127-831A-163
; Sequence 163, Application US/10127831A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C107
; CURRENT APPLICATION NUMBER: US/10/127, 831A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-831A-163

Query Match          1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
|
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 32
US-10-127-835A-163
; Sequence 163, Application US/10127835A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C102
; CURRENT APPLICATION NUMBER: US/10/127, 835A
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-835A-163

Query Match 1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
|
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 33
US-10-127-837A-163
; Sequence 163, Application US/10127837A
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C96
; CURRENT APPLICATION NUMBER: US/10/127, 837A
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-837A-163

Query Match 1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
|
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 34
US-10-127-842A-163
; Sequence 163, Application US/10127842A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.

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: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C100
: CURRENT APPLICATION NUMBER: US/10/127,842A
: CURRENT FILING DATE: 2002-10-15
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059184
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059352
: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/059588
: PRIOR FILING DATE: 1997-09-19
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 163
: LENGTH: 1968
: TYPE: DNA
: ORGANISM: Homo Sapien
: US-10-127-842A-163

Query Match          1.5%: Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
DB 1923 CTAACAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 35
US-10-127-850A-163
: Sequence 163, Application US/10127850A
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: Deforge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Zhang, Zemin
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C110
: CURRENT APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
```

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: CURRENT APPLICATION NUMBER: US/10/127,850A
: CURRENT FILING DATE: 2002-10-15
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059184
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059352
: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/059588
: PRIOR FILING DATE: 1997-09-19
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 163
: LENGTH: 1968
: TYPE: DNA
: ORGANISM: Homo Sapien
: US-10-127-850A-163

Query Match          1.5%: Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
DB 1923 CTAACAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 36
US-10-127-901A-163
: Sequence 163, Application US/10127901A
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: Deforge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C86
: CURRENT APPLICATION NUMBER: US/10/127,901A
: CURRENT FILING DATE: 2002-10-15
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
```

```
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-901A-163
```

```
Query Match 1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAA 1952
```

```
RESULT 37
US-10-128-689A-163
; Sequence 163, Application US/10128689A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C117
; CURRENT APPLICATION NUMBER: US/10/128, 689A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
```

```
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-128-689A-163
```

```
Query Match 1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAA 1952
```

```
RESULT 38
US-10-131-830A-163
; Sequence 163, Application US/10131830A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C137
; CURRENT APPLICATION NUMBER: US/10/131, 830A
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-830A-163
```

Query Match 1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTRAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040
|||||
DB 1923 CTRAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 39

US-10-131-833A-163
; Sequence 163, Application US/10131833A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C142
; CURRENT APPLICATION NUMBER: US/10/131,833A
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-833A-163

Query Match 1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTRAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040
|||||
DB 1923 CTRAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 40

US-10-131-837A-163
; Sequence 163, Application US/10131837A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C131
; CURRENT APPLICATION NUMBER: US/10/131,837A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-837A-163

Query Match 1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTRAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2040
|||||
DB 1923 CTRAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 41

US-10-125-930A-163
; Sequence 163, Application US/10125930A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.

```

: APPLICANT: Goddard,Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney,Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith,Victoria
: APPLICANT: Stewart,Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Matanabe, Colin K
: APPLICANT: Wood,William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C78
: CURRENT APPLICATION NUMBER: US/10/125, 930A
: CURRENT FILING DATE: 2002-04-19
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059184
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059352
: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/059588
: PRIOR FILING DATE: 1997-09-19
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 163
: LENGTH: 1968
: TYPE: DNA
: ORGANISM: Homo Sapien
US-10-125-930A-163

Query Match      1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 42
US-10-127-825A-163
: Sequence 163, Application US/10127825A
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Laureen
: APPLICANT: Deforge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Matanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
```

```

: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C84
: CURRENT APPLICATION NUMBER: US/10/127, 825A
: CURRENT FILING DATE: 2002-04-22
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059184
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059352
: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/059588
: PRIOR FILING DATE: 1997-09-19
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 163
: LENGTH: 1968
: TYPE: DNA
: ORGANISM: Homo Sapien
US-10-127-825A-163

Query Match      1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2011 CTAACAAAAAAAAAAAAAAAAAAAAA 2040
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAA 1952

RESULT 43
US-10-127-838B-163
: Sequence 163, Application US/10127838B
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Laureen
: APPLICANT: Deforge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Matanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C98
: CURRENT APPLICATION NUMBER: US/10/127, 838B
: CURRENT FILING DATE: 2002-04-22
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-838B-163
Query Match      1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2011 CTAACAAAAAAAAAAAAAAAAAAAAAAAAA 2040
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAA 1952
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RESULT 44
US-10-127-843A-163
; Sequence 163, Application US/10127843A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C09
; CURRENT FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
```

```

; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-843A-163
```

```

Query Match      1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 2011 CTAACAAAAAAAAAAAAAAAAAAAAAAAAA 2040
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAA 1952
```

```

RESULT 45
US-10-127-849A-163
; Sequence 163, Application US/10127849A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C103
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
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ORGANISM: Homo Sapien
US-10-127-849A-163

Query Match 1.5%; Score 30; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2011 CTAACAAAAA 2040
DB 1923 CTAACAAAAA 1952

Search completed: November 8, 2002, 15:51:31
Job time : 117.604 secs

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OM nucleic - nucleic search, using sw model

Run on: November 8, 2002, 09:20:29 : Search time 60.396 Seconds
(without alignments)
5201.412 Million cell updates/sec

Title: US-09-924-400-302

Perfect score: 2000

Sequence: 1 atgtgtgtgtgtgtgtgtgttc.....aaaaaaaaaaaaaaaaaaaaa 2000

Scoring table:

OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 205966 seqs, 78536166 residues

Word size : 15

Total number of hits satisfying chosen parameters: 10861

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/PCF_NEW_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
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4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	2.5	298	5	US-09-513-999C-3605
2	37	1.8	2331	6	US-10-125-923A-59
3	36	1.8	931	6	US-10-264-237-1316
4	36	1.8	1522	6	US-10-258-105-12
5	36	1.8	1996	6	US-10-264-237-1274
6	36	1.8	8238	6	US-10-240-434-43
7	35	1.8	114	6	US-10-240-425-582
8	35	1.8	563	6	US-10-266-829-12
9	35	1.8	983	6	US-10-230-437-47
10	35	1.8	1018	5	US-09-699-266A-1
11	35	1.8	1081	6	US-10-264-237-1295
12	35	1.8	1880	5	US-09-543-293C-21
13	35	1.8	1459	5	US-09-543-293C-21
14	35	1.8	1726	5	US-09-264-237-744
15	35	1.8	1726	5	US-09-674-988A-9
16	35	1.8	1968	6	US-10-131-813A-163
17	35	1.8	1968	6	US-10-131-819A-163
18	35	1.8	1968	6	US-10-131-823A-163
19	35	1.8	1968	6	US-10-131-824A-163
20	35	1.8	1968	6	US-10-131-826A-163
21	35	1.8	1968	6	US-10-131-829A-163
22	35	1.8	1968	6	US-10-125-926A-163
23	35	1.8	1968	6	US-10-127-831A-163
24	35	1.8	1968	6	US-10-127-835A-163
25	35	1.8	1968	6	US-10-127-837A-163
26	35	1.8	1968	6	US-10-127-842A-163

27	35	1.8	1968	6	US-10-127-850A-163	Sequence 163, App
28	35	1.8	1968	6	US-10-127-901A-163	Sequence 163, App
29	35	1.8	1968	6	US-10-128-689A-163	Sequence 163, App
30	35	1.8	1968	6	US-10-131-830A-163	Sequence 163, App
31	35	1.8	1968	6	US-10-131-833A-163	Sequence 163, App
32	35	1.8	1968	6	US-10-131-837A-163	Sequence 163, App
33	35	1.8	1968	6	US-10-125-930A-163	Sequence 163, App
34	35	1.8	1968	6	US-10-127-825A-163	Sequence 163, App
35	35	1.8	1968	6	US-10-127-838A-163	Sequence 163, App
36	35	1.8	1968	6	US-10-127-843A-163	Sequence 163, App
37	35	1.8	1968	6	US-10-127-849A-163	Sequence 163, App
38	35	1.8	1968	6	US-10-128-684A-163	Sequence 163, App
39	35	1.8	1968	6	US-10-128-685A-163	Sequence 163, App
40	35	1.8	1968	6	US-10-128-686A-163	Sequence 163, App
41	35	1.8	1968	6	US-10-128-690A-163	Sequence 163, App
42	35	1.8	1968	6	US-10-128-693A-163	Sequence 163, App
43	35	1.8	1968	6	US-10-131-821A-163	Sequence 163, App
44	35	1.8	1968	6	US-10-131-836A-163	Sequence 163, App
45	35	1.8	1968	6	US-10-137-872A-163	Sequence 163, App

ALIGNMENTS

```
RESULT 1
US-09-513-999C-3605
; Sequence 3605, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Mline Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59. US2. REG
; CURRENT APPLICATION NUMBER: US/09/513, 999C
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122, 487
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 3605
; LENGTH: 298
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 77..298
; US-09-513-999C-3605

Query Match      2.5%; Score 50; DB 5; Length 298;
Best local similarity 100.0%; Pred. No. 1.9e+13;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      811 CATGCCCTCACACACTGTCTGTGTGTACATGAGCAAAACAGCAAGT 860
      |||||||
Db      83 CATGCCCTCACACACTGTCTGTGTGTACATGAGCAAAACAGCAAGT 132

RESULT 2
US-10-125-923A-59
; Sequence 59, Application US/10125923A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
```

```
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C79
; CURRENT APPLICATION NUMBER: US/10/125,923A
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 59
; LENGTH: 2331
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-125-923A-59
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Query Match 1.8%; Score 37; DB 6; Length 2331;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1964 AGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 2273 AGCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2309
```

```
RESULT 3
US-10-264-237-1316
; Sequence 1316, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131PI
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1316
; LENGTH: 931
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-264-237-1316
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```
Query Match 1.8%; Score 36; DB 6; Length 931;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1965 GCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 876 GCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 911
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```
RESULT 4
US-10-258-105-12
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; Sequence 12, Application US/10258105
; GENERAL INFORMATION:
; APPLICANT: Wakamiya et al.
; TITLE OF INVENTION: Novel Collectin
; FILE REFERENCE: 19036/38785
; CURRENT APPLICATION NUMBER: US/10/258,105
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: PCT/JP01/03468
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: JP 2000-120358
; PRIOR FILING DATE: 2000-04-21
; NUMBER OF SEQ ID NOS: 61
; SEQ ID NO 12
; LENGTH: 1522
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (157)..(969)
US-10-258-105-12
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Query Match 1.8%; Score 36; DB 6; Length 1522;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1965 GCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1454 GCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1489
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```
RESULT 5
US-10-264-237-1274
; Sequence 1274, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131PI
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1274
; LENGTH: 1996
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1975)..(1975)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1980)..(1980)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-1274
```

```
Query Match 1.8%; Score 36; DB 6; Length 1996;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1965 GCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1917 GCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1952
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RESULT 6
US-10-240-454-43/C
; Sequence 43, Application US/10240454
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
```

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; APPLICANT: PIEPERBROCK, Christian
; TITLE OF INVENTION: Diagnosis of Diseases Associated with Metabolism
; FILE REFERENCE: 5013.1010
; CURRENT APPLICATION NUMBER: US/10/240.454
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/04016
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 68
; SEQ ID NO 43
; LENGTH: 8238
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-454-43
Query Match
Best Local Similarity 1.8%; Score 36; DB 6; Length 8238;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1965 GCTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
DB 2119 GCTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 2084

RESULT 7
US-10-240-425-582
; Sequence 582, Application US/10240425
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Wetzel, Jon C.
; APPLICANT: Scherf, Uwe
; APPLICANT: Vockley, Joseph G.
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240.425
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 582
; LENGTH: 114
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AF349119
US-10-240-425-582
Query Match
Best Local Similarity 1.8%; Score 35; DB 6; Length 114;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1965 GCTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 1999
DB 70 GCTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 104

RESULT 8
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```
US-10-266-829-12
; Sequence 12, Application US/10266829
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 29 Human secreted proteins
; FILE REFERENCE: P2041P1
; CURRENT APPLICATION NUMBER: US/10/266,829
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 09/756,168
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: PCT/US00/19735
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/145,220
; PRIOR FILING DATE: 1999-07-23
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-266-829-12
Query Match
Best Local Similarity 1.8%; Score 35; DB 6; Length 563;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1966 CTTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
DB 514 CTTAATAAAAAAAAAAAAAAAAAAAAAAAAAA 548

RESULT 9
US-10-230-437-47
; Sequence 47, Application US/10230437
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C94
; CURRENT APPLICATION NUMBER: US/10/230,437
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
```

SEQ ID NO 47
LENGTH: 983
TYPE: DNA
ORGANISM: Homo Sapien
US-10-230-437-47

Query Match 1.8%; Score 35; DB 6; Length 983;
Best Local Similarity 100.0%; Pred. No. 9.3e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1966 CTAACAAAAA
Db 940 CTAACAAAAA

RESULT 10
US-09-699-266A-1
Sequence 1, Application US/09699266A
GENERAL INFORMATION:
APPLICANT: Ma, Hongchang
APPLICANT: Morakinyo, Layo O.
APPLICANT: Odell, Joan T.
APPLICANT: Orozco Jr., Emil M.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: TRANSCRIPTION AND GENE EXPRESSION REGULATORS
FILE REFERENCE: B81164 US NA
CURRENT APPLICATION NUMBER: US/09/699,266A
CURRENT FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: PCT/US99/08385
PRIOR FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/083,212
PRIOR FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Microsoft Office 97
SEQ ID NO 1
LENGTH: 1018
TYPE: DNA
ORGANISM: Zea mays
US-09-699-266A-1

Query Match 1.8%; Score 35; DB 5; Length 1018;
Best Local Similarity 100.0%; Pred. No. 9.3e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1966 CTAACAAAAA
Db 972 CTAACAAAAA

RESULT 11
US-10-264-237-1295
Sequence 1295, Application US/10264237
GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA131P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 1295
LENGTH: 1081
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1076)..(1076)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:

NAME/KEY: misc_feature
LOCATION: (1078)..(1078)
OTHER INFORMATION: n equals a,t,g, or c
US-10-264-237-1295

Query Match 1.8%; Score 35; DB 6; Length 1081;
Best Local Similarity 100.0%; Pred. No. 9.3e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1966 CTAACAAAAA
Db 1023 CTAACAAAAA

RESULT 12
US-09-543-293C-21
Sequence 21, Application US/09543293C
GENERAL INFORMATION:
APPLICANT: Famodu, Omolayo O.
APPLICANT: Meyer, David J.
APPLICANT: Rafalski, J. Antoni
APPLICANT: Sakai, Hajime
APPLICANT: Tingey, Scott V.
TITLE OF INVENTION: Secretory Pathway Proteins
FILE REFERENCE: B81351 US NA
CURRENT APPLICATION NUMBER: US/09/543,293C
CURRENT FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/128,191
PRIOR FILING DATE: 1999-04-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Microsoft Office 97
SEQ ID NO 21
LENGTH: 1380
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1370)
OTHER INFORMATION: n = a, c, g or t
US-09-543-293C-21

Query Match 1.8%; Score 35; DB 5; Length 1380;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1966 CTAACAAAAA
Db 1285 CTAACAAAAA

RESULT 13
US-10-264-237-744
Sequence 744, Application US/10264237
GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA131P1
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR FILING DATE: 2001-05-18
PRIOR APPLICATION NUMBER: US 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2876
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 744
LENGTH: 1459
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (25)..(25)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:

US-10-264-237-744

Query Match 1.8%; Score 35; DB 6; Length 1459;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1966 CTAACAAAAAAAAAAAAAAAAAAAAA 2000
|||||
DB 1394 CTAACAAAAAAAAAAAAAAAAAAAAA 1428

RESULT 14

US-09-674-988A-9
; Sequence 9, Application US/09674988A
; GENERAL INFORMATION:
; APPLICANT: McElver, John A.
; APPLICANT: Zhao, Suling
; APPLICANT: Bowen, Benjamin A.
; TITLE OF INVENTION: Zea Mays Phosphate Transporter Genes
; FILE REFERENCE: 0859-PCT-US
; CURRENT APPLICATION NUMBER: US/09/674,988A
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/085,292
; PRIOR FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1726
; TYPE: DNA
; ORGANISM: Zea mays
US-09-674-988A-9

Query Match 1.8%; Score 35; DB 5; Length 1726;
Best Local Similarity 100.0%; Pred. No. 9.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1966 CTAACAAAAAAAAAAAAAAAAAAAAA 2000
|||||
DB 1687 CTAACAAAAAAAAAAAAAAAAAAAAA 1721

RESULT 15

US-10-131-813A-163
; Sequence 163, Application US/10131813A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C139
; CURRENT APPLICATION NUMBER: US/10/131,813A
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-813A-163

Query Match 1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1966 CTAACAAAAAAAAAAAAAAAAAAAAA 2000
|||||
DB 1923 CTAACAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 16

US-10-131-819A-163
; Sequence 163, Application US/10131819A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C134
; CURRENT APPLICATION NUMBER: US/10/131,819A
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-819A-163

;; PRIOR APPLICATION NUMBER: 60/059352
;; PRIOR FILING DATE: 1997-09-19
;; PRIOR APPLICATION NUMBER: 60/059588
;; PRIOR FILING DATE: 1997-09-19
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 550

;; SEQ ID NO 163
;; LENGTH: 1968
;; TYPE: DNA
;; ORGANISM: Homo Saplen
US-10-131-819A-163

Query Match 1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 17

US-10-131-823A-163

;; Sequence 163, Application US/10131823A

;; GENERAL INFORMATION:

;; APPLICANT: Baker, Kevin P.

;; APPLICANT: Beresini, Maureen

;; APPLICANT: Deforge, Laura

;; APPLICANT: Desnoyers, Luc

;; APPLICANT: Fliviaroff, Ellen

;; APPLICANT: Gao, Wei-Qiang

;; APPLICANT: Gerritsen, Mary E.

;; APPLICANT: Goddard, Audrey

;; APPLICANT: Godowski, Paul J.

;; APPLICANT: Gurney, Austin L.

;; APPLICANT: Sherwood, Steven

;; APPLICANT: Smith, Victoria

;; APPLICANT: Stewart, Timothy A.

;; APPLICANT: Tumas, Daniel

;; APPLICANT: Watanabe, Colin K

;; APPLICANT: Wood, William

;; APPLICANT: Zhang, Zemin

;; TITLE OF INVENTION: SECRETED AND TRANSEMEMBRANE POLYPEPTIDES AND NUCLEIC

;; FILE REFERENCE: P330R1C143

;; CURRENT APPLICATION NUMBER: US/10/131,823A

;; CURRENT FILING DATE: 2002-04-24

;; PRIOR APPLICATION NUMBER: 60/049911

;; PRIOR FILING DATE: 1997-06-18

;; PRIOR APPLICATION NUMBER: 60/056974

;; PRIOR FILING DATE: 1997-08-26

;; PRIOR APPLICATION NUMBER: 60/059113

;; PRIOR FILING DATE: 1997-09-17

;; PRIOR APPLICATION NUMBER: 60/059115

;; PRIOR FILING DATE: 1997-09-17

;; PRIOR APPLICATION NUMBER: 60/059117

;; PRIOR FILING DATE: 1997-09-17

;; PRIOR APPLICATION NUMBER: 60/059122

;; PRIOR FILING DATE: 1997-09-17

;; PRIOR APPLICATION NUMBER: 60/059184

;; PRIOR FILING DATE: 1997-09-17

;; PRIOR APPLICATION NUMBER: 60/059263

;; PRIOR FILING DATE: 1997-09-18

;; PRIOR APPLICATION NUMBER: 60/059352

;; PRIOR FILING DATE: 1997-09-19

;; PRIOR APPLICATION NUMBER: 60/059588

;; PRIOR FILING DATE: 1997-09-19

;; Remaining Prior Application data removed - See File Wrapper or PALM.

;; NUMBER OF SEQ ID NOS: 550

;; SEQ ID NO 163

;; LENGTH: 1968

;; TYPE: DNA

;; ORGANISM: Homo Saplen

US-10-131-823A-163

Query Match 1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 18

US-10-131-824A-163

;; Sequence 163, Application US/10131824A

;; GENERAL INFORMATION:

;; APPLICANT: Baker, Kevin P.

;; APPLICANT: Beresini, Maureen

;; APPLICANT: Deforge, Laura

;; APPLICANT: Desnoyers, Luc

;; APPLICANT: Fliviaroff, Ellen

;; APPLICANT: Gao, Wei-Qiang

;; APPLICANT: Gerritsen, Mary E.

;; APPLICANT: Goddard, Audrey

;; APPLICANT: Godowski, Paul J.

;; APPLICANT: Gurney, Austin L.

;; APPLICANT: Sherwood, Steven

;; APPLICANT: Smith, Victoria

;; APPLICANT: Stewart, Timothy A.

;; APPLICANT: Tumas, Daniel

;; APPLICANT: Watanabe, Colin K

;; APPLICANT: Wood, William

;; APPLICANT: Zhang, Zemin

;; TITLE OF INVENTION: SECRETED AND TRANSEMEMBRANE POLYPEPTIDES AND NUCLEIC

;; FILE REFERENCE: P330R1C126

;; CURRENT APPLICATION NUMBER: US/10/131,824A

;; CURRENT FILING DATE: 2002-04-24

;; PRIOR APPLICATION NUMBER: 60/049911

;; PRIOR FILING DATE: 1997-06-18

;; PRIOR APPLICATION NUMBER: 60/056974

;; PRIOR FILING DATE: 1997-08-26

;; PRIOR APPLICATION NUMBER: 60/059113

;; PRIOR FILING DATE: 1997-09-17

;; PRIOR APPLICATION NUMBER: 60/059115

;; PRIOR FILING DATE: 1997-09-17

;; PRIOR APPLICATION NUMBER: 60/059117

;; PRIOR FILING DATE: 1997-09-17

;; PRIOR APPLICATION NUMBER: 60/059122

;; PRIOR FILING DATE: 1997-09-17

;; PRIOR APPLICATION NUMBER: 60/059184

;; PRIOR FILING DATE: 1997-09-17

;; PRIOR APPLICATION NUMBER: 60/059263

;; PRIOR FILING DATE: 1997-09-18

;; PRIOR APPLICATION NUMBER: 60/059352

;; PRIOR FILING DATE: 1997-09-19

;; PRIOR APPLICATION NUMBER: 60/059588

;; PRIOR FILING DATE: 1997-09-19

;; Remaining Prior Application data removed - See File Wrapper or PALM.

;; NUMBER OF SEQ ID NOS: 550

;; SEQ ID NO 163

;; LENGTH: 1968

;; TYPE: DNA

;; ORGANISM: Homo Saplen

US-10-131-824A-163

Query Match 1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957


```
RESULT 19
US-10-131-826A-163
; Sequence 163, Application US/10131826A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-826A-163

Query Match          1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9,1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C138
; CURRENT APPLICATION NUMBER: US/10/131,829A
; PRIOR FILING DATE: 2002-04-27
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-829A-163

Query Match          1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9,1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 21
US-10-125-926A-163
; Sequence 163, Application US/10125926A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
```

```
APPLICANT: Wood,William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C80
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 163
LENGTH: 1968
TYPE: DNA
ORGANISM: Homo Sapien
US-10-125-926A-163
```

```
Query Match 1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9,1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957
```

```
RESULT 22
US-10-127-829A-163
Sequence 163, Application US/10127829A
GENERAL INFORMATION:
```

```
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C85
CURRENT APPLICATION NUMBER: US/10/127,829A
PRIOR FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
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PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 163
LENGTH: 1968
TYPE: DNA
ORGANISM: Homo Sapien
US-10-127-829A-163
```

```
Query Match 1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9,1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957
```

```
RESULT 23
US-10-127-831A-163
Sequence 163, Application US/10127831A
GENERAL INFORMATION:
```

```
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C107
CURRENT APPLICATION NUMBER: US/10/127,831A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
```

```

; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-831A-163

Query Match
Best Local Similarity 100.0%; Score 35; DB 6; Length 1968;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 24
US-10-127-835A-163
; Sequence 163, Application US/10127835A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumasz, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C102
; CURRENT APPLICATION NUMBER: US/10/127,835A
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
```

```

; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-835A-163

Query Match
Best Local Similarity 100.0%; Score 35; DB 6; Length 1968;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 25
US-10-127-837A-163
; Sequence 163, Application US/10127837A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumasz, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C096
; CURRENT APPLICATION NUMBER: US/10/127,837A
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-837A-163

Query Match
Best Local Similarity 100.0%; Score 35; DB 6; Length 1968;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
```

Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 26
US-10-127-842A-163

; Sequence 163, Application US/10127842A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C100
; CURRENT APPLICATION NUMBER: US/10/127, 842A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-842A-163

Query Match 1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 27
US-10-127-850A-163
; Sequence 163, Application US/10127850A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen

; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C110
; CURRENT APPLICATION NUMBER: US/10/127, 850A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-850A-163

Query Match 1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 28
US-10-127-901A-163
; Sequence 163, Application US/10127901A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria

```
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC86
; CURRENT APPLICATION NUMBER: US/10/127,901A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-901A-163

Query Match      1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
    |||||||||||||||||||||||||||||||||||
DB 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 29
US-10-128-689A-163
; Sequence 163, Application US/10128689A
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wel-Qiang
; APPLICANT: Gerltsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC117
; CURRENT APPLICATION NUMBER: US/10/128,689A
; CURRENT FILING DATE: 2002-10-15
```

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; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-128-689A-163

Query Match      1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
    |||||||||||||||||||||||||||||||||||
DB 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 30
US-10-131-830A-163
; Sequence 163, Application US/10131830A
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wel-Qiang
; APPLICANT: Gerltsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC137
; CURRENT APPLICATION NUMBER: US/10/131,830A
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
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; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-830A-163

Query Match      1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
    |||||||||||||||||||||||||||||||||||
Db  1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 31
US-10-131-833A-163
; Sequence 163, Application US/10131833A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C142
; CURRENT APPLICATION NUMBER: US/10/131,833A
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-833A-163

Query Match      1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
    |||||||||||||||||||||||||||||||||||
Db  1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 32
US-10-131-837A-163
; Sequence 163, Application US/10131837A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C131
; CURRENT APPLICATION NUMBER: US/10/131,837A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-837A-163

Query Match      1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-833A-163

Query Match      1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
    |||||||||||||||||||||||||||||||||||
Db  1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 32
US-10-131-837A-163
; Sequence 163, Application US/10131837A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C131
; CURRENT APPLICATION NUMBER: US/10/131,837A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-837A-163

Query Match      1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



```

; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C98
; CURRENT APPLICATION NUMBER: US/10/127,838B
; CURRENT FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-838B-163
```

```

Query Match          1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
    ||||||||||||||||||||||||||||||||||||
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957
```

```

RESULT 36
US-10-127-843A-163
; Sequence 163, Application US/10127843A
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerltsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C98
; CURRENT APPLICATION NUMBER: US/10/127,838B
; CURRENT FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-843A-163
```

```

; FILE REFERENCE: P3330R1C98
; CURRENT APPLICATION NUMBER: US/10/127,843A
; CURRENT FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-843A-163
```

```

Query Match          1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
    ||||||||||||||||||||||||||||||||||||
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957
```

```

RESULT 37
US-10-127-849A-163
; Sequence 163, Application US/10127849A
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerltsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C103
; CURRENT APPLICATION NUMBER: US/10/127,849A
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-849A-163
```



```

; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-849A-163

Query Match      1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9,1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 38
US-10-128-684A-163
; Sequence 163, Application US/10128684A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C118
; CURRENT APPLICATION NUMBER: US/10/128,684A
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-128-684A-163
```

```

; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-128-684A-163

Query Match      1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9,1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 39
US-10-128-685A-163
; Sequence 163, Application US/10128685A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C116
; CURRENT APPLICATION NUMBER: US/10/128,685A
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-128-685A-163
```

Query Match 1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 40
US-10-128-686A-163
Sequence 163, Application US/10128686A

GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey E.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C119
CURRENT APPLICATION NUMBER: US/10/128,686A
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 163
LENGTH: 1968
TYPE: DNA
ORGANISM: Homo Sapien
US-10-128-686A-163

Query Match 1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 41
US-10-128-690A-163
Sequence 163, Application US/10128690A
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey E.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C122
CURRENT APPLICATION NUMBER: US/10/128,690A
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 163
LENGTH: 1968
TYPE: DNA
ORGANISM: Homo Sapien
US-10-128-690A-163

Query Match 1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 42
US-10-128-693A-163

Sequence 163, Application US/10128693A
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang

```
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C120
; CURRENT APPLICATION NUMBER: US/10/128, 693A
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-128-693A-163

Query Match
Best Local Similarity 100.0%; Pred. No. 9,1e-07; Length 1968;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 43
US-10-131-821A-163
; Sequence 163, Application US/10131821A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
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; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C138
; CURRENT APPLICATION NUMBER: US/10/131, 831A
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-821A-163

Query Match
Best Local Similarity 100.0%; Pred. No. 9,1e-07; Length 1968;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957

RESULT 44
US-10-131-836A-163
; Sequence 163, Application US/10131836A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geriltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C135
; CURRENT APPLICATION NUMBER: US/10/131, 836A
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
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; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
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; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
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; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO: 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-836A-163
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DB 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957
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US-10-137-872A-163
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; Sequence 163, Application US/10137872A
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; GENERAL INFORMATION:
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; APPLICANT: Baker, Kevin P.
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; APPLICANT: Beresini, Maureen
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; APPLICANT: Desnoyers, Luc
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; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Goddard, Audrey
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; APPLICANT: Godowski, Paul J.
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; APPLICANT: Gurney, Austin L.
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; APPLICANT: Sherwood, Steven
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; APPLICANT: Smith, Victoria
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; APPLICANT: Stewart, Timothy A.
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; APPLICANT: Tumas, Daniel
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; APPLICANT: Watanabe, Colin K
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; APPLICANT: Wood, William
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; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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; FILE REFERENCE: P3330R1C150
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; CURRENT APPLICATION NUMBER: US/10/137, 872A
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; CURRENT FILING DATE: 2002-05-03
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; PRIOR APPLICATION NUMBER: 60/049911
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; PRIOR FILING DATE: 1997-06-18
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; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO: 163
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-137-872A-163
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Query Match 1.8%; Score 35; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 9.1e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 1966 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2000
DB 1923 CTAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1957
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Job time : 94.396 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 8, 2002, 13:01:09 ; Search time 87.1287 Seconds
(without alignments)
8143.939 Million cell updates/sec

Title: US-09-924-400-302

Perfect score: 2000

Sequence: 1 atggtgtgtgtgtgtgtc.....aaaaaaaaaaaaaaaaa 2000

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 320260 seqs, 177392727 residues

Word size : 15

Total number of hits satisfying chosen parameters: 20463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Published_Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCr_NEM_PUB.seq:*
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- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2000	100.0	2000	10 US-09-825-301-6	Sequence 6, Appl1
2	2000	100.0	2000	10 US-09-759-143-374	Sequence 374, App
3	2000	100.0	2000	10 US-09-780-669-374	Sequence 374, App
4	2000	100.0	2000	10 US-09-810-936-302	Sequence 302, App
5	2000	100.0	2000	10 US-09-822-827-374	Sequence 374, App
6	2000	100.0	2000	10 US-09-429-755-302	Sequence 302, App
7	1551	77.5	2040	10 US-09-825-301-7	Sequence 7, Appl1
8	1551	77.5	2040	10 US-09-759-143-375	Sequence 375, App
9	1551	77.5	2040	10 US-09-780-669-375	Sequence 375, App
10	1551	77.5	2040	10 US-09-810-936-303	Sequence 303, App
11	1551	77.5	2040	10 US-09-822-827-375	Sequence 375, App
12	1551	77.5	2040	10 US-09-429-755-303	Sequence 303, App
13	1128	56.4	1155	10 US-09-825-301-5	Sequence 5, Appl1
14	1128	56.4	1155	10 US-09-759-143-373	Sequence 373, App
15	1128	56.4	1155	10 US-09-780-669-373	Sequence 373, App
16	1128	56.4	1155	10 US-09-810-936-301	Sequence 301, App
17	1128	56.4	1155	10 US-09-822-827-373	Sequence 373, App
18	1128	56.4	1155	10 US-09-429-755-301	Sequence 301, App
19	1044	52.2	1590	10 US-09-810-936-323	Sequence 323, App

20	975	48.8	1155	10 US-09-810-936-328	Sequence 328, App
21	491	24.6	1512	10 US-09-759-143-368	Sequence 368, App
22	491	24.6	1512	10 US-09-780-669-368	Sequence 368, App
23	491	24.6	1512	10 US-09-810-936-294	Sequence 294, App
24	491	24.6	1512	10 US-09-822-827-368	Sequence 368, App
25	491	24.6	1512	10 US-09-429-755-294	Sequence 294, App
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27	252	12.6	1853	10 US-09-780-669-369	Sequence 369, App
28	252	12.6	1853	10 US-09-810-936-295	Sequence 295, App
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34	120	6.0	879	10 US-09-822-827-331	Sequence 531, App
35	120	6.0	879	10 US-09-429-755-314	Sequence 531, App
36	120	6.0	1059	10 US-09-759-143-372	Sequence 372, App
37	120	6.0	1059	10 US-09-780-669-372	Sequence 372, App
38	120	6.0	1059	10 US-09-810-936-298	Sequence 298, App
39	120	6.0	1059	10 US-09-822-827-372	Sequence 372, App
40	120	6.0	1059	10 US-09-429-755-298	Sequence 298, App
41	120	6.0	1851	10 US-09-825-301-1	Sequence 298, App
42	120	6.0	1851	10 US-09-759-143-366	Sequence 1, Appl1
43	120	6.0	1851	10 US-09-780-669-366	Sequence 366, App
44	120	6.0	1851	10 US-09-810-936-291	Sequence 291, App
45	120	6.0	1851	10 US-09-810-936-292	Sequence 292, App

ALIGNMENTS

RESULT 1
US-09-825-301-6
Sequence 6, Application US/09825301
Patent No. US20020009738A1
GENERAL INFORMATION:
APPLICANT: Houghton, Raymond L.
APPLICANT: Dillon, David C.
APPLICANT: Molesh, David A.
APPLICANT: Xu, Jiaqun
APPLICANT: Zehentner, Barbara
TITLE OF INVENTION: PERSING, David H.
TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
FILE REFERENCE: 210121.513
CURRENT APPLICATION NUMBER: US/09/825,301
CURRENT FILING DATE: 2001-04-02
NUMBER OF SEQ ID NOS: 77
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-825-301-6

Query Match 100.0%; Score 2000; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGGTGTGAGTGATTCATCGCGGCTCTTGTGTAAGCAATTTGTC 60
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Db 1 ATGGTGTGAGTGATTCATCGCGGCTCTTGTGTAAGCAATTTGTC 60
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Db 61 AGAGCAAGATGGGCAAGTGTGCTCCGTCTCCCTGTCAGGAGAGCGGCAAG 120
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OY 121 AGCAAGTGGGCACTTCTGGAACACGACACTCTGCTATGAAGCACTCAGAGCAAG 180
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Db 121 AGCAAGTGGGCACTTCTGGAACACGACACTCTGCTATGAAGCACTCAGAGCAAG 180
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OY 181 ATGGGCAATGTGGCCGCACTGTCTCCCTGTCAGGAGGAGGAGCAAGCACTG 240
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Db 181 ATGGGCAAGTGTGGCCGCTCTCCCTGCTGACAGGGGAGTGGCAAGCAACGCTG 240
Qy 241 GCGCGTTCTGGAGACACAGAGACCTGCTATGAAGACACTCAGAAACAAGTGGGCAAG 300
Db 241 GCGCGTTCTGGAGACACAGAGACCTGCTATGAAGACACTCAGAAACAAGTGGGCAAG 300
Qy 301 TGTGTCTCCACTGCTTCCCTGCTGACAGGGGAGCGGCAAGCAAGTGGGCGCTTGG 360
Db 301 TGTGTCTCCACTGCTTCCCTGCTGACAGGGGAGCGGCAAGCAAGTGGGCGCTTGG 360
Qy 361 GGAGACTGAGTACAGTGCCTTTCATGAGAGCCCAAGTACCAAGTCCGTGGAGAAATGTC 420
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Db 421 GACAAGCTCCACAGAGTGCCTGGTGGGTAAGTCCCAAAAAGATCTCATGCTCATG 480
Qy 481 CTCAGGACACTGACGTGACAGAAAGAGCAAGCAAAAAGAGACTGCTCTACATCTGGCC 540
Db 481 CTCAGGACACTGACGTGACAGAAAGAGCAAGCAAAAAGAGACTGCTCTACATCTGGCC 540
Qy 541 TCTGCAATGGGAATTCGAAGTAGTAATACTCGTGGACAGACGATGCAACTTAT 600
Db 541 TCTGCAATGGGAATTCGAAGTAGTAATACTCGTGGACAGACGATGCAACTTAT 600
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Qy 901 CTGATAGATATGGAAGAGACTGCTCTCACTTGTGATGTTGGATGTCAGCAAGTATA 960
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Qy 961 GTCAGCCTTCTACTTGAAGCAAAATATTGATGATCTTCTCAAGATCTATCTGACAGACG 1020
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Qy 1321 AATGCTAATATGATTAATTTCTCAAGAGAGACAGAACACCTGAAATCAGCAATTT 1380
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Qy 1441 AAACAGATGCCAAATATCTTCTGAAGAACGCAACCCAGAACAAAGCTTAAACCTGACA 1500
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Qy 1561 TTTATGCTATCGAAGAAATGAAGACGAGAAAGTACTCATGTGCGATTTCCAGAAAC 1620
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Qy 1621 CTGACTAATGGTGCACCTGCGCAATGGCAATGGATGATGATTAATTCCTCAAGGAGAGC 1680
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Qy 1681 AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAGATATCAACAGTGAAGAA 1740
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Qy 1861 CTTAGTTGTGAAGAAAGAAAGACATCTTGCAATGAATATGATGTTGCGGGAAGAAAT 1920
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Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
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RESULT 2
US-09-759-143-374
: Sequence 374, Application US/09759143
: Patent No. US2002022248A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Jennifer L.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yugu
: APPLICANT: Henderson, Robert A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Panger, Gary R.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darrick
: APPLICANT: Li, Samuel
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

;; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
;; FILE REFERENCE: 210121.427C23
;; CURRENT APPLICATION NUMBER: US/09/759,143
;; CURRENT FILING DATE: 2001-01-12
;; NUMBER OF SEQ ID NOS: 934
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO: 374
;; LENGTH: 2000
;; TYPE: DNA
;; ORGANISM: Homo sapien
US-09-759-143-374

Query Match 100.0%; Score 2000; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 AGGAGCAAGATGGGCAAGTGTGTCCTTCCCTGCTGCGAGGAGAGCGGCAAG 120
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DB 121 AGCAAGTGGGCACTTCTGTGAGACCAAGCAAGTCTGTATGAAGACTCAGAGCAAG 180
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DB 361 GGAGACTACGATGACAGTGCCTTTCATGAGCCAGGTACCAAGTCCGAGGAAGTCTG 420
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QY 541 TGTGCCAATGGGAATTCAGAAAGTAAAGTCTGCTGGACAGAGATGTCAACTTAAT 600
DB 541 TGTGCCAATGGGAATTCAGAAAGTAAAGTCTGCTGGACAGAGATGTCAACTTAAT 600
QY 601 GTCCCTTGAACAAAAGAGAGACGCTGTGATTAAGCCGCTACAAATGCGCAAGAGTGA 660
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QY 661 TGTGCTTATATGTGCTGGAACATGAGTCAAAATATTCAGATGATGATGAAAT 720
DB 661 TGTGCTTATATGTGCTGGAACATGAGTCAAAATATTCAGATGATGATGAAAT 720
QY 721 ACCACTCTGACACTGATCTATCTATTAATGAAGATTAATGAGCAAGCACTGCTTGA 780
DB 721 ACCACTCTGACACTGATCTATCTATTAATGAAGATTAATGAGCAAGCACTGCTTGA 780
QY 781 TATGAGTGTGATATGCAATCAAAAAGCAAGCATGAGGCTCACACCACTGTTACTTGTGTA 840
DB 781 TATGAGTGTGATATGCAATCAAAAAGCAAGCATGAGGCTCACACCACTGTTACTTGTGTA 840
QY 841 CATGACCAAAAACAGCAAGTCTGTAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900

DB 841 CATGACCAAAAACAGCAAGTCTGTAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
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DB 901 CTGATAGATATGGAAGAGCTGCTCATACTTGTGATGATGATGATGATGATGATGATGAT 960
QY 961 GTGAGCCTTCTACTTGAAGAAATATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
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DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCGAGTTACTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTTAAATCTTCTGAAACAGCAATTCAGAAAGCACTTAAAG 1140
DB 1081 AAGAAAAACAGATGCTTAAATCTTCTGAAACAGCAATTCAGAAAGCACTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGTCAAAAAGTTCAAAAGGCAAGTGAAGCCAGCAGAGAA 1200
DB 1141 CTGACATCAGAGAGAGTCAAAAAGTTCAAAAGGCAAGTGAAGCCAGCAGAGAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGATGATGATGATGATGATGATGATGATGAT 1260
DB 1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 1261 AAGCATGAAGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
DB 1261 AAGCATGAAGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
QY 1321 AATGATATATGATATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB 1321 AATGATATATGATATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCAATTTAGTTCTGACTCAAAAGAA 1440
DB 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGCAATTTAGTTCTGACTCAAAAGAA 1440
QY 1441 AAGCAATGCAAAATATCTTCTGAAACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1500
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QY 1561 TTTATGCTATCGAAGAAATGAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1620
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QY 1621 CTGACTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
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QY 1741 CAATAATGATCTCAGAAAGCAATTTTGTGAAGAACAGAACTGGAATATTTACAGATGAG 1800
DB 1741 CAATAATGATCTCAGAAAGCAATTTTGTGAAGAACAGAACTGGAATATTTACAGATGAG 1800
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QY 1861 CTTAGTTGTGAAGAAAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
DB 1861 CTTAGTTGTGAAGAAAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1920
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Db 1921 GCCATGCTAAGACTGAGCTAGACACAAATGAAATCAGAGCCAGCTTAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 3

US-09-780-669-374
; Sequence 374, Application US/09780669
; Patent No. US20020051977A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780.669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-780-669-374

Query Match 100.0%; Score 2000; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 AGGAGCAAGATGGGCAAGTGTGCTGCTGCTCCCTGCTGAGGAGAGCGGCAAG 120
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Qy 361 GGAGACTACGATGACAGTGCCTTCATGAGGCCAGTACCAAGCTCCCTGAGAGATCTG 420
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Db 1381 CCTGACACAGAAATGAGAGATATCAGAAATTTGCAATTTAGTTTGTGACTACAAAGAA 1440
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Db 1441 AAACAGATGCCAAATACTCTTCTGAAAACAGAACCCAGAACACTTAAAGCTGACA 1500
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Db 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGATGAAATAGTACGTTGGGGAGAAAT 1920
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Db 1921 GCCATGCTAAGACTGAGCTAGACACATGAAACATCAGAGCGCTAATAAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 4
US-09-810-936-302
; Sequence 302, Application US/09810936
; Patent No. US2002068285A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, David C.
; APPLICANT: Reiter, Marc W.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-936-302

Query Match 100.0%: Score 2000: DB 10: Length 2000:
Best Local Similarity 100.0%: Pred. No. 0:
Matches 2000: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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Db 1 ATGGTGGTTGAGGTGATTCATGCCGGCTGCTCTTCTGTGAAGAACCAATTTGGTCTC 60
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Db 61 AGGAGCAAGATGGGCAAGTGTGTGTCCTGCTTCCCTGTCGACAGGAGAGCGCCAG 120
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Db 121 AGCAAGTGGGCACTTCTGGAAGCAAGACGATCTGCTATGAAGACACTCAGAGCCAG 180
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Qy 301 TGGTGTGTCACACTGCTTCCCTGTCGACAGGAGAGCGGCAAGAGTGGGCGCTTG 360
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Qy 421 GACAACTCCACAGAGCTGCTGTTGGGTTAAAGTCCCGCAAGAAAGATCATGCTCAT 480
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Qy 481 CTGAGGACACATGACGTAAGAAAGCAAGAAAGCAAGAAAGCAAGTCTGCTGCTGCT 540
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Db 601 GTCTCTGACAAACAAAGAGAGAGACGCTCTGATTAAGAGCCGTACATGCCAGAAATGAA 660
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Db 721 ACCACTCTGACATGACGCTATCTATTAATGAAGATTAATGAGCAAGACGCTCTTA 780
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Db 781 TATGCTGTGATATGCAATCAAAAAACAGCATGAGCTTCACACACTGTTACTTGGTGA 840
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Qy 961 GTGAGCTTCTACTTACGCAAAATATGATGATATCTTCAAGATCATGTCAGACAG 1020
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Qy 1201 ATGTCTCAGAACGAGAAATTAATTAAGGATGATAGAGGTTGAAGAAATGAAG 1260
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Db 1321 AATGCTAATATGATTAATCTCTCAAAGAGAGCAGAACCTGAAATATCAGCAATTT 1380
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Db 1381 CTTGACAAACGAAAGTAAAGATATCAGAAATTTGCGAATTAATGTTCTGACTACAAAGAA 1440
Qy 1441 AAAAGATGCCAAATATCTCTGAAAAACGCAACCCAGAACAAAGCTTAAAGCTGACA 1500
Db 1441 AAAAGATGCCAAATATCTCTGAAAAACGCAACCCAGAACAAAGCTTAAAGCTGACA 1500
Qy 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGCGAGTAAATGSCCAGCCAGACTAGAAAT 1560
Db 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGCGAGTAAATGSCCAGCCAGACTAGAAAT 1560
Qy 1561 TTTATGCTATCGAAGAAATGAGAACGACGAAAGTACTCATGTCGGATTTCCAGAAAAAC 1620
Db 1561 TTTATGCTATCGAAGAAATGAGAACGACGAAAGTACTCATGTCGGATTTCCAGAAAAAC 1620
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Db 1621 CTGACTAATGTCGCTGCTGCTGCGAATGATGATGATTAATTTCTCCAGAGAAAGAC 1680
Qy 1681 AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAGATCACAGTACAGAA 1740
Db 1681 AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAGATCACAGTACAGAA 1740
Qy 1741 CAAAATGATCTCAGAAAGCAATTTTGTGAAGACAGAACTGGAATTTACACAGATAG 1800
Db 1741 CAAAATGATCTCAGAAAGCAATTTTGTGAAGACAGAACTGGAATTTACACAGATAG 1800
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Qy 1861 CTTAGTGTGAAGAAAGAAAGACATCTTTCATGATAATATAGCTTTCGCGGAGAAATTT 1920
Db 1861 CTTAGTGTGAAGAAAGAAAGACATCTTTCATGATAATATAGCTTTCGCGGAGAAATTT 1920
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Db 1921 GCCATGCTAAGACTGAGAGCTAGACAAATGAACATCAGAGCCAGCTAAAAAAGAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 5

US-09-822-827-374
; Sequence 374, Application US/09822827
; Patent No. US2002008160A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822.827

; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-374
Query Match 100.0%; Score 2000; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGTGTTGAGTTGATTCATGCGGCTGCTCTTCTGTGAAGAACCATTTGCTCTC 60
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Qy 61 AGAGCAAGATGGGCAAGTGTGCTGCGGTTGCTTCCCTCTGCTGAGGAGAGGGGCAAG 120
Db 61 AGAGCAAGATGGGCAAGTGTGCTGCGGTTGCTTCCCTCTGCTGAGGAGAGGGGCAAG 120
Qy 121 AGCAACGTGGGCACTTCTGGAGACACGACGACTCTGCTATGAAGACACTCAGAGCAAG 180
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Db 541 TCTGCAATGGGAATTCAGAAATAGTAAACTCTGCTGACAGAGATGCTCAACTTAAT 600
Qy 601 GTCTTGAACAACAAAAGAGAGAGCTGTGATTAAGGCCGTACATATGCGAGAGATGAA 660
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Qy 661 TGTGCTTAATGTTGCTGAGAACATGGCAGCTGATCCAAATTTCCAGATGAGATGGAAT 720
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Qy 721 ACCACTCTGACACTACGCTATCTATATGAATGAATTAATGAGCAAGCAAGCAAGCTGCTTA 780
Db 721 ACCACTCTGACACTACGCTATCTATATGAATGAATTAATGAGCAAGCAAGCAAGCTGCTTA 780
Qy 781 TATGCTGTGATATGCAATCAAAAAACAGATGAGCTGCTACACCACTGTTCTGCTGCTA 840
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Qy 841 CATGAGCAAAACAGCAAGTGTGAATTTTATTCAGAAAGAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAACAGCAAGTGTGAATTTTATTCAGAAAGAAAGCAATTTAAATGCA 900

Qy	901	CTGATAGATATGGAAGACTGCTCTCATACTTGCTGTATATGTTGGATCAAGCATATA	960
Dp	901	CTGGATATGATATGGAAGACTGCTCTCAACTTGGTGTATGTTGGATCAAGCATATA	960
Qy	961	GTCAGCCTTACTTGTAGCAAAATATATGATATCTTCCAAAGATCTATCGACAGACG	1020
Dp	961	GTCAGCCTTACTTGTAGCAAAATATGATATCTTCCAAAGATCTATCTGGACAGACG	1020
Qy	1021	GCCAGAGATATGCTGTTTCTTACTCATCATATGTAATTTGGCACTTACTTTCGACTAC	1080
Dp	1021	GCCAGAGATATGCTGTTTCTTACTCATCATATGTAATTTGGCACTTACTTTCGACTAC	1080
Qy	1081	AAAGAAAACAGATGCTAAAAATCTTGTGAAAACAGCAATCCAGAACAAAGACTTAAG	1140
Dp	1081	AAAGAAAACAGATGCTAAAAATCTTGTGAAAACAGCAATCCAGAACAAAGACTTAAG	1140
Qy	1141	CTGCATCAGAGGAAGTGCACAAAGCTTCAAAAGGAGTGAATAATAGCAGCCAGAGAA	1200
Dp	1141	CTGCATCAGAGGAAGTGCACAAAGCTTCAAAAGGAGTGAATAATAGCAGCCAGAGAA	1200
Qy	1201	ATGCTTCAGAACACAGAAATAAATAAGATGGTGTAGAGAGTGTGAAGAATAATGAG	1260
Dp	1201	ATGCTTCAGAACACAGAAATAAATAAGATGGTGTAGAGAGCTTGAAGAATAATGAG	1260
Qy	1261	AAGCATGAAGTATATTAATGTGGATTACTAGAAAACCTGACTAATGTGTCACTGTGCG	1320
Dp	1261	AAGCATGAAGTATATTAATGTGGATTACTAGAAAACCTGACTAATGTGTCACTGTGCG	1320
Qy	1321	AATGCTATATGATTAATCTCTCAAGGAAGACAGAACCTGAAATTCACCAATTT	1380
Dp	1321	AATGCTATATGATTAATCTCTCAAGGAAGACAGAACCTGAAATTCACCAATTT	1380
Qy	1381	CCTGACACAGAAAGTGAAGAGTATCACAATAATTCGAAATTTAGTTTCTGCATACAAAGA	1440
Dp	1381	CCTGACACAGAAAGTGAAGAGTATCACAATAATTTGGAAATTTAGTTTCTGCATACAAAGA	1440
Qy	1441	AAACAGATGCCAAATATCTTCTGAAAACAGCAACCAGAACAAAGACTTAAGCTGACA	1500
Dp	1441	AAACAGATGCCAAATATCTTCTGAAAACAGCAACCAGAACAAAGACTTAAGCTGACA	1500
Qy	1501	TCACAGAAAGTGCACAAAGGCTTGAGGGCAGTGAATAATGGCAGCCAGACTTGAATAAT	1560
Dp	1501	TCACAGAAAGTGCACAAAGGCTTGAGGGCAGTGAATAATGGCAGCCAGACTTGAATAAT	1560
Qy	1561	TTTATGCTATCGAAGAAATGAAGAAGCAGCAAGTACTCATGTGGATTCOCAGAAAAC	1620
Dp	1561	TTTATGCTATCGAAGAAATGAAGAAGCAGCAAGTACTCATGTGGATTCOCAGAAAAC	1620
Qy	1621	CTGACTAATGSGTGCACCTGCTGGCAATGGTGTATGATGATTAATTCCTCAGGAAGAGC	1680
Dp	1621	CTGACTAATGSGTGCACCTGCTGGCAATGGTGTATGATGATTAATTCCTCAGGAAGAGC	1680
Qy	1681	AGAACACCTTAAAGCCAGCAATTTCTGTGACACTGAGAAATGAAGATATCACAGTGCAG	1740
Dp	1681	AGAACACCTTAAAGCCAGCAATTTCTGTGACACTGAGAAATGAAGATATCACAGTGCAG	1740
Qy	1741	CAAAATATATCTCAGAAAGCAATTTTGTGAAGAACAGAACTGGAATTTTACAGATGAG	1800
Dp	1741	CAAAATATATCTCAGAAAGCAATTTTGTGAAGAACAGAACTGGAATTTTACAGATGAG	1800
Qy	1801	ATTCTGATTCATGAGAAAGACAGATAGAAAGTGTGAAAAAATAATTCGTGAGCTTCT	1860
Dp	1801	ATTCTGATTCATGAGAAAGACAGATAGAAAGTGTGAAAAAATAATTCGTGAGCTTCT	1860
Qy	1861	CTTATGTTGTAAAGAAAGAAAGCATCTTGTCATGAATAATAGTACCTTGGGGAGAAATTT	1920
Dp	1861	CTTATGTTGTAAAGAAAGAAAGCATCTTGTCATGAATAATAGTACCTTGGGGAGAAATTT	1920
Qy	1921	GCCATGCTAAGACGCGGAGTACAGACAAATGAAGAAACATCAGAGCTCAAAAAA	1980
Dp	1921	GCCATGCTAAGACGCGGAGTACAGACAAATGAAGAAACATCAGAGCTCAAAAAA	1980
Qy	1981	AAAAAAAAAAAAAAAAAAAA 2000	

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Db      1981 AAAAAAAAAAAAAAAAAAAAAA 2000

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RESULT 6
; Sequence 302, Application US/09429755A
; Patent No. US20020111467A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Reiter, Marc W.
; APPLICANT: Dillon, David C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-302

Query Match      100.0%; Score 2000; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGGGCGTTGAGGTTGATTCATCCGCGCTGCGCTCTCTGTGGAAGAGCATTTGGCTC 60
DB      1 ATGGGCGTTGAGGTTGATTCATCCGCGCTGCGCTCTCTGTGGAAGAGCATTTGGCTC 60

QY      61 AGGAGCAAGATGGGCAATGGTGTGCTGCCGTTGCTTCCCTGCTGACAGGAGCGGCAAG 120
DB      61 AGGAGCAAGATGGGCAATGGTGTGCTGCCGTTGCTTCCCTGCTGACAGGAGCGGCAAG 120

QY      121 AGCAACGTTGGGCACTTCTGGAGACCAGAGCACTCTCTATGAAGACACTCAGAGCAAG 180
DB      121 AGCAACGTTGGGCACTTCTGGAGACCAGAGCACTCTCTATGAAGACACTCAGAGCAAG 180

QY      181 ATGGGCAAGTGTGGCGCGCACTGCTTCCCTGCTGACAGGGGAGATGGCAAGCAAGTGTG 240
DB      181 ATGGGCAAGTGTGGCGCGCACTGCTTCCCTGCTGACAGGGGAGATGGCAAGCAAGTGTG 240

QY      241 GCGCGCTTGTGAGACCAAGCAAGCACTGTCTATGAAGCACTCAGAGCAAGATGGGCAAG 300
DB      241 GCGCGCTTGTGAGACCAAGCAAGCACTGTCTATGAAGCACTCAGAGCAAGATGGGCAAG 300

QY      301 TGTGCTCTCCCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGCAAGTGGGCGCTTGG 360
DB      301 TGTGCTCTCCCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGCAAGTGGGCGCTTGG 360

QY      361 GGAGACTCGATGAGAGGCTTCTATGAGAGCCAGGATACCAACGCGTGGAGAGATCTG 420
DB      361 GGAGACTCGATGAGAGGCTTCTATGAGAGCCAGGATACCAACGCGTGGAGAGATCTG 420

QY      421 GACAAGCTCCACAGAGCTGCTGGTGGGGTTAAAGTATCCCAAGAAAGATTCATCTGATG 480
DB      421 GACAAGCTCCACAGAGCTGCTGGTGGGGTTAAAGTATCCCAAGAAAGATTCATCTGATG 480

QY      481 CTCAGGGAAGCTGAGCTGACCAAGAGCAAGCAAGCAAGAGAGAGCTCTTACATCTGGCC 540
DB      481 CTCAGGGAAGCTGAGCTGACCAAGAGCAAGCAAGCAAGAGAGAGCTCTTACATCTGGCC 540

QY      541 TCTGCCAATGGGAATTCGAAAGTGTGTAAGAGCCCTTACAAATGCCAGGAAGATGAA 600
DB      541 TCTGCCAATGGGAATTCGAAAGTGTGTAAGAGCCCTTACAAATGCCAGGAAGATGAA 600

QY      601 GTCTTGGCAACAAAGAGGAGCAAGCTCTGTATTAAGCCCTTACAAATGCCAGGAAGATGAA 660

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Db 601 GTCCCTTACACAAAAAGAGACAGCTGTATAAGCCGCTACAAATCCCGAAGAAAGAA 660
Qy 661 TGTCCGTTAATGTTGTGGAACATGAGCATGATCCAAATATTTCCAGATGATGAAAT 720
Db 661 TGTCCGTTAATGTTGTGGAACATGAGCATGATCCAAATATTTCCAGATGATGAAAT 720
Qy 721 ACCACTGTGACACTAGCTATCTATATGAATAAATTAATGGCCAAAGCACTGCTTA 780
Db 721 ACCACTGTGACACTAGCTATCTATATGAATAAATTAATGGCCAAAGCACTGCTTA 780
Qy 781 TATGTCCTGATATCGAATCAAAAAACAGATGGCTCACACGACTGTTACTTGGTGA 840
Db 781 TATGTCCTGATATCGAATCAAAAAACAGATGGCTCACACGACTGTTACTTGGTGA 840
Qy 841 CATGAGCAAAAACAGCAAGTCGTAAATTTTAAATCAAGAAAAAGGAAATTAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGTCGTAAATTTTAAATCAAGAAAAAGGAAATTAATGCA 900
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Db 901 CTGATATGATATGGAAGAGCTGCTCTCATCTGCTATGTTGTGATCAGCAAGTATA 960
Qy 961 GTCAAGCTTCTACTTGACAAAATATTGATGATCTTCTCAAGATCTATCTGACAGAG 1020
Db 961 GTCAAGCTTCTACTTGACAAAATATTGATGATCTTCTCAAGATCTATCTGACAGAG 1020
Qy 1021 GCCAGAGATATGCTGTTTGTAGTCATCATGATATTTGGCCAGTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTGTAGTCATCATGATATTTGGCCAGTACTTCTGACTAC 1080
Qy 1081 AAGAAAAACAGATGCTAAAAATCTCTTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
Db 1081 AAGAAAAACAGATGCTAAAAATCTCTTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
Qy 1141 CTGACATCAAGAGAGAGTACAAAGTTCAAAAGGCGTGAATATACCGACGAGAGAA 1200
Db 1141 CTGACATCAAGAGAGAGTACAAAGTTCAAAAGGCGTGAATATACCGACGAGAGAA 1200
Qy 1201 ATGCTCAAGAACAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAAAGAAATAG 1260
Db 1201 ATGCTCAAGAACAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAAAGAAATAG 1260
Qy 1261 AAGCAGAAAGTAATTAATGTTGGGATTACTAGAAAACTGACTAAATGGTGTCTGCG 1320
Db 1261 AAGCAGAAAGTAATTAATGTTGGGATTACTAGAAAACTGACTAAATGGTGTCTGCG 1320
Qy 1321 AATGCTGATATGATTAATTTCTCAAGAGAGAGAGCACTGTGAATTTGACTACAAAGAA 1380
Db 1321 AATGCTGATATGATTAATTTCTCAAGAGAGAGAGCACTGTGAATTTGACTACAAAGAA 1380
Qy 1381 CTTGACAAAGAAAGTGAAGATATACAGAAATTTGCAATTAATTTGACTACAAAGAA 1440
Db 1381 CTTGACAAAGAAAGTGAAGATATACAGAAATTTGCAATTAATTTGACTACAAAGAA 1440
Qy 1441 AAACAGATGCCAAATATCTCTTGAAAAACAGCAATCCAGAACAGACTTAAGCTGACA 1500
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Db 1501 TCAGAGAAAGATCAAAAGGCTTGAGGAGAGTGAATTTGGCCAGGAGAGCTAGAAAT 1560
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Db 1561 TTTATGCTTATCGAAGAAATGAAGAGCAGGAACTATGTCGATTTCCAGAAAG 1620
Qy 1621 CTGACTAATATGTTGCTGCTGCAATGATGATGATGATTAATTTCTCCAGAGAGAGC 1680
Db 1621 CTGACTAATATGTTGCTGCTGCAATGATGATGATGATTAATTTCTCCAGAGAGAGC 1680
Qy 1681 AGAACACCTTAAGCCAGCAATTTCTGACATGAGAGAAATTAATTTCTCCAGAGAGAG 1740
Db 1681 AGAACACCTTAAGCCAGCAATTTCTGACATGAGAGAAATTAATTTCTCCAGAGAGAG 1740

Db 1681 AGAACACCTTAAGCCAGCAATTTCTGACATGAGAGAAATTAATTTCTCCAGAGAGAG 1740
Qy 1741 CAAATATGATCTAGAGCAATTTTGTGAAGACAGAACTGGAAATATTACAGATAG 1800
Db 1741 CAAATATGATCTAGAGCAATTTTGTGAAGACAGAACTGGAAATATTACAGATAG 1800
Qy 1801 ATTCTGATTCAGAGAAAGAGAGATGAAAGTGGTTGAAAAATGAATTTGAGCTTCT 1860
Db 1801 ATTCTGATTCAGAGAAAGAGAGATGAAAGTGGTTGAAAAATGAATTTGAGCTTCT 1860
Qy 1861 CTTAGCTTGAAGAAAGAAAGACATCTGATGAATTAATGATGCTGGGGAAGAAAT 1920
Db 1861 CTTAGCTTGAAGAAAGAAAGACATCTGATGAATTAATGATGCTGGGGAAGAAAT 1920
Qy 1921 GCCATGCTAAGACTGAGCTAGACAAATGAATGAATCAGAGCCAGCTAAAAA 1980
Db 1921 GCCATGCTAAGACTGAGCTAGACAAATGAATGAATCAGAGCCAGCTAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 7
US-09-825-301-7
; Sequence 7, Application US/09825301
; Patent No. US2002009738A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Dillon, David C.
; APPLICANT: Molesh, David A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Zehntner, Barbara
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
; FILE REFERENCE: 210121.513
; CURRENT APPLICATION NUMBER: US/09/825.301
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-825-301-7

Query Match 77.5%; Score 1551; DB 10; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTGGTTGAGGTTGATTCATGCGCGCTGCGCTCTCTGTGAAGAGCCATTTGGTCTC 60
Db 1 ATGGTGGTTGAGGTTGATTCATGCGCGCTGCGCTCTCTGTGAAGAGCCATTTGGTCTC 60
Qy 61 AGGAGCAAGATGGGCAAGTGGTCTGCTGCTTCCCTGCTGTCAGAGGAGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGGTCTGCTGCTTCCCTGCTGTCAGAGGAGAGCGGCAAG 120
Qy 121 AGCAAGCTGGGCACTTCTGAGACACGACGACTCTGCTATGAAGACATCAGAGCAAG 180
Db 121 AGCAAGCTGGGCACTTCTGAGACACGACGACTCTGCTATGAAGACATCAGAGCAAG 180
Qy 181 ATGGGCAAGTGGGCGCGCCCTGCTTCCCTGCTGTCAGAGGAGGAGTGGCAAGCAAG 240
Db 181 ATGGGCAAGTGGGCGCGCCCTGCTTCCCTGCTGTCAGAGGAGGAGTGGCAAGCAAG 240
Qy 241 GGGCTTCTGAGAGACGACGACTGCTATGAAGACATCAGAGCAAGATGGGCAAG 300
Db 241 GGGCTTCTGAGAGACGACGACTGCTATGAAGACATCAGAGCAAGATGGGCAAG 300
Qy 301 TGGTGTGCTGCTGCTTCCCTGCTGAGGAGGAGGAGGAGCAAGGATGGGCGCTTG 360
Db 301 TGGTGTGCTGCTGCTTCCCTGCTGAGGAGGAGGAGGAGCAAGGATGGGCGCTTG 360

Db 301 TGGTGTCCACTGTTCCCTGCTGTCAGAGGGGAGCGCAAGACAGATGGGCGCTTG 360
QY 361 GGAGACTAGATGACAGTGGCTTCATGAGCCAGGTACAGCTCCGTGGAGAAATCTCG 420
Db 361 GGAGACTAGATGACAGTGGCTTCATGAGCCAGGTACAGCTCCGTGGAGAAATCTCG 420
QY 421 GACAACTCCACAGAGCTCCGTGGGTTAAAGTCCAGAAAGATGTCATCGCATG 480
Db 421 GACAACTCCACAGAGCTCCGTGGGTTAAAGTCCAGAAAGATGTCATCGCATG 480
QY 481 CTCAGGAGACTGACGTGAACAAGAGCAACAAAGAGAGCTCTCTACATCTGGCC 540
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Db 541 TCTGCCAATGGGAATCAAGAGTAAACCTCTCTGAGAGAGATGTCACCTTAAT 600
QY 601 GTCTTTGACAAACAAAGAGAGAGCTGTGATTAAGCCGTACAAATGCCAGAAATGAA 660
Db 601 GTCTTTGACAAACAAAGAGAGAGCTGTGATTAAGCCGTACAAATGCCAGAAATGAA 660
QY 661 TGTGCTTAATGTGCTGGAACATGGCAGTATCCAAATATTCAGATGATGTAAT 720
Db 661 TGTGCTTAATGTGCTGGAACATGGCAGTATCCAAATATTCAGATGATGTAAT 720
QY 721 ACCACTCTGACAGCTCTATATGAAGTAAATTAATGCCAAACAGCTGCTTA 780
Db 721 ACCACTCTGACAGCTCTATATGAAGTAAATTAATGCCAAACAGCTGCTTA 780
QY 781 TATGCTGTGATATCGAATCAAAAAACAAGCATGGCTCACACAGCTGTTACTTGGTGA 840
Db 781 TATGCTGTGATATCGAATCAAAAAACAAGCATGGCTCACACAGCTGTTACTTGGTGA 840
QY 841 CATGACAAAACAGCAAGCTGTAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
Db 841 CATGACAAAACAGCAAGCTGTAATTTTATCAAGAAAAAGCGAATTTAAATGCA 900
QY 901 CTGGATAGATGGAAGAGCTGCTCATCTGCTGATGTTGGTGGATCAGCAATATA 960
Db 901 CTGGATAGATGGAAGAGCTGCTCATCTGCTGATGTTGGTGGATCAGCAATATA 960
QY 961 GTGAGCTTCTACTTGAGCAAAATATTTGATGATCTTCTCAAGATCTATCTGAGACAG 1020
Db 961 GTGAGCTTCTACTTGAGCAAAATATTTGATGATCTTCTCAAGATCTATCTGAGACAG 1020
QY 1021 GCCAGAGATGCTGTTCTAGTCAATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
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QY 1081 AAGAAACAGATGCTTAATAATCTTCTGAAAAACAGCAATCCAGAACAGCTTAAG 1140
Db 1081 AAGAAACAGATGCTTAATAATCTTCTGAAAAACAGCAATCCAGAACAGCTTAAG 1140
QY 1141 CTGACATCTCAGAGAGAGTACAAAGGTTCAAGGAGTGAATATGCCAGCAGAGAAA 1200
Db 1141 CTGACATCTCAGAGAGAGTACAAAGGTTCAAGGAGTGAATATGCCAGCAGAGAAA 1200
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Db 1201 ATGCTCAAGAACCAAGAAATTAATTAAGATGTGATAGAGAGTTGAAGAAATGAAG 1260
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Db 1261 AAGCATGAAGTAAATATGAGGATTAATGAAACCTGACTAATGCTGCTGCTGGC 1320
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Db 1321 AATGCTGAATGATTAATCTTCAAGAGAGAGCAACACCTGAAAAATGCAATTT 1380
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QY 1441 AAGACAGTGCAGAAATATCTTCTGAAAAACAGCAACCCAGAAACAGTAAAGCTGACA 1500
Db 1441 AAGACAGTGCAGAAATATCTTCTGAAAAACAGCAACCCAGAAACAGTAAAGCTGACA 1500
QY 1501 TCAGAGAGAGTACACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCAGAG 1551
Db 1501 TCAGAGAGAGTACACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCAGAG 1551

RESULT 8
US-09-759-143-375
; Sequence 375, Application US/09759143
; Patent No. US200202248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Wang, Aljun
; APPLICANT: L1, Samuel
; APPLICANT: Skelky, Yasil A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-375

Query Match 77.5%; Score 151; DB 10; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGTGAGTGGTATTCATGCGCGGCTCTTCTGTGAAGAACATTTGGCTTC 60
Db 1 ATGCTGTGAGTGGTATTCATGCGCGGCTCTTCTGTGAAGAACATTTGGCTTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGTTCCTGCTGCGAGGAGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGTGCTGCGTTCCTGCTGCGAGGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGACACAGAGACTGTGTAAGACACTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTGAGACACAGAGACTGTGTAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGGCGGCACTGCTCCCTGCTGAGGGGGAGTGGCAAGCAACGTC 240
Db 181 ATGGGCAAGTGGGCGGCACTGCTCCCTGCTGAGGGGGAGTGGCAAGCAACGTC 240
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Db 241 GCGGCTTCTGAGACACAGACGACTGCTATGAACACTCAGAAAGATGGGCAAG 300
QY 301 TGGTGTGCACTGTTCCCTGCTGACAGGGGAGCGCAAGAGCAAGGTGGGCGCTTGG 360
Db 301 TGGTGTGCACTGTTCCCTGCTGACAGGGGAGCGCAAGAGCAAGGTGGGCGCTTGG 360

QY 361 GGAGACTACGATGACAGTGCCTTCATGAGCCAGGTACCACTCCGTGGAGAGATCTG 420
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Db 361 GGAGACTACGATGACAGTGCCTTCATGAGCCAGGTACCACTCCGTGGAGAGATCTG 420
QY 421 GACAAGCTCCACAGAGTGCCTGGTGGGTTAAAGTCCCAAGAAAGATCTATGTCATG 480
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Db 421 GACAAGCTCCACAGAGTGCCTGGTGGGTTAAAGTCCCAAGAAAGATCTATGTCATG 480
QY 481 CTCAGGAGACTGACGTGACCAAGAGGACCAAGGAGAGGAGTCTCATCTTGACC 540
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Db 481 CTCAGGAGACTGACGTGACCAAGAGGACCAAGGAGAGGAGTCTCATCTTGACC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGACAGACGATGTCACTTAAT 600
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Db 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGACAGACGATGTCACTTAAT 600
QY 601 GTCCCTTGACCAAAAAAGAGACAGCTCTGTATAAGGCCGTACAAATGCCAAGAGATGAA 660
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Db 601 GTCCCTTGACCAAAAAAGAGACAGCTCTGTATAAGGCCGTACAAATGCCAAGAGATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTTCCAGATGATGGAAT 720
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Db 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTTCCAGATGATGGAAT 720
QY 721 ACCACTCTGACCTACGCTATCTATATGAAAGATAAATTAATGACCAGACCTGCTTTA 780
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Db 721 ACCACTCTGACCTACGCTATCTATATGAAAGATAAATTAATGACCAGACCTGCTTTA 780
QY 781 TATGTCGTGATATGCAATCAAAAAAGAGATGGCCCTACACCACTGTACTTGCTGTTA 840
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Db 781 TATGTCGTGATATGCAATCAAAAAAGAGATGGCCCTACACCACTGTACTTGCTGTTA 840
QY 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATCA 900
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Db 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATCA 900
QY 901 CTGATATGATATGGAAGAGATGCTCTCATCTGCTGATGTTGGATCAGCAATGTA 960
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Db 901 CTGATATGATATGGAAGAGATGCTCTCATCTGCTGATGTTGGATCAGCAATGTA 960
QY 961 GTGAGCCTTCTACTGAGCAAAATATGATGATCTCTCTCAAGATCTATCTGAGACAGCG 1020
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Db 961 GTGAGCCTTCTACTGAGCAAAATATGATGATCTCTCTCAAGATCTATCTGAGACAGCG 1020
QY 1021 GCCAGAGATGCTGTTTCTAGTCATCATCATTAATTTCCAGTACTTTCGACTAC 1080
|||||
Db 1021 GCCAGAGATGCTGTTTCTAGTCATCATCATTAATTTCCAGTACTTTCGACTAC 1080
QY 1081 AAAAGAAAAAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAAAGACTTAAAG 1140
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Db 1081 AAAAGAAAAAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAAAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGTGCACAAAGGTTCAAGGCGAGTGAATPAGCCAGACGAGAAA 1200
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Db 1141 CTGACATCAGAGAGAGTGCACAAAGGTTCAAGGCGAGTGAATPAGCCAGACGAGAAA 1200
QY 1201 ATGCTCTCAAGAACAGAAATTAATTAAGATGCTGATAGAGAGGTTGAAGAAATGAG 1260
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Db 1201 ATGCTCTCAAGAACAGAAATTAATTAAGATGCTGATAGAGAGGTTGAAGAAATGAG 1260
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Db 1261 AAGCATGAAATTAATATGTTGGATTTACTAGAAAACTGACTTAATGTTGCTACTGCTGC 1320
QY 1321 AATGCTGATATGATTAATCTCTCAAGAGAGACAGAAACCTGAAATACAGCAATTT 1380
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Db 1321 AATGCTGATATGATTAATCTCTCAAGAGAGACAGAAACCTGAAATACAGCAATTT 1380
QY 1381 CCTGACAAAGAAATGAGAGATATCAGAAATTTGCGAATAGTTTCTGACTACAAAGAA 1440
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Db 1381 CCTGACAAAGAAATGAGAGATATCAGAAATTTGCGAATAGTTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAAAATCTCTTCTGAAAAACAGAAACCCAGAAAGACTTAAAGCTGACA 1500
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Db 1441 AAACAGATGCCAAAAATCTCTTCTGAAAAACAGAAACCCAGAAAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGTCCAAAGGCTTGAGGGCGAGTGAATGGCCAGCCAGAG 1551
Db 1501 TCAGAGAGAGAGTCCAAAGGCTTGAGGGCGAGTGAATGGCCAGCCAGAG 1551
RESULT 9
US-09-780-669-375
: Sequence 375, Application US/09780669
: Patent No. US2002051977A1
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, David C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yuqi
: APPLICANT: Henderson, Robert A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Derrick
: APPLICANT: Li, Samuel
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William
: APPLICANT: Hurst, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghton, Raymond L.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.427C24
: CURRENT APPLICATION NUMBER: US/09/780.669
: CURRENT FILING DATE: 2001-02-09
: NUMBER OF SEQ ID NOS: 943
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 375
: LENGTH: 2040
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-780-669-375
Query Match 77.5%; Score 1551; DB 10; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1551; Conservative 0;
QY 1 ATGCTGTTGAGTGTGATTCATCCATGCCGCTGCTCTTCTGTGAAGAACCATTTGCTCTC 60
Db 1 ATGCTGTTGAGTGTGATTCATCCATGCCGCTGCTCTTCTGTGAAGAACCATTTGCTCTC 60
QY 61 AGAGCAAGATGGCAAGTGTGCTGCCGTTGCTTCCCTCTCTCAGGAGAGCGGCAAG 120
Db 61 AGAGCAAGATGGCAAGTGTGCTGCCGTTGCTTCCCTCTCTCAGGAGAGCGGCAAG 120
QY 121 AGCAAGCGGGCAGCTTTCGAGACACAGAGACTCTGCTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAAGCGGGCAGCTTTCGAGACACAGAGACTCTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGCAAGTGTGCTCCGCACTGCTCCCTGCTGCAAGGGGAGTGGCAAGCAAGTG 240
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QY 241 GGGCCTTCTGAGAACACAGAGACTCTGCTATGAAAGACTCAGAAACAGATGGCAAG 300
Db 241 GGGCCTTCTGAGAACACAGAGACTCTGCTATGAAAGACTCAGAAACAGATGGCAAG 300
QY 301 TGTGTCGCGCCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGTGGGCGTTGG 360
Db 301 TGTGTCGCGCCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGTGGGCGTTGG 360

QY 361 GGAGACTAGATGACAGTGCCTTCATGAGCCAGGTACACAGTCCGTGGAGAAATCTG 420
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 DB 361 GGAGACTAGATGACAGTGCCTTCATGAGCCAGGTACACAGTCCGTGGAGAAATCTG 420
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 DB 481 CTCAGGAGACACTGAGCTGAACAAGAGCAAGCAAAAGAGACTGCTTACATCTGGCC 540
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 DB 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCTCTGAGACAGAGATGTCACATTAAT 600
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 QY 721 ACCACTCTGACTAGCTATCTATATGAAGATPAAATATGAGCCCAAGACAGTCTCTTA 780
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 DB 721 ACCACTCTGACTAGCTATCTATATGAAGATPAAATATGAGCCCAAGACAGTCTCTTA 780
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 DB 781 TATGGTGTGATATGCAATCAAAAAACAAGCATGGCCCTCACACACTGTTACTTGGTGA 840
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 DB 841 CATGAGCAAAAAACAGCAAGTCTGAAATTTTATCAAGAAAAACGGAATTTAAATGCA 900
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 DB 961 GTGAGCTTCTACTGAGCAAAATATGATGATATCTTCAAGATCATCTGAGACAGAG 1020
 QY 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
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 DB 1261 AAGCATGAAGATTAATTAATGAGGATTAAGTGAAGAACTGATTAAGTGTGCTGCTGGC 1320
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 DB 1321 AATGATTAATGATTAATCTCTCAAGAGAGAGCAACCTGAAATACGCAATTT 1380
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 DB 1441 AACAGATGCCAAATACTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
 QY 1501 TCAGAGGAAGAGTCCACAAAGGCTTGAGGGCAGTGAATAATGCGCAGCCAGAG 1551
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 DB 1501 TCAGAGGAAGAGTCCACAAAGGCTTGAGGGCAGTGAATAATGCGCAGCCAGAG 1551
 RESULT 10
 US-09-810-936-303
 ; Sequence 303, Application US/09810936
 ; Patent No. US20020068285A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Frudakis, Tony N.
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Smith, John M.
 ; APPLICANT: Misher, Linda E.
 ; APPLICANT: Dillon, David C.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yashir A.W.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Day, Craig H.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 ; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
 ; FILE REFERENCE: 210121.419C11
 ; CURRENT FILING DATE: 2001-03-16
 ; NUMBER OF SEQ ID NOS: 334
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 303
 ; LENGTH: 2040
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-09-810-936-303
 Query Match 77.5%; Score 1511; DB 10; Length 2040;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAGTGGTGGAGTGGATTCATGCGCGCTGCTTCTGTGAAAGAACCATTTGGTCTC 60
 |||||
 DB 1 ATGAGTGGTGGAGTGGATTCATGCGCGCTGCTTCTGTGAAAGAACCATTTGGTCTC 60
 QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGCTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
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 DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCGCTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
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 DB 121 AGCAAGTGGGCACTTCTGGAGACGACGAGACTGCTATGAAAGACACTCAGAGACAAAG 180
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 DB 181 ATGGGCAAGTGTGCGCGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGACAGTG 240
 QY 241 GCGGCTTCTGAGACCCACAGACGACTGCTATGAAAGACACTCAGAAAGATGGGCAAG 300
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 DB 241 GCGGCTTCTGAGACCCACAGACGACTGCTATGAAAGACACTCAGAAAGATGGGCAAG 300
 QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGGAGGCGGCAAGGATGGGCGCTTGG 360
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 DB 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGGAGGCGGCAAGGATGGGCGCTTGG 360
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 DB 361 GGAGACTAGATGACAGTGCCTTCATGAGCCAGGTACACAGTCCGTGGAGAAATCTG 420
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 DB 421 GACAAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAGAAAGATCTCATCTGATG 480


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Db 781 TATGGTGTGATATGTAATCAAAAAACAAGCATGGGCTCACACCACTGTTACTGGGTGA 840
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Db 961 GTCACGCTTCTACTGAGCAAAATATGATATCTTCAAGATCTATCTGGACAGAG 1020
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Oy 1321 AATGATGATATGATTAATCTCTCAAAAGAGAGAGAGCAACCTGAAATAATGAGCAATT 1380
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Db 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGGCAGTGAATAATGGCGACGAGAG 1551

RESULT 12
US-09-429-755-303
; Sequence 303. Application US/09429755A
; Patent No. US20020111467A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, David C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-303

Query Match          77.5%; Score 1551; DB 10; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGTGTGTTGAGGTGATTCATGCCGGCTGCTTCTGTGAAGAACCAATTTGGTCTC 60
Db 1 ATGTGTGTTGAGGTGATTCATGCCGGCTGCTTCTGTGAAGAACCAATTTGGTCTC 60
Oy 61 AAGAGCAAGATGAGCAAGTGTGCTGCTTCCCTGCTGCGAGGAGAGCGGCAAG 120
Db 61 AAGAGCAAGATGAGCAAGTGTGCTGCTTCCCTGCTGCGAGGAGAGCGGCAAG 120
Oy 121 AACCAAGTGGGACCTTCTGGAAGCCAGACGACTGCTATGAAAGCACTCAGAGCAAG 180
Db 121 AACCAAGTGGGACCTTCTGGAAGCCAGACGACTGCTATGAAAGCACTCAGAGCAAG 180
Oy 181 ATGGGCAAGTGGTGCAGCTGCTTCCCTGCTGCGAGGAGAGTGGCAAGCAAGCTG 240
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Oy 361 GGAGACTACGATGACAGTCCCTTCATGAGCCAGGTACACGCTCCGTGGAGAAGTCTG 420
Db 361 GGAGACTACGATGACAGTCCCTTCATGAGCCAGGTACACGCTCCGTGGAGAAGTCTG 420
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Db 721 ACCACTCTGCACCTACGCTATCTATATGAAGATTAATTAATGCGCAAAAGCCTGCTTA 780
Oy 781 TATGGTGTGATATGGAATCAAAAAACAAGCATGGGCTCACACCACTGTTACTGGGTGA 840
Db 781 TATGGTGTGATATGGAATCAAAAAACAAGCATGGGCTCACACCACTGTTACTGGGTGA 840
Oy 841 CATGAGCAAAAACACAGCAAGTCTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
Db 841 CATGAGCAAAAACACAGCAAGTCTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
Oy 901 CTGGATAGATATGGAAGGACTGCTCATCTTCTGTATGTGTGGATCAGCAAGTATA 960
Db 901 CTGGATAGATATGGAAGGACTGCTCATCTTCTGTATGTGTGGATCAGCAAGTATA 960
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RESULT 14
US-09-759-143-373
; Sequence 373, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jlang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-373

Query Match          56.4%; Score 1128; DB 10; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTGTTGAGTTGATTCATGCGCGGCTGCTTCTTGTAAGAAAGCATTTGGTCTC 60
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QY 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAACGTG 240
DB 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAACGTG 240

QY 241 GGGCGTTTGGAGACGACGACGACTGCTATGAAGACACTCAGAAACAAGTGGGCAAG 300
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QY 301 TGGTCTGCACTGCTTCCCTGCTGCAAGGAGGAGCGCAAGAGTGGGCGCTTGG 360
DB 301 TGGTCTGCACTGCTTCCCTGCTGCAAGGAGGAGCGCAAGAGTGGGCGCTTGG 360

QY 361 GGAGACTAGATGACAGTGCCTTTCATGAGCCAGGTACCAAGTCCGTTGAGAAATCTG 420
DB 361 GGAGACTAGATGACAGTGCCTTTCATGAGCCAGGTACCAAGTCCGTTGAGAAATCTG 420

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DB 421 GACAAGCTCCACAGAGCGCTGGTGGGTAAGTCCCAAGAAAGATCTCATCGTCAG 480

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RESULT 15
US-09-780-669-373
; Sequence 373, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jlang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hurl, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
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; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-780-669-373

Query Match      56.4%; Score 1128; DB 10; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGTTGATTCATCCCGCTCCCTCTCTGTGAAGAGCCATTGGTCTC 60
DB 1 ATGGTGGTTGAGTTGATTCATCCCGCTCCCTCTCTGTGAAGAGCCATTGGTCTC 60

QY 61 AGGAGCAAGATGGGCAAGTGGTGGTCCGTTGCTTCCCTGCTGACAGGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGGTGGTCCGTTGCTTCCCTGCTGACAGGAGCGGCAAG 120

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DB 121 AGCAAGCTGGGCACTTGTGGAGACAGAGACTGCTGTGAAGACATCAGGAGCAAG 180

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DB 361 GGAGACTACAGTACAGTGGCTTTCATGAGAGCCAGTACACGTCCTGAGAGAGATCTG 420

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DB 421 GACAGACTCCACAGAGCTGCTGCTGGGAGTAACTCCCGAGAAAGATTCATGTCATG 480

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DB 541 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCCTGCTGACAGACGATGCAACTTAAT 600

QY 601 GTCTTTACACAACAAAAAGAGAGAGCTGTGATAAAGCCGTACATATCCAGGAAGATGAA 660
DB 601 GTCTTTACACAACAAAAAGAGAGAGCTGTGATAAAGCCGTACATATCCAGGAAGATGAA 660

QY 661 TGTGCGTTAATGTTGCTGGAACATGGCAGTGCATCAATAATTCAGATGAGTATGAAAT 720
DB 661 TGTGCGTTAATGTTGCTGGAACATGGCAGTGCATCAATAATTCAGATGAGTATGAAAT 720

QY 721 ACCACTCTGACACTACGCTATCTATATGAAGATTAATTAATGGCCAAAGCACTGCTTTA 780
DB 721 ACCACTCTGACACTACGCTATCTATATGAAGATTAATTAATGGCCAAAGCACTGCTTTA 780

QY 781 TATGCTCTGATATCGATCAAAAAACAGCAGTGGCTCACACCACTGTTACTTGGTGA 840
DB 781 TATGCTCTGATATCGATCAAAAAACAGCAGTGGCTCACACCACTGTTACTTGGTGA 840

QY 841 CATGAGCAAAAACAGCAAGTGTGTAATTTTATCAAGAAAAAGGAAATTTTAAATGCA 900
DB 841 CATGAGCAAAAACAGCAAGTGTGTAATTTTATCAAGAAAAAGGAAATTTTAAATGCA 900
```

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QY 901 CTGATAGATATGGAAGAGACTGCTCTCATACTGCTGTATGTTGGATCAGCAAGTATA 960
DB 901 CTGATAGATATGGAAGAGACTGCTCTCATACTGCTGTATGTTGGATCAGCAAGTATA 960

QY 961 GTCAGCCTTCTACTTGGACAAAATATGANGATATCTTCTCAAGATCTATCTGGACAGC 1020
DB 961 GTCAGCCTTCTACTTGGACAAAATATGANGATATCTTCTCAAGATCTATCTGGACAGC 1020

QY 1021 GCCAGAGATATGCTGTTTCTAGCATCATCATATTAATTTGCCAGTACTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGCATCATCATATTAATTTGCCAGTACTTCTGACTAC 1080

QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGTAAAAACAGCAATCCAGAA 1128
DB 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGTAAAAACAGCAATCCAGAA 1128

RESULT 16
US-09-810-936-301
; Sequence 301, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, David C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 301
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-936-301

Query Match      56.4%; Score 1128; DB 10; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGTTGATTCATCCCGCTCCCTCTCTGTGAAGAGCCATTGGTCTC 60
DB 1 ATGGTGGTTGAGTTGATTCATCCCGCTCCCTCTCTGTGAAGAGCCATTGGTCTC 60

QY 61 AGGAGCAAGATGGGCAAGTGGTGGTCCGTTGCTTCCCTGCTGACAGGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGGTGGTCCGTTGCTTCCCTGCTGACAGGAGCGGCAAG 120

QY 121 AGCAAGCTGGGCACTTGTGGAGACAGAGACTGCTGTGAAGACATCAGGAGCAAG 180
DB 121 AGCAAGCTGGGCACTTGTGGAGACAGAGACTGCTGTGAAGACATCAGGAGCAAG 180

QY 181 ATGGGCAAGTGGTGGTCCGCTCCCTGCTGACAGGAGGAGTGGCAAGCAAGCTG 240
DB 181 ATGGGCAAGTGGTGGTCCGCTCCCTGCTGACAGGAGGAGTGGCAAGCAAGCTG 240

QY 241 GGGGCTTGTGAGACACAGAGACTGCTGTGAAGACATCAGGAGCAAGGAGCAAG 300
DB 241 GGGGCTTGTGAGACACAGAGACTGCTGTGAAGACATCAGGAGCAAGGAGCAAG 300

QY 301 TGGTGGTGGCACTGCTTCCCTGCTGACAGGAGGAGGCAAGGAGTGGGCGTTGG 360
DB 301 TGGTGGTGGCACTGCTTCCCTGCTGACAGGAGGAGGCAAGGAGTGGGCGTTGG 360
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QY	361	GGAGACTACGATACAGAGTGCCTTCATGAGAGCCAGGATACCAAGTCCGCGGAGGAAGATCTG	420
Dp	361	GGAGACTACGATACAGAGTGCCTTCATGAGAGCCAGGATACCAAGTCCGCGGAGGAAGATCTG	420
QY	421	GACAAGCTCCACAGAGCTGCTGGTGGGTTAAAGTCCCGAAGAAAGATCTATGCTCATG	480
Dp	421	GACAAGCTCCACAGAGCTGCTGGTGGGTTAAAGTCCCGAAGAAAGATCTATGCTCATG	480
QY	481	CTCAGGACACTGACGTGAACAAGAAAGCAACAAAGAAAGAGATGCTCTACATCTGGCC	540
Dp	481	CTCAGGACACTGACGTGAACAAGAAAGCAACAAAGAAAGAGATGCTCTACATCTGGCC	540
QY	541	TTCGCCAATGGGAATTCAGAAGTAGTAAACCTCGCTGGGACAGAGATGTCACACTTAT	600
Dp	541	TTCGCCAATGGGAATTCAGAAGTAGTAAACCTCGCTGGGACAGAGATGTCACACTTAT	600
QY	601	GTCCTTGACAAACAAAAGAGAGACGCTCGATTAAGAGCCGTCACATGCGACAGAAAGATGA	660
Dp	601	GTCCTTGACAAACAAAAGAGAGACGCTCGATTAAGAGCCGTCACATGCGACAGAAAGATGA	660
QY	661	TGTGCGTTAATGTTGCTGGAACATGGCACTGATTCCAATATATCCAGATGAGTATGGAAT	720
Dp	661	TGTGCGTTAATGTTGCTGGAACATGGCACTGATTCCAATATATCCAGATGAGTATGGAAT	720
QY	721	ACCACTGTGACATACGCTATCTTATATGAAGATTAATTAATGGCCAAAGCACTGCTCTA	780
Dp	721	ACCACTGTGACATACGCTATCTTATATGAAGATTAATTAATGGCCAAAGCACTGCTCTA	780
QY	781	TATGTCGCTATATCGAATTCAAAAAACAAGCATGGCGTCCACACACTGTAATCTGGTGTGA	840
Dp	781	TATGTCGCTATATCGAATTCAAAAAACAAGCATGGCGTCCACACACTGTAATCTGGTGTGA	840
QY	841	CATGACGAAAAACAGCAAGTCTGGAATTTTAAATTCACAGAAAAAAGCAATTTAAATGCA	900
Dp	841	CATGACGAAAAACAGCAAGTCTGGAATTTTAAATTCACAGAAAAAAGCAATTTAAATGCA	900
QY	901	CTGATATGATATGGAAGAGACTGCTCATACACTGTCGTATGTTGGATACGCAAGATGA	960
Dp	901	CTGATATGATATGGAAGAGACTGCTCATACACTGTCGTATGTTGGATACGCAAGATGA	960
QY	961	GTCAGCCTTCTACTTGAGCAAAATATATGATGTATCTTCCAAAGATCTATCTGAGACAG	1020
Dp	961	GTCAGCCTTCTACTTGAGCAAAATATATGATGTATCTTCCAAAGATCTATCTGAGACAG	1020
QY	1021	GCCAGAGATATGCTGTTCTAGTATCATATCATATGTAATTTGCCAATTTACTTCTGATAC	1080
Dp	1021	GCCAGAGATATGCTGTTCTAGTATCATATCATATGTAATTTGCCAATTTACTTCTGATAC	1080
QY	1081	AAAGAAAAACAGATGCTAAAAAATCTTCTTGAAAGACAGAAATCCAGAA 1128	
Dp	1081	AAAGAAAAACAGATGCTAAAAAATCTTCTTGAAAGACAGAAATCCAGAA 1128	

RESULT 17
US-09-822-827-373
; Sequence 373, Application US/09822827
; Patent No. US20020081680A1

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: APPLICANT: Xu, Jiangchun
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.534C1
: CURRENT APPLICATION NUMBER: US/09/822,827
: CURRENT FILING DATE: 2001-03-28
: NUMBER OF SEQ ID NOS: 982
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 373
: LENGTH: 1155
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-822-827-373

```

Query Match 56.48; Score 1128; DB 10; Length 1155;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	1	ATGAGGTTGAGAGTGAATTCATGCGGGCTGCCTTTCTGTGAAACACATTTGGTCTC	60
Db	1	ATGGTGTTGAGAGTTGAATTCATGCGGGCTGCCTTTCTGTGAAACACATTTGGTCTC	60
OY	61	AGGAGCAAGATGGGCAAGTGGTGCTGCCGTTCCTCCCTGCTGCAGGGAGAGCGGCAAG	120
Db	61	AGGAGCAAGATGGGCAAGTGGTGCTGCCGTTCCTCCCTGCTGCAGGGAGAGCGGCAAG	120
OY	121	AGCAACGTGGGCACTTCTGTGAGAGACCAGCACTTGTCTATGAAAGACACTCAGAGGCAAG	180
Db	121	AGCAACGTGGGCACTTCTGTGAGAGACCAGCACTTGTCTATGAAAGACACTCAGAGGCAAG	180
OY	181	ATGGGCAAGTGGTGCGCGGCACCTGCTTCCCTGCTCAGGGGAGTGGCAAGGCAACCTG	240
Db	181	ATGGGCAAGTGGTGCGCGGCACCTGCTTCCCTGCTCAGGGGAGTGGCAAGGCAACCTG	240
OY	241	GGCGCTTCTGGAGACCAAGCAAGCACTCTATGAAAGACACTCAGGACAAAGATGGGCAAG	300
Db	241	GGCGCTTCTGGAGACCAAGCAAGCACTCTATGAAAGACACTCAGGACAAAGATGGGCAAG	300
OY	301	TGGTCTGCCACACTGCTTCCCTGCTGCAAGGGGAGCGGCAGAGCAAGTGGGCGCTTGG	360
Db	301	TGGTCTGCCACACTGCTTCCCTGCTGCAAGGGGAGCGGCAGAGCAAGTGGGCGCTTGG	360
OY	361	GGAGACTGAGATGACAGTGGCCCTTCAATGGAGCCAGGTACCAAGTGCCTGGAGCAAGATCTG	420
Db	361	GGAGACTGAGATGACAGTGGCCCTTCAATGGAGCCAGGTACCAAGTGCCTGGAGCAAGATCTG	420
OY	421	GACAAAGCTCCACAGAGCTGCCTGCTGGGGGTAAGTCCCGAGAAAGATCTCATCTCATG	480
Db	421	GACAAAGCTCCACAGAGCTGCCTGCTGGGGGTAAGTCCCGAGAAAGATCTCATCTCATG	480
OY	481	CTCAGGGCACTGACCTGTAACAAGAGCAAGCAAGCAAGAGAGACTGCTTACATCTGGCC	540
Db	481	CTCAGGGCACTGACCTGTAACAAGAGCAAGCAAGCAAGAGAGACTGCTTACATCTGGCC	540
OY	541	TCTGCGCATGGGAATTCAAGAACTACTAAACCTCGCTGAGACAGACGATGTCAACTTAAT	600
Db	541	TCTGCGCATGGGAATTCAAGAACTACTAAACCTCGCTGAGACAGACGATGTCAACTTAAT	600
OY	601	GTCTTGGACAACAAAGAGGAGGACAGCTCTGATTAAGGGCGCTACAATGGCCAGGAGATGAA	660
Db	601	GTCTTGGACAACAAAGAGGAGGAGGACAGCTCTGATTAAGGGCGCTACAATGGCCAGGAGATGAA	660
OY	661	TGTGCGTTAATGTTGCTGTGAAACATGGCACTGATCCAAATATTCAGAGTACGATGGAAT	720
Db	661	TGTGCGTTAATGTTGCTGTGAAACATGGCACTGATCCAAATATTCAGAGTACGATGGAAT	720
OY	721	ACCACTGCACTAGCGTATCTATATGAAGTAATTAATGAGCCAAAGCACTGCTCTTA	780
Db	721	ACCACTGCACTAGCGTATCTATATGAAGTAATTAATTAATGAGCCAAAGCACTGCTCTTA	780
OY	781	TATGTCGTGATATGCAATCAAAAAACAAGCATGGCCTCACACCACTGTACTTGGTGA	840
Db	781	TATGTCGTGATATGCAATCAAAAAACAAGCATGGCCTCACACCACTGTACTTGGTGA	840
OY	841	CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAAGCGAATTTAAATGCA	900
Db	841	CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAAGCGAATTTAAATGCA	900
OY	901	CTGGATATATATGGAAGGACGTGCTCATACTGTGATGTTGTTGGATACACCAAGTATA	960
Db	901	CTGGATATATATGGAAGGACGTGCTCATACTGTGATGTTGTTGGATACACCAAGTATA	960
OY	961	GTCACCTCTTCACTTGAGCAAAATTTATATGATCTTCTCAAGATCTATCTGAGAGAGC	1020
Db	961	GTCACCTCTTCACTTGAGCAAAATTTATGATCTTCTCAAGATCTATCTGAGAGAGC	1020
OY	1021	GCCAGAGATATGCTGTTTCTAATGATCATCATGTAAATTTGCCAGTTACTTTCGACTAC	1080
Db	1021	GCCAGAGATATGCTGTTTCTAATGATCATCATGTAAATTTGCCAGTTACTTTCGACTAC	1080

Db 1021 GCCAGAGATGCTGTTTCTAGTCATCATCATGTAATTTCCAGTCTTCTGACTAC 1080
Qy 1081 AAAGAAAAAGATGCTAAAAATCTCTTCTGAAAAAGCAATCCAGAA 1128
Db 1081 AAAGAAAAAGATGCTAAAAATCTCTTCTGAAAAAGCAATCCAGAA 1128

RESULT 18

US-09-429-755-301
; Sequence 301, Application us/09429755A
; Patent No. US20020111467A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 301
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-301

Query Match 56.4%; Score 1128; DB 10; Length 1155;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGTTGAGTTGATTCATCCGGCTGCTCTTCTGTGAAGAACCAATTTGCTGC 60
Db 1 ATGCTGTTGAGTTGATTCATCCGGCTGCTCTTCTGTGAAGAACCAATTTGCTGC 60
Qy 61 AGAGCAAGATGGGCAAGTGTGCTGCGTGTCTCCCTGCTCAGGGAAGGGGCAAG 120
Db 61 AGAGCAAGATGGGCAAGTGTGCTGCGTGTCTCCCTGCTCAGGGAAGGGGCAAG 120
Qy 121 AGCAAGCTGGGCACTTCTGAGACACAGACACTCTGCTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAAGCTGGGCACTTCTGAGACACAGACACTCTGCTATGAAGACACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGTGCTGCGTGTCTCCCTGCTGCAAGGGGGAAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGTGCTGCGTGTCTCCCTGCTGCAAGGGGGAAGTGGCAAGCAAGCTG 240
Qy 241 GGGCTTCTGGAGACACAGACACTCTGCTATGAAGACACTCAGAGCAAGTGGGCAAG 300
Db 241 GGGCTTCTGGAGACACAGACACTCTGCTATGAAGACACTCAGAGCAAGTGGGCAAG 300
Qy 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGGGAAGGGCAAGCAAGTGGGCAAGTGG 360
Db 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGGGGAAGGGCAAGCAAGTGGGCAAGTGG 360
Qy 361 GGAACACTACATGACATGCTTATGAGAGCCCAAGTACCAAGTCCGTGGAAGAAATCTG 420
Db 361 GGAACACTACATGACATGCTTATGAGAGCCCAAGTACCAAGTCCGTGGAAGAAATCTG 420
Qy 421 GACAAGCTCCACAGAGCTGGCTGGTGGGGAATGCCCAAGAAAGAAATCTATGTCATG 480
Db 421 GACAAGCTCCACAGAGCTGGCTGGTGGGGAATGCCCAAGAAAGAAATCTATGTCATG 480
Qy 481 CTCAGGCACTGACGTGAACAAGAGACAAAGCAAAAGAGACTGCTCTCATCTGCGCC 540
Db 481 CTCAGGCACTGACGTGAACAAGAGACAAAGCAAAAGAGACTGCTCTCATCTGCGCC 540
Qy 541 TCTGCCAATGGGAATTAAGAAATCTCTGCTGCAAGAGATGTCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTAAGAAATCTCTGCTGCAAGAGATGTCAACTTAAT 600

Db 541 TCTGCCAATGGGAATTAAGAAATCTCTGCTGCAAGAGATGTCAACTTAAT 600
Qy 601 GTCTGTGACAAACAAAGAGGACAGCTCTGATTAAGGCGCTACATGCGCAGGAATGAA 660
Db 601 GTCTGTGACAAACAAAGAGGACAGCTCTGATTAAGGCGCTACATGCGCAGGAATGAA 660
Qy 661 TGTGCGTTAATGTTGCTGGAACATGGCAGCTGATCCAAATATTTCCAGATGATGAAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGGCAGCTGATCCAAATATTTCCAGATGATGAAAT 720
Qy 721 ACCACTGTGCACTACGCTATATTAAGAGATAAATTAATGAGCAAGCACTGCTCTTA 780
Db 721 ACCACTGTGCACTACGCTATATTAAGAGATAAATTAATGAGCAAGCACTGCTCTTA 780
Qy 781 TATGCTGTGATATGCAATCAAAACAAAGATGGCTCACACCACTGTTACTGTGTA 840
Db 781 TATGCTGTGATATGCAATCAAAACAAAGATGGCTCACACCACTGTTACTGTGTA 840
Qy 841 CATGAGCAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Qy 901 CTGATAGATATGGAAGAGCTGCTCATACTTCTGATATGTTGATGACGCAAGTATA 960
Db 901 CTGATAGATATGGAAGAGCTGCTCATACTTCTGATATGTTGATGACGCAAGTATA 960
Qy 961 GTCAAGCTTCTACTGAGCAAAATATGATGATATCTCTCAAGATATATCGACAGACG 1020
Db 961 GTCAAGCTTCTACTGAGCAAAATATGATGATATCTCTCAAGATATATCGACAGACG 1020
Qy 1021 GCCAGAGATAGTGTGTTTCTAGTCATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
Db 1021 GCCAGAGATAGTGTGTTTCTAGTCATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
Qy 1081 AAAGAAAAAGATGCTAAAAATCTCTTCTGAAAAAGCAATCCAGAA 1128
Db 1081 AAAGAAAAAGATGCTAAAAATCTCTTCTGAAAAAGCAATCCAGAA 1128

RESULT 19

US-09-810-936-323
; Sequence 323, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Lynda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 323
; LENGTH: 1590
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-810-936-323

Query Match 52.2%; Score 1044; DB 10; Length 1590;
Best Local Similarity 99.9%; Pred. No. 0;

Matches 1094; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 34 TCTTCTGTGAAGAACCAATTTGTTCTCAGAGCAAGATGGGCAAGTGTGCTGCTGCTGC 93
Db 34 TCTTCTGTGAAGAACCAATTTGTTCTCAGAGCAAGATGGGCAAGTGTGCTGCTGCTGC 93

Db 469 TCTTCTGTGAAGAACCATTTGGTCTCAGAGCAAGATGGGCAAGTGGTGTCCGTTGC 528
QY 94 TTCCCTGCTGAGAGAGGCGGCAAGACAGTGGGCACTTGTGAGACCAAGCAGCAGC 153
Db 529 TTCCCTGCTGAGAGAGGCGGCAAGACAGTGGGCACTTGTGAGACCAAGCAGCAGC 588
QY 154 TCTGCTATGAAGACACTCAGAGAGCAAGATGGGCAAGTGGTGGCCGCTCTCCCTGC 213
Db 589 TCTGCTATGAAGACACTCAGAGAGCAAGATGGGCAAGTGGTGGCCGCTCTCCCTGC 648
QY 214 TGCAGGGGAGTGGCAAGACAGCACTGGGCGCTTCTGAGACCAAGCAGCAGCTCTATG 273
Db 649 TGCAGGGGAGTGGCAAGACAGCACTGGGCGCTTCTGAGACCAAGCAGCAGCTCTATG 708
QY 274 AAGACACTCAGAGAACAGATGGGCAAGTGGTGGCCGCTCTCCCTGCGCAGGGG 333
Db 709 AAGACACTCAGAGAACAGATGGGCAAGTGGTGGCCGCTCTCCCTGCGCAGGGG 768
QY 334 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTAGCAGTGCCTTCAATGGAGCC 393
Db 769 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTAGCAGTGCCTTCAATGGAGCC 828
QY 394 AGCTACCAAGCTCGTGAGAGAGATGGCAAGCTCCACAGAGCTGCTGGGGTAAA 453
Db 829 AGGTACCAAGCTCGTGAGAGAGATGGCAAGCTCCACAGAGCTGCTGGGGTAAA 888
QY 454 GTCCCGAGAAAGATCTCATGTCTCAGGAGACAGTGAACAAAGAAAGACAG 513
Db 889 GTCCCGAGAAAGATCTCATGTCTCAGGAGACAGTGAACAAAGAAAGACAG 948
QY 514 CAAAGAGAGACTGCTCATCATGTGCGCTCTGCAATGGGAATTCAGAAAGTAAACATC 573
Db 949 CAAAGAGAGACTGCTCATCATGTGCGCTCTGCAATGGGAATTCAGAAAGTAAACATC 1008
QY 574 CTGCTGACAGACGATGTCACTTAATGTCTTGAACAAAGAGAGCAGCTCTGATA 633
Db 1009 CTGCTGACAGACGATGTCACTTAATGTCTTGAACAAAGAGAGCAGCTCTGATA 1068
QY 634 AAGGCGGTACATGGCAGGAAGATGAATGTGGTTAATGTCTGGAACATGGCAGTAT 693
Db 1069 AAGGCGGTACATGGCAGGAAGATGAATGTGGTTAATGTCTGGAACATGGCAGTAT 1128
QY 694 CCAATTAATTCAGATGAGATGGAATACCACTCTGCACTAGCTATCTATATGAAGAT 753
Db 1129 CCAATTAATTCAGATGAGATGGAATACCACTCTGCACTAGCTATCTATATGAAGAT 1188
QY 754 AATTAATGCGCAAGACACTGCTTAAATGCTGATATGCAATCAAAAAACAAGCAT 813
Db 1189 AATTAATGCGCAAGACACTGCTTAAATGCTGATATGCAATCAAAAAACAAGCAT 1248
QY 814 GGCCTCACACCACTGTTACTTGGTGTACATGAGCAAAAAACAGCAAGTCTGAAATTTTAA 873
Db 1249 GGCCTCACACCACTGTTACTTGGTGTACATGAGCAAAAAACAGCAAGTCTGAAATTTTAA 1308
QY 874 ATCAAGAAAAAAGCGAATTTAATGATGCACTGATAGATGAGAGAGCACTGCTCATACTT 933
Db 1309 ATCAAGAAAAAAGCGAATTTAATGATGCACTGATAGATGAGAGAGCACTGCTCATACTT 1368
QY 934 GCTGATGTGTGATGATGAGCAAGATAGTACAGCTTCTACTTGAAGCAAAATATGATGTA 993
Db 1369 GCTGATGTGTGATGATGAGCAAGATAGTACAGCTTCTACTTGAAGCAAAATATGATGTA 1428
QY 994 TCTTCTCAAGATCTATCTGAGAGAGAGGCGCAGAGATATGCTGTTATGATCATCTAT 1053
Db 1429 TCTTCTCAAGATCTATCTGAGAGAGAGGCGCAGAGATATGCTGTTATGATCATCTAT 1488
QY 1054 GTAAATTTGCCAGTTACTTCTGACTACAAAGAAAAACAGATCTTAAATCTCTTGAA 1113
Db 1489 GTAAATTTGCCAGTTACTTCTGACTACAAAGAAAAACAGATCTTAAATCTCTTGAA 1548
QY 1114 AACAGCAATCCAGAA 1128
Db 1549 AACAGCAATCCAGAA 1563

RESULT 20
US-09-810-936-328
; Sequence 328, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Mishner, Linda E.
; APPLICANT: Dillon, David C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 328
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-810-936-328
Query Match 48.8%; Score 975; DB 10; Length 1155;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1125; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGTGTGTGAGTTGATTTCATGCGCGGCTGCTCTTCTGTGAAGAACGATTTGGTCTC 60
Db 1 ATGTGTGTGAGTTGATTTCATGCGCGGCTGCTCTTCTGTGAAGAACGATTTGGTCTC 60
QY 61 AGGAGCAGATGGGCAAGTGGTGTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Db 61 AGGAGCAGATGGGCAAGTGGTGTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGGAAGACAGCAGACTGCTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGGAAGACAGCAGACTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTCAGGGGAGTGGCAAGACAGT 240
Db 181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTCAGGGGAGTGGCAAGACAGT 240
QY 241 GCGGCTTCTGAGAGACAGCAGCACTCTGTAAGAACACTCAGAGCAAGTGGGCAAG 300
Db 241 GCGGCTTCTGAGAGACAGCAGCACTCTGTAAGAACACTCAGAGCAAGTGGGCAAG 300
QY 301 TGGTCTGCACTGCTTCCCTGCTGAGAGGAGCGCAAGAGAGTGGGCGCTTGG 360
Db 301 TGGTCTGCACTGCTTCCCTGCTGAGAGGAGCGCAAGAGAGTGGGCGCTTGG 360
QY 361 GGAGACTACAGATGAGAGTCCCTTCAATGAGCCAGGTACCAAGTCCGTGAGAAATGTC 420
Db 361 GGAGACTACAGATGAGAGTCCCTTCAATGAGCCAGGTACCAAGTCCGTGAGAAATGTC 420
QY 421 GACAACTCCACAGAGCTGCGCTGGTGGGTAAGTCCCAAGAAAGATTCATGCTGTAAG 480
Db 421 GACAACTCCACAGAGCTGCGCTGGTGGGTAAGTCCCAAGAAAGATTCATGCTGTAAG 480
QY 481 CTCAGGAGACTGAGCTGGAACAAGAGCAAGCAAAAGAGACTGCTTACATCTGGCC 540
Db 481 CTCAGGAGACTGAGCTGGAACAAGAGCAAGCAAAAGAGACTGCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGAGAGAGATGTCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGAGAGAGATGTCAACTTAAT 600


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QY 601 GTCCTTGACAAACAAAAGAGACAGCTCTGATTAAGCCGTACAAATCCAGAGATGAA 660
      |||||||
Db 601 GTCCTTGACAAACAAAAGAGAGAGCTCTGATTAAGCCGTACAAATCCAGAGATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGGCAGTGCATCAATATTCAGATGAGTGAAT 720
      |||||||
Db 661 TGTGCGTTAATGTTGCTGGAACATGGCAGTGCATCAATATTCAGATGAGTGAAT 720
QY 721 ACCACTGTCGACATCGCTATCTATTAATGAATTAATTAATGACCAAGCAGCTCTTA 780
      |||||||
Db 721 ACCACTGTCGACATCGCTATCTATTAATGAATTAATTAATGACCAAGCAGCTCTTA 780
QY 781 TATGTCCTGATATCGAATCAAAAACACAGATGGCCTCACACCACTGTTACTGTGTA 840
      |||||||
Db 781 TATGTCCTGATATCGAATCAAAAACACAGATGGCCTCACACCACTGTTACTGTGTA 840
QY 841 CATGACGAAAAACAGACAGTCTGTAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
      |||||||
Db 841 CATGACGAAAAACAGACAGTCTGTAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATATGATATGGAAGAGACTGCTCTACTGCTGATGTTGATGATGAGACAGATATA 960
      |||||||
Db 901 CTGATATGATATGGAAGAGACTGCTCTACTGCTGATGTTGATGATGAGACAGATATA 960
QY 961 GTCAGCCTTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAGC 1020
      |||||||
Db 961 GTCAGCCTTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAGC 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGCATCATCATTAATTTGCCAGTACTTCTGACTAC 1080
      |||||||
Db 1021 GCCAGAGATATGCTGTTTCTAGCATCATCATTAATTTGCCAGTACTTCTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAATCTCTTGAAGAACAGCAATCCAGAA 1128
      |||||||
Db 1081 AAGAAAAACAGATGCTAAATCTCTTGAAGAACAGCAATCCAGAA 1128

RESULT 21
US-09-759-143-368
; Sequence 368, Application US/09759143
; Patient No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuxui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Wang, Samuel
; APPLICANT: Hepler, Yashir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 368
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-368
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Query Match 24.6%; Score 491; DB 10; Length 1512;
Best Local Similarity 99.4%; Pred. No. 2,9e-175;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 34 TCTTCTGTAAGAACCATTTGGTCTCAGAGCAAGATGGGGCAAGTGTGCTGCCCTGTC 93
      |||||||
Db 256 TCTTCTGTAAGAACCATTTGGTCTCAGAGCAAGATGGGGCAAGTGTGCTGCCCTGTC 315
QY 94 TTCCCTGCTGCAAGGAGAGAGCGCCAAAGACAGTGGGGCACTTCTGAGACCAAGAC 153
      |||||||
Db 316 TTCCCTGCTGCAAGGAGAGAGCGCCAAAGACAGTGGGGCACTTCTGAGACCAAGAC 375
QY 154 TCTGCTATGGAACACTCAGAGAGCAAGATGGGCAAGTGTGTCGCCCACTCTCCCTGC 213
      |||||||
Db 376 TCTGCTATGGAAGCACTCAGAGAGCAAGATGGGCAAGTGTGTCGCCCACTCTCCCTGC 435
QY 214 TGCAGGGGGAGTGGCAAGCAACGTGGGGGCTTCTGGAACCAAGCAAGCACTGCTGATG 273
      |||||||
Db 436 TGCAGGGGGAGTGGCAAGCAACGTGGGGGCTTCTGGAACCAAGCAAGCACTGCTGATG 495
QY 274 AAGCACTCAGAAACAAGATGGGCAAGTGGTGGCTGCACTGCTCCCTGCTGAGGGGG 333
      |||||||
Db 496 AAGCACTCAGAAACAAGATGGGCAAGTGGTGGCTGCACTGCTCCCTGCTGAGGGGG 555
QY 334 AGCGGCAAGACAAAGTGGGGCGCTTGGGGAGACTACGATACAGTGCCTTCATGAGACCC 393
      |||||||
Db 556 AGCGCAAGACAAAGTGGGGCGCTTGGGGAGACTACGATACAGTGCCTTCATGAGACCC 615
QY 394 AGGTACCAAGTCCGTGGAGAAGATCTGACAAAGTCCACAGAGCTGCTGGGGGTTAA 453
      |||||||
Db 616 AGGTACCAAGTCCGTGGAGAAGATCTGACAAAGTCCACAGAGCTGCTGGGGGTTAA 675
QY 454 GTCCCCAGAAAGATCTCATCTCATCTGATGCTCAGGAGACACTGACGTGAACAAGAGACAG 513
      |||||||
Db 676 GTCCCCAGAAAGATCTCATCTCATCTGATGCTCAGGAGACACTGACGTGAACAAGAGACAG 735
QY 514 CAAAAGAGAGCTGCTACATCTGGCCTTGGCCAAATGGGAATTCAGAAATGTTAAATCTC 573
      |||||||
Db 736 CAAAAGAGAGCTGCTACATCTGGCCTTGGCCAAATGGGAATTCAGAAATGTTAAATCTC 795
QY 574 CTGCTGACAGAGAGATGCACTTAATGTCCTTGACAAACAAAAGAGACAGCTGTGATA 633
      |||||||
Db 796 CTGCTGACAGAGAGATGCACTTAATGTCCTTGACAAACAAAAGAGACAGCTGTGATA 855
QY 634 AAGGCCGTACATGCCAGGAAGATGATGCGTTAATGTTGCTGGAACATGGCACTGAT 693
      |||||||
Db 856 AAGGCCGTACATGCCAGGAAGATGATGCGTTAATGTTGCTGGAACATGGCACTGAT 915
QY 694 CCAAAATTTCCAGATGAGTGAATAACCACTCT 728
      |||||||
Db 916 CCAAAATTTCCAGATGAGTGAATAACCACTCT 950

RESULT 22
US-09-780-669-368
; Sequence 368, Application US/09780669
; Patient No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuxui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
```



```

; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 368
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-780-669-368
```

```

Query Match          24.6%; Score 491; DB 10; Length 1512;
Best Local Similarity 99.4%; Pred. No. 2.9e-175;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```

QY 34 TCTTGTGTAAGACCATTTGGTCTCAGAGCAAGATGGGCAAGTGTGTCGCCGTTGC 93
   |||||||
DB 256 TCTTGTGTAAGACCATTTGGTCTCAGAGCAAGATGGGCAAGTGTGTCGCCGTTGC 315
   |||||||
QY 94 TTCCCTGCTGAGGAGGCGGCAAGACAGTGGGCAAGTGTGTCGCCGTTGCCCTTC 153
   |||||||
DB 316 TTCCCTGCTGAGGAGGCGGCAAGACAGTGGGCAAGTGTGTCGCCGTTGCCCTTC 375
   |||||||
QY 154 TCTGCTATGAACACACTCAGAGCAAGATGGGCAAGTGTGTCGCCGTTGCCCTTC 213
   |||||||
DB 376 TCTGCTATGAACACACTCAGAGCAAGATGGGCAAGTGTGTCGCCGTTGCCCTTC 435
   |||||||
QY 214 TGCAGGGGAGTGGCAAGACAGTGGGCAAGTGTGTCGCCGTTGCCCTTCCTATG 273
   |||||||
DB 436 TGCAGGGGAGTGGCAAGACAGTGGGCAAGTGTGTCGCCGTTGCCCTTCCTATG 495
   |||||||
QY 274 AAGACACTCAGGAAAGATGGGCAAGTGGTGTGTCGCCCTTCCCTGCGCAGGGGG 333
   |||||||
DB 496 AAGACACTCAGGAAAGATGGGCAAGTGGTGTGTCGCCCTTCCCTGCGCAGGGGG 555
   |||||||
QY 334 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTAGATGACAGTGCCTTCATGAGCCC 393
   |||||||
DB 556 AGCRCAAGAGCAAGTGGGCGCTTGGGAGACTAGATGACAGTGCCTTCATGAGCCC 615
   |||||||
QY 394 AGGTACCACTCCGTGGAGAGATCTGCACAGTCCACAGAGTGCCTGTTGGGGTAAA 453
   |||||||
DB 616 AGGTACCACTCCGTGGAGAGATCTGCACAGTCCACAGAGTGCCTGTTGGGGTAAA 675
   |||||||
QY 454 GTCCCCAGAAAGATCTCATGTCATGCTCAGGAGCACTGACGTGAACAAAGAGCAAG 513
   |||||||
DB 676 GTCCCCAGAAAGATCTCATGTCATGCTCAGGAGCACTGACGTGAACAAAGAGCAAG 735
   |||||||
QY 514 CAAAAGAGAGTCTCTCATATCTGGCCTCTGCCAATGGGAATTCAGAAATGATAAACTC 573
   |||||||
DB 736 CAAAAGAGAGTCTCTCATATCTGGCCTCTGCCAATGGGAATTCAGAAATGATAAACTC 795
   |||||||
QY 574 CTGCTGGAGACAGATGTCACCTTAATGTCTTGACACAAAGAGAGACAGCTGTGATA 633
   |||||||
DB 796 STGCTGGAGACAGATGTCACCTTAATGTCTTGACACAAAGAGAGACAGCTGTGATA 855
   |||||||
QY 634 AAGGCCGTACATGCGCAGGAAGATGAATGTGGTAAATGTTCTGGAAATGGCACTGAT 693
   |||||||
DB 856 AAGGCCGTACATGCGCAGGAAGATGAATGTGGTAAATGTTCTGGAAATGGCACTGAT 915
   |||||||
QY 694 CCAATATATTCAGATGAGTATGGAATAACACTCT 728
   |||||||
DB 916 CCAATATATTCAGATGAGTATGGAATAACACTCT 950
   |||||||
```

```

; Sequence 294, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 294
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-936-294
```

```

Query Match          24.6%; Score 491; DB 10; Length 1512;
Best Local Similarity 99.4%; Pred. No. 2.9e-175;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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```

QY 34 TCTTGTGTAAGACCATTTGGTCTCAGAGCAAGATGGGCAAGTGTGTCGCCGTTGC 93
   |||||||
DB 256 TCTTGTGTAAGACCATTTGGTCTCAGAGCAAGATGGGCAAGTGTGTCGCCGTTGC 315
   |||||||
QY 94 TTCCCTGCTGAGGAGGCGGCAAGACAGTGGGCAAGTGTGTCGCCGTTGCCCTTC 153
   |||||||
DB 316 TTCCCTGCTGAGGAGGCGGCAAGACAGTGGGCAAGTGTGTCGCCGTTGCCCTTC 375
   |||||||
QY 154 TCTGCTATGAACACACTCAGAGCAAGATGGGCAAGTGTGTCGCCGTTGCCCTTC 213
   |||||||
DB 376 TCTGCTATGAACACACTCAGAGCAAGATGGGCAAGTGTGTCGCCGTTGCCCTTC 435
   |||||||
QY 214 TGCAGGGGAGTGGCAAGACAGTGGGCAAGTGTGTCGCCGTTGCCCTTCCTATG 273
   |||||||
DB 436 TGCAGGGGAGTGGCAAGACAGTGGGCAAGTGTGTCGCCGTTGCCCTTCCTATG 495
   |||||||
QY 274 AAGACACTCAGGAAAGATGGGCAAGTGGTGTGTCGCCCTTCCCTGCGCAGGGGG 333
   |||||||
DB 496 AAGACACTCAGGAAAGATGGGCAAGTGGTGTGTCGCCCTTCCCTGCGCAGGGGG 555
   |||||||
QY 334 AGCGGCAAGAGCAAGTGGGCGCTTGGGAGACTAGATGACAGTGCCTTCATGAGCCC 393
   |||||||
DB 556 AGCRCAAGAGCAAGTGGGCGCTTGGGAGACTAGATGACAGTGCCTTCATGAGCCC 615
   |||||||
QY 394 AGGTACCACTCCGTGGAGAGATCTGCACAGTCCACAGAGTGCCTGTTGGGGTAAA 453
   |||||||
DB 616 AGGTACCACTCCGTGGAGAGATCTGCACAGTCCACAGAGTGCCTGTTGGGGTAAA 675
   |||||||
QY 454 GTCCCCAGAAAGATCTCATGTCATGCTCAGGAGCACTGACGTGAACAAAGAGCAAG 513
   |||||||
DB 676 GTCCCCAGAAAGATCTCATGTCATGCTCAGGAGCACTGACGTGAACAAAGAGCAAG 735
   |||||||
QY 514 CAAAAGAGAGTCTCTCATATCTGGCCTCTGCCAATGGGAATTCAGAAATGATAAACTC 573
   |||||||
DB 736 CAAAAGAGAGTCTCTCATATCTGGCCTCTGCCAATGGGAATTCAGAAATGATAAACTC 795
   |||||||
QY 574 CTGCTGGAGACAGATGTCACCTTAATGTCTTGACACAAAGAGAGACAGCTGTGATA 633
   |||||||
DB 796 STGCTGGAGACAGATGTCACCTTAATGTCTTGACACAAAGAGAGACAGCTGTGATA 855
   |||||||
QY 634 AAGGCCGTACATGCGCAGGAAGATGAATGTGGTAAATGTTCTGGAAATGGCACTGAT 693
   |||||||
DB 856 AAGGCCGTACATGCGCAGGAAGATGAATGTGGTAAATGTTCTGGAAATGGCACTGAT 915
   |||||||
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QY 694 CCAATATTCAGATGATGAAATACCACTCT 728
|
Db 916 CCAATATTCAGATGATGAAATACCACTCT 950

RESULT 24
US-09-822-827-368
; Sequence 368, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822, 827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 368
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-368

Query Match 24.6%; Score 491; DB 10; Length 1512;
Best Local Similarity 99.4%; Pred. No. 2,9e-175;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAGCCATTGGTCTCAGAGCAAGATGGCAAGTGTGCTGCGCTTGC 93
|
Db 256 TCTTCTGTGAAGAGCCATTGGTCTCAGAGCAAGATGGCAAGTGTGCTGCGCTTGC 315
QY 94 TTCCCTGTGTCAGAGGAGGCGGCAAGCAAGTGGGCACTTCTGAGACACAGAGAC 153
|
Db 316 TTCCCTGTGTCAGAGGAGGCGGCAAGCAAGTGGGCACTTCTGAGACACAGAGAC 375
QY 154 TCTGCTATGAAGACACTCAGAGAGCAAGATGGCAAGTGTGCTGCGCTTGCCTGC 213
|
Db 376 TCTGCTATGAAGACACTCAGAGAGCAAGATGGGCAAGTGTGCTGCGCTTGCCTGC 435
QY 214 TGCAGGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACACAGAGACTGCTATG 273
|
Db 436 TGCAGGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACACAGAGACTGCTATG 495
QY 274 AAGCACTCAGAGCAAGATGGGCAAGTGGTGTCCACTGCTCCCTGCTGAGGGGG 333
|
Db 496 AAGCACTCAGAGCAAGATGGGCAAGTGGTGTCCACTGCTCCCTGCTGAGGGGG 555
QY 334 AGCGGCAAGCAAGATGGGCGCTTGGGGAGACTACAGATGACAGTGCCTTCATGAGGCC 393
|
Db 556 AGCGGCAAGCAAGATGGGCGCTTGGGGAGACTACAGATGACAGTGCCTTCATGAGGCC 615
QY 394 AGGTAACACGTCCTGAGAGAGATCTGGACAGCTCCACAGAGCTGCTGGGGTAAA 453
|
Db 616 AGGTAACACGTCCTGAGAGAGATCTGGACAGCTCCACAGAGCTGCTGGGGTAAA 675
QY 454 GTCCCGAAGAAAGATCTCATGCTGCTCAGGAGCACTGACGTAAGCAAGAAAGAAAG 513
|
Db 676 GTCCCGAAGAAAGATCTCATGCTGCTCAGGAGCACTGACGTAAGCAAGAAAGAAAG 735
QY 514 CAAAAGAGAGTCTCATGCTGCTCAGGAGCACTGACGTAAGCAAGAAAGAAAGTCT 573
|
Db 736 CAAAAGAGAGTCTCATGCTGCTCAGGAGCACTGACGTAAGCAAGAAAGTCT 795
QY 574 CTGCTGACAGAGATGTCAACTTAATGCTTGTGACAAAGAGAGAGAGAGAGAGAG 633
|
Db 796 CTGCTGACAGAGATGTCAACTTAATGCTTGTGACAAAGAGAGAGAGAGAGAGAG 855
QY 634 AAGGCGCTACAAATGCCAGAGAGATGATGCTTAATGTTGCGGAACATGGAGCTGAT 693
|
Db 856 AAGGCGCTACAAATGCCAGAGAGATGATGCTTAATGTTGCGGAACATGGAGCTGAT 915

QY 694 CCAATATTCAGATGATGAAATACCACTCT 728
|
Db 916 CCAATATTCAGATGATGAAATACCACTCT 950

RESULT 25
US-09-429-755-294
; Sequence 294, Application US/09429755A
; Patent No. US2002011467A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, David C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429, 755A
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 294
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-294

Query Match 24.6%; Score 491; DB 10; Length 1512;
Best Local Similarity 99.4%; Pred. No. 2,9e-175;
Matches 691; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAGCCATTGGTCTCAGAGCAAGATGGCAAGTGTGCTGCGCTTGC 93
|
Db 256 TCTTCTGTGAAGAGCCATTGGTCTCAGAGCAAGATGGCAAGTGTGCTGCGCTTGC 315
QY 94 TTCCCTGTGTCAGAGGAGGCGGCAAGCAAGTGGGCACTTCTGAGACACAGAGAC 153
|
Db 316 TTCCCTGTGTCAGAGGAGGCGGCAAGCAAGTGGGCACTTCTGAGACACAGAGAC 375
QY 154 TCTGCTATGAAGACACTCAGAGAGCAAGATGGGCAAGTGTGCTGCGCTTGCCTGC 213
|
Db 376 TCTGCTATGAAGACACTCAGAGAGCAAGATGGGCAAGTGTGCTGCGCTTGCCTGC 435
QY 214 TGCAGGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACACAGAGACTGCTATG 273
|
Db 436 TGCAGGGGGAGTGGCAAGCAAGTGGGCGCTTCTGAGACACAGAGACTGCTATG 495
QY 274 AAGCACTCAGAGCAAGATGGGCAAGTGGTGTCCACTGCTCCCTGCTGAGGGGG 333
|
Db 496 AAGCACTCAGAGCAAGATGGGCAAGTGGTGTCCACTGCTCCCTGCTGAGGGGG 555
QY 334 AGCGGCAAGCAAGATGGGCGCTTGGGGAGACTACAGATGACAGTGCCTTCATGAGGCC 393
|
Db 556 AGCGGCAAGCAAGATGGGCGCTTGGGGAGACTACAGATGACAGTGCCTTCATGAGGCC 615
QY 394 AGGTAACACGTCCTGAGAGAGATCTGGACAGCTCCACAGAGCTGCTGGGGTAAA 453
|
Db 616 AGGTAACACGTCCTGAGAGAGATCTGGACAGCTCCACAGAGCTGCTGGGGTAAA 675
QY 454 GTCCCGAAGAAAGATCTCATGCTGCTCAGGAGCACTGACGTAAGCAAGAAAGAGAG 513
|
Db 676 GTCCCGAAGAAAGATCTCATGCTGCTCAGGAGCACTGACGTAAGCAAGAAAGAGAG 735
QY 514 CAAAAGAGAGTCTCATGCTGCTCAGGAGCACTGACGTAAGCAAGAAAGAGAGAGAG 573
|
Db 736 CAAAAGAGAGTCTCATGCTGCTCAGGAGCACTGACGTAAGCAAGAAAGAGAGAGAG 795
QY 574 CTGCTGACAGAGATGTCAACTTAATGCTTGTGACAAAGAGAGAGAGAGAGAGAGAG 633
|
Db 796 CTGCTGACAGAGATGTCAACTTAATGCTTGTGACAAAGAGAGAGAGAGAGAGAGAG 855

APPLICANT: Reed, Steven G.
APPLICANT: Smith, John M.
APPLICANT: Smith, Linda E.
APPLICANT: Dillon, David C.
APPLICANT: Retter, Marc W.
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Harlocker, Susan T.
APPLICANT: Day, Craig H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT OF BREAST CANCER
FILE REFERENCE: 210121.419C11
CURRENT APPLICATION NUMBER: US/09/810, 936
CURRENT FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 334
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 295
LENGTH: 1853
TYPE: DNA
ORGANISM: Homo sapien
US-09-810-936-295

Query Match 12.6% Score 252; DB 10; Length 1853;
Best Local Similarity 99.7%; Pred. No. 8.8e-86;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAACCATTTGCTCAGAGCAAGATGGGCAAGTGTGCTGCGCTTGC 93
DB 256 TCTTCTGTGAAGAACCATTTGCTCAGAGCAAGATGGGCAAGTGTGCTGCGCTTGC 315
QY 94 TTCCCTGCTGCAAGGAGGAGGCAAGCAAGCTGGGCACTTGTGAGACCAAGAGAGC 153
DB 316 TTCCCTGCTGCAAGGAGGAGGCAAGCAAGCTGGGCACTTGTGAGACCAAGAGAGC 375
QY 154 TCTGCTATGAAGACACACAGCAAGATGGGCAAGTGTGCTGCGCTTGCCTTGC 213
DB 376 TCTGCTATGAAGACACACAGCAAGATGGGCAAGTGTGCTGCGCTTGCCTTGC 435
QY 214 TGCAGGGGAGTGGCAAGAGCAAGCAAGCTTGTGAGACCAAGAGCTGTATG 273
DB 436 TGCAGGGGAGTGGCAAGAGCAAGCAAGCTTGTGAGACCAAGAGCTGTATG 495
QY 274 AAGACACTCAGGAACAAGATGGGCAAGTGTGCTGCGCTTGCCTTGCCTTGC 333
DB 496 AAGACACTCAGGAACAAGATGGGCAAGTGTGCTGCGCTTGCCTTGCCTTGC 555
QY 334 AGC 336
DB 556 AGC 558

RESULT 29
US-09-822-827-369
Sequence 369, Application US/09822827
Patent No. US20020081680A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TREATMENT OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822, 827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 369
LENGTH: 1853
TYPE: DNA
ORGANISM: Homo sapien
US-09-822-827-369

Query Match 12.6% Score 252; DB 10; Length 1853;
Best Local Similarity 99.7%; Pred. No. 8.8e-86;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAACCATTTGCTCAGAGCAAGATGGGCAAGTGTGCTGCGCTTGC 93
DB 256 TCTTCTGTGAAGAACCATTTGCTCAGAGCAAGATGGGCAAGTGTGCTGCGCTTGC 315
QY 94 TTCCCTGCTGCAAGGAGGAGGCAAGCAAGCTGGGCACTTGTGAGACCAAGAGAGC 153
DB 316 TTCCCTGCTGCAAGGAGGAGGCAAGCAAGCTGGGCACTTGTGAGACCAAGAGAGC 375
QY 154 TCTGCTATGAAGACACACAGCAAGATGGGCAAGTGTGCTGCGCTTGCCTTGC 213
DB 376 TCTGCTATGAAGACACACAGCAAGATGGGCAAGTGTGCTGCGCTTGCCTTGC 435
QY 214 TGCAGGGGAGTGGCAAGAGCAAGCAAGCTTGTGAGACCAAGAGCTGTATG 273
DB 436 TGCAGGGGAGTGGCAAGAGCAAGCAAGCTTGTGAGACCAAGAGCTGTATG 495
QY 274 AAGACACTCAGGAACAAGATGGGCAAGTGTGCTGCGCTTGCCTTGCCTTGC 333
DB 496 AAGACACTCAGGAACAAGATGGGCAAGTGTGCTGCGCTTGCCTTGCCTTGC 555
QY 334 AGC 336
DB 556 AGC 558

RESULT 30
US-09-429-755-295
Sequence 295, Application US/09429755A
Patent No. US20020111467A1
GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Retter, Marc W.
APPLICANT: Dillon, David C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C6
CURRENT APPLICATION NUMBER: US/09/429, 755A
CURRENT FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 315
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 295
LENGTH: 1853
TYPE: DNA
ORGANISM: Homo sapien
US-09-429-755-295

Query Match 12.6% Score 252; DB 10; Length 1853;
Best Local Similarity 99.7%; Pred. No. 8.8e-86;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 TCTTCTGTGAAGAACCATTTGCTCAGAGCAAGATGGGCAAGTGTGCTGCGCTTGC 93
DB 256 TCTTCTGTGAAGAACCATTTGCTCAGAGCAAGATGGGCAAGTGTGCTGCGCTTGC 315
QY 94 TTCCCTGCTGCAAGGAGGAGGCAAGCAAGCTGGGCACTTGTGAGACCAAGAGAGC 153
DB 316 TTCCCTGCTGCAAGGAGGAGGCAAGCAAGCTGGGCACTTGTGAGACCAAGAGAGC 375
QY 154 TCTGCTATGAAGACACACAGCAAGATGGGCAAGTGTGCTGCGCTTGCCTTGC 213
DB 376 TCTGCTATGAAGACACACAGCAAGATGGGCAAGTGTGCTGCGCTTGCCTTGC 435
QY 214 TGCAGGGGAGTGGCAAGAGCAAGCAAGCTTGTGAGACCAAGAGCTGTATG 273
DB 436 TGCAGGGGAGTGGCAAGAGCAAGCAAGCTTGTGAGACCAAGAGCTGTATG 495
QY 274 AAGACACTCAGGAACAAGATGGGCAAGTGTGCTGCGCTTGCCTTGCCTTGC 333
DB 496 AAGACACTCAGGAACAAGATGGGCAAGTGTGCTGCGCTTGCCTTGCCTTGC 555

OY 334 AGC 336
|||
Db 556 AGC 558

RESULT 31

US-09-759-143-531
; Sequence 531, Application US/09759143
; Patent No. US20020022248A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darlick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
NUMBER OF FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 531
LENGTH: 879
TYPE: DNA
ORGANISM: Homo sapiens
US-09-759-143-531

Query Match 6.0%; Score 120; DB 10; Length 879;
Best Local Similarity 99.1%; Pred. No. 2.5e-36;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 507 GGACAAGCAAAAGAGAGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 566
|||||
Db 333 GGACAAGCAAAAGAGAGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 392
OY 567 AAAACTCGCTGGAGACAGATGTCACACTTAATGCTTGCACACAAAAAGAGACAGC 626
|||||
Db 393 AAAACTCGCTGGAGACAGATGTCACACTTAATGCTTGCACACAAAAAGAGACAGC 452
OY 627 TCTGATTAAGGCCGTCACATATGCCAGGAAGATGATGCGGTAAATGTTGCTGGAACATGG 686
|||||
Db 453 TCTGATTAAGGCCGTCACATATGCCAGGAAGATGATGCGGTAAATGTTGCTGGAACATGG 512
OY 687 CACTGATCCCAATATTCAGATGAGTATGGAATACCACTCT 728
|||||
Db 513 CACTGATCCCAATATTCAGATGAGTATGGAATACCACTCT 554

RESULT 32

US-09-780-669-531
; Sequence 531, Application US/09780669
; Patent No. US20020051977A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darlick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hurlal, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
NUMBER OF FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 531
LENGTH: 879
TYPE: DNA
ORGANISM: Homo sapiens
US-09-780-669-531

Query Match 6.0%; Score 120; DB 10; Length 879;
Best Local Similarity 99.1%; Pred. No. 2.5e-36;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 507 GGACAAGCAAAAGAGAGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 566
|||||
Db 333 GGACAAGCAAAAGAGAGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 392
OY 567 AAAACTCGCTGGAGACAGATGTCACACTTAATGCTTGCACACAAAAAGAGACAGC 626
|||||
Db 393 AAAACTCGCTGGAGACAGATGTCACACTTAATGCTTGCACACAAAAAGAGACAGC 452
OY 627 TCTGATTAAGGCCGTCACATATGCCAGGAAGATGATGCGGTAAATGTTGCTGGAACATGG 686
|||||
Db 453 TCTGATTAAGGCCGTCACATATGCCAGGAAGATGATGCGGTAAATGTTGCTGGAACATGG 512
OY 687 CACTGATCCCAATATTCAGATGAGTATGGAATACCACTCT 728
|||||
Db 513 CACTGATCCCAATATTCAGATGAGTATGGAATACCACTCT 554

RESULT 33

US-09-810-936-314
; Sequence 314, Application US/09810936
; Patent No. US20020068285A1

GENERAL INFORMATION:

APPLICANT: Frudakis, Tony N.
APPLICANT: Reed, Steven G.
APPLICANT: Smith, John M.
APPLICANT: Misner, Linda E.
APPLICANT: Dillon, Davin C.
APPLICANT: Retter, Marc W.
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Harlocker, Susan L.
APPLICANT: Day, Craig H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE REFERENCE: 210121.419C11
CURRENT APPLICATION NUMBER: US/09/810,936
NUMBER OF FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 334
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 314
LENGTH: 879
TYPE: DNA

Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAAAGAGAGACTGCTCTACATCTGGCTCTGGCAATGGGAATTCAGAACTACT 566
|||||
Db 276 GGACAGCAAAAGAGAGAGACTGCTCTACATCTGGCTCTGGCAATGGGAATTCAGAACTACT 335

QY 567 AAAACTCTGCTGGACAGACGATGTCACCTTAATGTCCTTGACACAAAAAGAGACAGC 626
|||||
Db 336 AAAACTCTGCTGGACAGACGATGTCACCTTAATGTCCTTGACACAAAAAGAGACAGC 395

QY 627 TGTGATTAAGGCCGTCACATGCGCAGAGACATTAATGTCCTTAATGTCCTGGAACATGG 686
|||||
Db 396 TGTGATTAAGGCCGTCACATGCGCAGAGACATTAATGTCCTTAATGTCCTGGAACATGG 455

QY 687 CACTGATCCAAATATTCAGATGAGTGAATACCACTCT 728
|||||
Db 456 CACTGATCCAAATATTCAGATGAGTGAATACCACTCT 497

RESULT 37

US-09-780-669-372
; Sequence 372; Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedyick, Thomas S.
; APPLICANT: Carter, Darriok
; APPLICANT: Wang, Aljun
; APPLICANT: Li, Samuel
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780.669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 372
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-780-669-372

Query Match 6.0%; Score 120; DB 10; Length 1059;
Best Local Similarity 99.1%; Pred. No. 2.5e-36;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAAAGAGAGACTGCTCTACATCTGGCTCTGGCAATGGGAATTCAGAACTACT 566
|||||
Db 276 GGACAGCAAAAGAGAGACTGCTCTACATCTGGCTCTGGCAATGGGAATTCAGAACTACT 335

QY 567 AAAACTCTGCTGGACAGACGATGTCACCTTAATGTCCTTGACACAAAAAGAGACAGC 626
|||||
Db 336 AAAACTCTGCTGGACAGACGATGTCACCTTAATGTCCTTGACACAAAAAGAGACAGC 395

QY 627 TGTGATTAAGGCCGTCACATGCGCAGAGACATTAATGTCCTTAATGTCCTGGAACATGG 686
|||||
Db 396 TGTGATTAAGGCCGTCACATGCGCAGAGACATTAATGTCCTTAATGTCCTGGAACATGG 455

QY 687 CACTGATCCAAATATTCAGATGAGTGAATACCACTCT 728
|||||
Db 456 CACTGATCCAAATATTCAGATGAGTGAATACCACTCT 497

RESULT 38

US-09-810-936-298
; Sequence 298; Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810.936
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 298
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-936-298

Query Match 6.0%; Score 120; DB 10; Length 1059;
Best Local Similarity 99.1%; Pred. No. 2.5e-36;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAGCAAAAGAGAGACTGCTCTACATCTGGCTCTGGCAATGGGAATTCAGAACTACT 566
|||||
Db 276 GGACAGCAAAAGAGAGACTGCTCTACATCTGGCTCTGGCAATGGGAATTCAGAACTACT 335

QY 567 AAAACTCTGCTGGACAGACGATGTCACCTTAATGTCCTTGACACAAAAAGAGACAGC 626
|||||
Db 336 AAAACTCTGCTGGACAGACGATGTCACCTTAATGTCCTTGACACAAAAAGAGACAGC 395

QY 627 TGTGATTAAGGCCGTCACATGCGCAGAGACATTAATGTCCTTAATGTCCTGGAACATGG 686
|||||
Db 396 TGTGATTAAGGCCGTCACATGCGCAGAGACATTAATGTCCTTAATGTCCTGGAACATGG 455

QY 687 CACTGATCCAAATATTCAGATGAGTGAATACCACTCT 728
|||||
Db 456 CACTGATCCAAATATTCAGATGAGTGAATACCACTCT 497

RESULT 39

US-09-822-827-372
; Sequence 372; Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.53A1
; CURRENT APPLICATION NUMBER: US/09/822.827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 372
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-372

Query Match 6.0%; Score 120; DB 10; Length 1059;
 Best Local Similarity 99.1%; Pred. No. 2.5e-36;
 Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAAGCAAAAGAGAGCTGCTTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 566
 Db 276 GGACAAAGCAAAAGAGAGCTGCTTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 335
 QY 567 AAAAATCTCTGCTGGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAGAGACAGC 626
 Db 336 AAAAATCTCTGCTGGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAGAGACAGC 395
 QY 627 TCTGATTAAGGCGGTACAAATGCCAGAAAGATGAATGTGCTTAATGTGCTGGAACATGG 686
 Db 396 TCTGATTAAGGCGGTACAAATGCCAGAAAGATGAATGTGCTTAATGTGCTGGAACATGG 455
 QY 687 CACTGATCCAAATATTCAGATGATGTGGAATACCACTCT 728
 Db 456 CACTGATCCAAATATTCAGATGATGTGGAATACCACTCT 497

RESULT 40

US-09-429-755-298
 ; Sequence 298, Application US/09429755A
 ; Patent No. US2002011467A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Frudakis, Tony N.
 ; APPLICANT: Smith, John M.
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Misher, Lynda
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Dillon, Davin C.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 ; FILE REFERENCE: 210121.419C6
 ; CURRENT APPLICATION NUMBER: US/09/429,755A
 ; CURRENT FILING DATE: 1999-10-28
 ; NUMBER OF SEQ ID NOS: 315
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 298
 ; LENGTH: 1059
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; US-09-429-755-298

Query Match 6.0%; Score 120; DB 10; Length 1059;
 Best Local Similarity 99.1%; Pred. No. 2.5e-36;
 Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAAGCAAAAGAGAGCTGCTTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 566
 Db 276 GGACAAAGCAAAAGAGAGCTGCTTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 335
 QY 567 AAAAATCTCTGCTGGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAGAGACAGC 626
 Db 336 AAAAATCTCTGCTGGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAGAGACAGC 395
 QY 627 TCTGATTAAGGCGGTACAAATGCCAGAAAGATGAATGTGCTTAATGTGCTGGAACATGG 686
 Db 396 TCTGATTAAGGCGGTACAAATGCCAGAAAGATGAATGTGCTTAATGTGCTGGAACATGG 455
 QY 687 CACTGATCCAAATATTCAGATGATGTGGAATACCACTCT 728
 Db 456 CACTGATCCAAATATTCAGATGATGTGGAATACCACTCT 497

RESULT 41

US-09-825-301-1/C
 ; Sequence 1, Application US/09825301
 ; Patent No. US20020009738A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Dillon, Davin C.

; APPLICANT: Molesch, David A.
 ; APPLICANT: Xu, JIANGCHUN
 ; APPLICANT: Zehentner, Barbara
 ; APPLICANT: Persing, David H.
 ; TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
 ; FILE REFERENCE: 210121.513
 ; CURRENT APPLICATION NUMBER: US/09/825,301
 ; CURRENT FILING DATE: 2001-04-02
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 1851
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; US-09-825-301-1

Query Match 6.0%; Score 120; DB 10; Length 1851;
 Best Local Similarity 99.1%; Pred. No. 2.3e-36;
 Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAAGCAAAAGAGAGCTGCTTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 566
 Db 791 GGACAAAGCAAAAGAGAGCTGCTTACATCTGGCCTCTGCCAATGGGAATTCAGAACTAGT 732
 QY 567 AAAAATCTCTGCTGGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAGAGACAGC 626
 Db 731 AAAAATCTCTGCTGGACAGAGATGTCAACTTAATGTCTTGACAAACAAAAGAGACAGC 672
 QY 627 TCTGATTAAGGCGGTACAAATGCCAGAAAGATGAATGTGCTTAATGTGCTGGAACATGG 686
 Db 671 TCTGATTAAGGCGGTACAAATGCCAGAAAGATGAATGTGCTTAATGTGCTGGAACATGG 612
 QY 687 CACTGATCCAAATATTCAGATGATGTGGAATACCACTCT 728
 Db 611 CACTGATCCAAATATTCAGATGATGTGGAATACCACTCT 570

RESULT 42

US-09-759-143-366/C
 ; Sequence 366, Application US/09759143
 ; Patent No. US2002022248A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, JIANGCHUN
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Hendersen, Robert A.
 ; APPLICANT: Fanger, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvik, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE REFERENCE: 210121.427C23
 ; CURRENT APPLICATION NUMBER: US/09/759,143
 ; CURRENT FILING DATE: 2001-01-12
 ; NUMBER OF SEQ ID NOS: 934
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 366
 ; LENGTH: 1851
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; US-09-759-143-366


```
Query Match          6.0%; Score 120; DB 10; Length 1851;
Best Local Similarity 99.1%; Pred. No. 2.3e-36;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 507 GGACAGCAAAAGAGGACTGCTTACATCTGCGCTCTGCCAATGGGAATTCAGAACTAGT 566
      |||
Db 791 GGACAGCAAAAGAGGACTGCTTACATCTGCGCTCTGCCAATGGGAATTCAGAACTAGT 732

Qy 567 AAACTCTGCTGGACAGACGATGCACACTTAATGCTTGCACACAAAAGAGACAGC 626
      |||
Db 731 AAACTCTGCTGGACAGACGATGCACACTTAATGCTTGCACACAAAAGAGACAGC 672

Qy 627 TCTGATAAAGCCGCTACAAATGCCAGAGATGAATGTCGTTAATGTTGCTGGAACATGG 686
      |||
Db 671 TCTGACAAAGCCGCTACAAATGCCAGAGATGAATGTCGTTAATGTTGCTGGAACATGG 612

Qy 687 CACTGATCCAAATATTCAGATGAGTATGAAATACCACTCT 728
      |||
Db 611 CACTGATCCAAATATTCAGATGAGTATGAAATACCACTCT 570

RESULT 43
US-09-780-669-366/c
; Sequence 366, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, JIANGCHUN
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: JIANG, YUQU
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hurai, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 366
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-780-669-366

Query Match          6.0%; Score 120; DB 10; Length 1851;
Best Local Similarity 99.1%; Pred. No. 2.3e-36;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 507 GGACAGCAAAAGAGGACTGCTTACATCTGCGCTCTGCCAATGGGAATTCAGAACTAGT 566
      |||
Db 791 GGACAGCAAAAGAGGACTGCTTACATCTGCGCTCTGCCAATGGGAATTCAGAACTAGT 732

Qy 567 AAACTCTGCTGGACAGACGATGCACACTTAATGCTTGCACACAAAAGAGACAGC 626
      |||
Db 731 AAACTCTGCTGGACAGACGATGCACACTTAATGCTTGCACACAAAAGAGACAGC 672

Qy 627 TCTGATAAAGCCGCTACAAATGCCAGAGATGAATGTCGTTAATGTTGCTGGAACATGG 686
      |||
Db 611 TCTGATAAAGCCGCTACAAATGCCAGAGATGAATGTCGTTAATGTTGCTGGAACATGG 686
```

```
Db 671 TCTGCAAAAGCCGCTACAAATGCCAGAGATGAATGTCGTTAATGTTGCTGGAACATGG 612
Qy 687 CACTGATCCAAATATTCAGATGAGTATGAAATACCACTCT 728
      |||
Db 611 CACTGATCCAAATATTCAGATGAGTATGAAATACCACTCT 570

RESULT 44
US-09-810-936-291/c
; Sequence 291, Application US/09810936
; Patent No. US2002008285A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 291
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-936-291

Query Match          6.0%; Score 120; DB 10; Length 1851;
Best Local Similarity 99.1%; Pred. No. 2.3e-36;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 507 GGACAGCAAAAGAGGACTGCTTACATCTGCGCTCTGCCAATGGGAATTCAGAACTAGT 566
      |||
Db 791 GGACAGCAAAAGAGGACTGCTTACATCTGCGCTCTGCCAATGGGAATTCAGAACTAGT 732

Qy 567 AAACTCTGCTGGACAGACGATGCACACTTAATGCTTGCACACAAAAGAGACAGC 626
      |||
Db 731 AAACTCTGCTGGACAGACGATGCACACTTAATGCTTGCACACAAAAGAGACAGC 672

Qy 627 TCTGATAAAGCCGCTACAAATGCCAGAGATGAATGTCGTTAATGTTGCTGGAACATGG 686
      |||
Db 671 TCTGCAAAAGCCGCTACAAATGCCAGAGATGAATGTCGTTAATGTTGCTGGAACATGG 612

Qy 687 CACTGATCCAAATATTCAGATGAGTATGAAATACCACTCT 728
      |||
Db 611 CACTGATCCAAATATTCAGATGAGTATGAAATACCACTCT 570

RESULT 45
US-09-810-936-292/c
; Sequence 292, Application US/09810936
; Patent No. US2002008285A1
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 292
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-936-292
```

```
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810,936
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 292
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-936-292

Query Match      6.08; Score 120; DB 10; Length 1851;
Best Local Similarity 99.1%; Pred. No. 2,3e-36;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 507 GGACAAAGCAAAAGAGACTGCTTACATCTGGCCCTGCGCAATGGGAATTCAGAACTAGT 566
Db 791 GGACAAAGCAAAAGAGACTGCTTACATCTGGCCCTGCGCAATGGGAATTCAGAACTAGT 732
QY 567 AAAACTCTGCTGTGACAGAGATGTCAACTTAATGTCTTGACAACAACAAAAAGAGACAGC 626
Db 731 AAAACTCTGCTGTGACAGAGATGTCAACTTAATGTCTTGACAACAACAAAAAGAGACAGC 672
QY 627 TCTGATAAAGCCCTACATATGCCAGAGATGAATGTGCGTTAATGTTGCTGGAACATGG 686
Db 671 TCTGACAAAGCCCTACATATGCCAGAGATGAATGTGCGTTAATGTTGCTGGAACATGG 612
QY 687 CACTGATCCAATATTCAGATGAGTATGGAAATACCACTCT 728
Db 611 CACTGATCCAATATTCAGATGAGTATGGAAATACCACTCT 570
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Search completed: November 8, 2002, 15:53:37
Job time : 113.129 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 8, 2002, 09:07:24 : Search time 3942.57 Seconds
(without alignments)
12754.351 Million cell updates/sec

Title: US-09-924-400-302
Perfect score: 2000
Sequence: 1 atgtgtgttgagtgatc.....aaaaaaaaaaaaaaaaaaaa 2000

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

Word size : 15

Total number of hits satisfying chosen parameters: 1091550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending_Patents_NA_Main:*

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3: /cgn2_6/ptodata/1/pna/US0950_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US0950_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US0950_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US0950_COMB.seq:*
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43: /cgn2_6/ptodata/1/pna/US0950_COMB.seq:*
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Result				SUMMARIES	
No.	Score	Query Match	Length DB	ID	Description
1	2000	100.0	2000	1	Sequence 302, App
2	2000	100.0	2000	1	Sequence 302, App
3	2000	100.0	2000	1	Sequence 302, App
4	2000	100.0	2000	1	Sequence 302, App
5	2000	100.0	2000	1	Sequence 302, App
6	2000	100.0	2000	1	Sequence 302, App
7	2000	100.0	2000	1	Sequence 302, App
8	2000	100.0	2000	1	Sequence 302, App
9	2000	100.0	2000	1	Sequence 302, App
10	2000	100.0	2000	1	Sequence 302, App
11	2000	100.0	2000	1	Sequence 302, App
12	2000	100.0	2000	1	Sequence 302, App
13	2000	100.0	2000	1	Sequence 302, App
14	2000	100.0	2000	1	Sequence 302, App
15	2000	100.0	2000	1	Sequence 302, App
16	2000	100.0	2000	1	Sequence 302, App
17	2000	100.0	2000	1	Sequence 302, App
18	2000	100.0	2000	1	Sequence 302, App
19	2000	100.0	2000	1	Sequence 302, App
20	2000	100.0	2000	1	Sequence 302, App
21	2000	100.0	2000	1	Sequence 302, App

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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22 2000 100.0 2000 28 US-09-709-729-374 Sequence 374, App
23 2000 100.0 2000 29 US-09-759-143-374 Sequence 374, App
24 2000 100.0 2000 30 US-09-780-669-374 Sequence 374, App
25 2000 100.0 2000 31 US-09-810-936-302 Sequence 302, App
26 2000 100.0 2000 31 US-09-822-827-374 Sequence 374, App
27 2000 100.0 2000 32 US-09-825-301-6 Sequence 6, App1
28 2000 100.0 2000 32 US-09-852-911-374 Sequence 374, App
29 2000 100.0 2000 33 US-09-895-793-374 Sequence 374, App
30 2000 100.0 2000 33 US-09-895-814-374 Sequence 374, App
31 2000 100.0 2000 34 US-09-924-400-302 Sequence 302, App
32 2000 100.0 2000 38 US-10-006-920-374 Sequence 374, App
33 2000 100.0 2000 38 US-10-010-940-374 Sequence 374, App
34 2000 100.0 2000 38 US-10-012-896-374 Sequence 374, App
35 2000 100.0 2000 39 US-10-079-137B-302 Sequence 302, App
36 2000 100.0 2000 40 US-10-144-678A-374 Sequence 374, App
37 2000 100.0 2000 42 US-10-212-679-302 Sequence 302, App
38 1551 77.5 2040 16 PCT-US02-24917-303 Sequence 303, App
39 1551 77.5 2040 16 US-09-288-946-375 Sequence 375, App
40 1551 77.5 2040 16 US-09-289-198-303 Sequence 303, App
41 1551 77.5 2040 18 US-09-429-755-303 Sequence 303, App
42 1551 77.5 2040 18 US-09-443-686-375 Sequence 375, App
43 1551 77.5 2040 18 US-09-483-672A-375 Sequence 375, App
44 1551 77.5 2040 20 US-09-534-825A-303 Sequence 303, App
45 1551 77.5 2040 20 US-09-536-857-375 Sequence 375, App
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ALIGNMENTS

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RESULT 1
PCT-US02-24917-302
; Sequence 302, Application PC/TUS0224917
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, Davin C.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.4191PC
; CURRENT APPLICATION NUMBER: PCT/US02/24917
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-24917-302
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Query Match 100.0%; Score 2000; DB 1; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6, 6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ATGGTGTAGGTTGATTCATCCGCGGCTCTCTGTGAAGAACCATTTGGCTC 60
Db 1 ATGGTGTAGGTTGATTCATCCGCGGCTCTCTGTGAAGAACCATTTGGCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGGTGGTCCCTGCTCAGAGAGGAGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGGTGGTGGTCCCTGCTCAGAGAGGAGCAAG 120
QY 121 AGCAAGCTGGGCACTTGTGAGACACGACGACTCTCTATGAAGACATTCAGAGCAAG 180
Db 121 AGCAAGCTGGGCACTTGTGAGACACGACGACTCTCTATGAAGACATTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGGCGGCACTGCTCCCTGCTGCAAGGGGAGTGGCAAGACAACTG 240
Db 181 ATGGGCAAGTGGTGGGCGGCACTGCTCCCTGCTGCAAGGGGAGTGGCAAGACAACTG 240
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QY 241 GGGCGTTCTGGAGACGACGAGCTGTCTATGAAGAACTCAGGAACAAGATGGCAAG 300
Db 241 GGGCGTTCTGGAGACGACGAGCTGTCTATGAAGAACTCAGGAACAAGATGGCAAG 300
QY 301 TGTGCTGCCACACTCTTCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGTGGCGCTGG 360
Db 301 TGTGCTGCCACACTCTTCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGTGGCGCTGG 360
QY 361 GGAGACTACGATGACAGTGGCTTCATGAGCGCCAGTACACGTCCTGGAGAAAGATCTG 420
Db 361 GGAGACTACGATGACAGTGGCTTCATGAGCGCCAGTACACGTCCTGGAGAAAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGGTGGGTAAGTCCCGAGAAAGATCTCATCTGATG 480
Db 421 GACAAGCTCCACAGAGCTGCTGGTGGGTAAGTCCCGAGAAAGATCTCATCTGATG 480
QY 481 CTCAGGACACCTGACGTGAACAGAGACACAAAGAGGACTGCTTACATCTGGCC 540
Db 481 CTCAGGACACCTGACGTGAACAGAGACACAAAGAGGACTGCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTGAGAAATGTAATCTCTGTCGACAGAGATGCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTGAGAAATGTAATCTCTGTCGACAGAGATGCAACTTAAT 600
QY 601 GTCCCTGACAAACAAAAGAGGACAGCTCTGATTAAGGCCCTACAAATGCCAGGAAGTGA 660
Db 601 GTCCCTGACAAACAAAAGAGGACAGCTCTGATTAAGGCCCGTACAAATGCCAGGAAGTGA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGGCAGTGAATCCAAATATTCACATGATGCAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGGCAGTGAATCCAAATATTCACATGATGCAAT 720
QY 721 ACCACCTGACACTGCTATCTATATGAAGATTAATTAAGGCAAGAGCTGCTTA 780
Db 721 ACCACCTGACACTGCTATCTATATGAAGATTAATTAAGGCAAGAGCTGCTTA 780
QY 781 TATGTCCTGATATGCAATCAAAAACAGCATGGCCACACACCTGTTACTGGTGA 840
Db 781 TATGTCCTGATATGCAATCAAAAACAGCATGGCCACACACCTGTTACTGGTGA 840
QY 841 CATGAGCAAAAACAGCAAGTCGTGAATTTTTTAATCAAGAAAAAGGATTTAAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGTCGTGAATTTTTTAATCAAGAAAAAGGATTTAAATGCA 900
QY 901 CTGATATGATATGGAAGAGCTGCTCATCTGCTGCTATGTTGTGTGATCAGCAAGTATA 960
Db 901 CTGATATGATATGGAAGAGCTGCTCATCTGCTGCTATGTTGTGTGATCAGCAAGTATA 960
QY 961 GTGAGCCTTCTACTTGAAGCAAAATATTGATGTATCTTCTCAAGATCTATCTGACAGAG 1020
Db 961 GTGAGCCTTCTACTTGAAGCAAAATATTGATGTATCTTCTCAAGATCTATCTGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAAATTTGCCAGTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAAATTTGCCAGTACTTCTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAATAATCTCTTGAAAAACGCAATCCAGAAACAGACTTTAAAG 1140
Db 1081 AAAGAAAAACAGATGCTAAATAATCTCTTGAAAAACGCAATCCAGAAACAGACTTTAAAG 1140
QY 1141 CTGACATCAGAGGAGAGTGCACAAAGGTTCAAGGCGAGTGAATAATACCCAGAGAGAAA 1200
Db 1141 CTGACATCAGAGGAGAGTGCACAAAGGTTCAAGGCGAGTGAATAATACCCAGAGAGAAA 1200
QY 1201 ATGTCTCAAGACACAGAAATTAATTAAGATGCTGATTAAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGACACAGAAATTAATTAAGATGCTGATTAAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGTATATATGTTGGATTACTTGAAAAACCTGACTATATGTTGCTGCTGGC 1320
Db 1261 AAGCATGAAGTATATATGTTGGATTACTTGAAAAACCTGACTATATGTTGCTGCTGGC 1320
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QY 1321 AATGTGATATGATTAATTCCTCCAAAGGAAAGGACAAACACCGAAATACAGATTT 1380
Db 1321 AATGTGATATGATTAATTCCTCCAAAGGAAAGGACAAACCGAAATACAGATTT 1380
QY 1381 CCTGACAAACGAAAGTGAAGAGTATCACAGAAATTTGCGAATTAGTTCTGACTACAAAGAA 1440
Db 1381 CCTGACAAACGAAAGTGAAGAGTATCACAGAAATTTGCGAATTAGTTCTGACTACAAAGAA 1440
QY 1441 AACAAGATGCCAAAATATCTCTTCGAAAAACAGCAACCCAGAAACAGACTTAAAGTGTACA 1500
Db 1441 AACAAGATGCCAAAATATCTCTTCGAAAAACAGCAACCCAGAAACAGACTTAAAGTGTACA 1500
QY 1501 TCAGAGGAAGAGTACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAGCTAGAAAT 1560
Db 1501 TCAGAGGAAGAGTACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAGCTAGAAAT 1560
QY 1561 TTTATGCGTATCGAAGAAATGAAGAGCAGGAAGTACTCATGTGCGAATTCGCCAGAAAC 1620
Db 1561 TTTATGCGTATCGAAGAAATGAAGAGCAGGAAGTACTCATGTGCGAATTCGCCAGAAAC 1620
QY 1621 CTGACTAATGTGCGCACTGCTGGCAATGCGTATGATGATTAATTCCTCCAAAGAAAGC 1680
Db 1621 CTGACTAATGTGCGCACTGCTGGCAATGCGTATGATGATTAATTCCTCCAAAGAAAGC 1680
QY 1681 AGAACACCTGAAAGCCAGCAATTTCTTGACACTGAGAAATGAAGAGTATCACAGTACGAA 1740
Db 1681 AGAACACCTGAAAGCCAGCAATTTCTTGACACTGAGAAATGAAGAGTATCACAGTACGAA 1740
QY 1741 CAAATGATCTACGAAACCAATTTTGTGAAGACGAACACGGAATTTACAGATGAG 1800
Db 1741 CAAATGATCTACGAAACCAATTTTGTGAAGACGAACACGGAATTTACAGATGAG 1800
QY 1801 ATTCGATTCATGAAAGAAAGCAGATAGAGTGTGTAAGAAATGAATTCGAGCTTCT 1860
Db 1801 ATTCGATTCATGAAAGAAAGCAGATAGAGTGTGTAAGAAATGAATTCGAGCTTCT 1860
QY 1861 CTTAGTCTAGAAAGAAAGAGACATCTTGCATGAAATAGTACGTTGCGGGAAGAAATT 1920
Db 1861 CTTAGTCTAGAAAGAAAGAGACATCTTGCATGAAATAGTACGTTGCGGGAAGAAATT 1920
QY 1921 GCCATGCTAAGACTGAGACTGACACAAATGAACAATCAGAGCCACACTAAAAAAGAAAA 1980
Db 1921 GCCATGCTAAGACTGAGACTGACACAAATGAACAATCAGAGCCACACTAAAAAAGAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 2
US-09-288-946-374
: Sequence 374, Application US/09288946
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer Lynn
: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
: TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
: FILE REFERENCE: 210121.427C7
: CURRENT APPLICATION NUMBER: US/09/288, 946
: NUMBER OF SEQ ID NOS: 381
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 374
: LENGTH: 2000
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-288-946-374

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Query Match	100.0%;	Score 2000;	DB 16;	Length 2000;
Best Local Similarity	100.0%;	Pred. No. 6.6e-226;		
Matches 2000; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

OY	1	ATGCGTGTGAGGTTGATTCATGCCGGCTGCTCTTCTGTGGAAAGCAACCCATTGGTCTC	60
OY	1	ATGGGTGTGAGGTTGATTCATGCCGGCTGCTCTTCTGTGGAAAGCAACCCATTGGTCTC	60
DB	1	ATGGGTGTGAGGTTGATTCATGCCGGCTGCTCTTCTGTGGAAAGCAACCCATTGGTCTC	60
OY	61	AGGACCAAGATGGGCAAGTGGTGGCCGTTGGCTTCCCTCTCTGCAGGGAGACGGCCAG	120
DB	61	AGGACCAAGATGGGCAAGTGGTGGCCGTTGGCTTCCCTCTCTGCAGGGAGACGGCCAG	120
OY	121	AGCAACGTTGGGCACTTCTGGAGACCAAGCAGCAGCTTGTATGAAGACACTGAGAGCAAG	180
DB	121	AGCAACGTTGGGCACTTCTGGAGACCAAGCAGCAGCTTGTATGAAGACACTGAGAGCAAG	180
OY	181	ATGGGCAAGTGTGGCCGCACTGCTTCCCTGCTCAGGGGAGAGTGGGAACGACAGGTG	240
DB	181	ATGGGCAAGTGTGGCCGCACTGCTTCCCTGCTCAGGGGAGAGTGGGAACGACAGGTG	240
OY	241	GCGCGTTCTGGAGACCAAGCAGCAGCTCTGTATGAAGACACTCAGGAAACAAGTGGGCAG	300
DB	241	GCGCGTTCTGGAGACCAAGCAGCAGCTCTGTATGAAGACACTCAGGAAACAAGTGGGCAG	300
OY	301	TGGTCTGCCACACTGCTTCCCTGCTCAGGGGAGAGGCAAGAGCAAGGTGGCGCTTGG	360
DB	301	TGGTCTGCCACACTGCTTCCCTGCTCAGGGGAGAGGCAAGAGCAAGGTGGCGCTTGG	360
OY	361	GGAAGCACTACGATGAGACAGTGCCTTCAATGAGACCCAGCTACCACTCCGTGGAGAAATCTG	420
DB	361	GGAAGCACTACGATGAGACAGTGCCTTCAATGAGACCCAGCTACCACTCCGTGGAGAAATCTG	420
OY	421	GACAAGCTCCACAGAGCTGCGTGGGGGTAAAGTCCCGAGAAAGATCTCATCTGCATNG	480
DB	421	GACAAGCTCCACAGAGCTGCGTGGGGGTAAAGTCCCGAGAAAGATCTCATCTGCATNG	480
OY	481	CTCAGGGCACTAGACGTGAACAAGAAGCAACAAGAAAGAGACTCTTACATCTGGCC	540
DB	481	CTCAGGGCACTAGACGTGAACAAGAAGCAACAAGAAAGAGACTCTTACATCTGGCC	540
OY	541	TCTGCCAATGGGAATTCAGAAAGTACTTAAACTCTCTGTGGACAGCAGATGTCACTTAAT	600
DB	541	TCTGCCAATGGGAATTCAGAAAGTACTTAAACTCTCTGTGGACAGCAGATGTCACTTAAT	600
OY	601	GTCCTTGACAAACAAAAGAGGACAGCTCGTGAATGAAGGCCGTACATGGCAGAGAACTGA	660
DB	601	GTCCTTGACAAACAAAAGAGGACAGCTCGTGAATGAAGGCCGTACATGGCAGAGAACTGA	660
OY	661	TGTGGCTTAATGTTGCTGGAAACATGGCAGCTGATCCAAATATTCAGATGAGTATGAAAT	720
DB	661	TGTGGCTTAATGTTGCTGGAAACATGGCAGCTGATCCAAATATTCAGATGAGTATGAAAT	720
OY	721	ACCACTCTGCACTACCGCTATCTATATGATGAAGATAATTAATGAGCCAAAGCACTGCTTTA	780
DB	721	ACCACTCTGCACTACCGCTATCTATATGATGAAGATAATTAATGAGCCAAAGCACTGCTTTA	780
OY	781	TATGTCGTGATATGCAATCAAAAACAAGCATGGCCCTCACACCACTGATCTTGCTGTTA	840
DB	781	TATGTCGTGATATGCAATCAAAAACAAGCATGGCCCTCACACCACTGATCTTGCTGTTA	840
OY	841	CATGAGCAAAAAACAGCAAGTCTGTAATTTTTTAATCAAGAAAAAGCGAATTTAAATGCA	900
DB	841	CATGAGCAAAAAACAGCAAGTCTGTAATTTTTTAATCAAGAAAAAGCGAATTTAAATGCA	900
OY	901	CTGGATAGATATGAGAGGACGTGCTCTCATCTTCTGTATGTTGTGATCAGCAAGTATA	960
DB	901	CTGGATAGATATGAGAGGACGTGCTCTCATCTTCTGTATGTTGTGATCAGCAAGTATA	960
OY	961	GTCACCTTCTACTTGAGCAAAATATGATGATATTTCTCAAGATCTATCTGGAGAGAGC	1020
DB	961	GTCACCTTCTACTTGAGCAAAATATGATGATATTTCTCAAGATCTATCTGGAGAGAGC	1020
OY	1021	GCCAGAGATATGCTGTTTCTAGTATGATCATCTGTAATTTGGCACTTACTTCTGATAC	1080
DB	1021	GCCAGAGATATGCTGTTTCTAGTATGATCATCTGTAATTTGGCACTTACTTCTGATAC	1080
OY	1081	AAAGAAAAACAGATCTTAAAAATCTTCTGTGAAAACAGCAATCCAGAAACAAGACTTAAAG	1140

|||||
Db 1081 AAAGAAAAAGATGCTAAAAATCTCTTCTGAAACAGCAATCCAGAACAGCTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGTGCACAAAGGTTCAAAGGCGTGAATAATACCCGCGCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGTGCACAAAGGTTCAAAGGCGTGAATAATACCCGCGCAGAGAAA 1200
QY 1201 ATGCTCTCAAGACAGAAATTAATTAAGATGTCATAGAGAGGTGAAGAAATGAAG 1260
Db 1201 ATGCTCTCAAGACAGAAATTAATTAAGATGTCATAGAGAGGTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATTAATGCGGATTAATGCGGATTAATGCGGATTAATGCGGATTA 1320
Db 1261 AAGCATGAAGATTAATTAATGCGGATTAATGCGGATTAATGCGGATTAATGCGGATTA 1320
QY 1321 AATGGTATATGATTAATTAATCTCTCAAGAGAGAGCAACCTGAAATTCAGCAATTT 1380
Db 1321 AATGGTATATGATTAATTAATCTCTCAAGAGAGAGCAACCTGAAATTCAGCAATTT 1380
QY 1381 CTTGACACAGAAAGTGAAGATATCACAGAAATTTGCAATTAATTTCTGACTACAAAGAA 1440
Db 1381 CTTGACACAGAAAGTGAAGATATCACAGAAATTTGCAATTAATTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAATATCTCTTCTGAAACAGCAACCCAGACAGACTTAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATATCTCTTCTGAAACAGCAACCCAGACAGACTTAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGTGCACAAAGGCTTGAGGCGAGTGAATAATGCGCGCAGAGCTGAAAT 1560
Db 1501 TCAGAGAGAGAGTGCACAAAGGCTTGAGGCGAGTGAATAATGCGCGCAGAGCTGAAAT 1560
QY 1561 TTTATGGCTATCGAAGAAATGAAGAACACAGGAATGCTCATGTGCGATTCGCCAGAAAC 1620
Db 1561 TTTATGGCTATCGAAGAAATGAAGAACACAGGAATGCTCATGTGCGATTCGCCAGAAAC 1620
QY 1621 CTGACTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
Db 1621 CTGACTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
QY 1681 AGAAGACCTGAAGCCAGCAATTTCTGACACTGAGAAATGAAGATTCACAGTGAAGAA 1740
Db 1681 AGAAGACCTGAAGCCAGCAATTTCTGACACTGAGAAATGAAGATTCACAGTGAAGAA 1740
QY 1741 CAAAATGATATCTGAGAGCAATTTTGTGAAGAACAGAACTGGAATATTACAGATGAG 1800
Db 1741 CAAAATGATATCTGAGAGCAATTTTGTGAAGAACAGAACTGGAATATTACAGATGAG 1800
QY 1801 ATTCTGATTCATGAAGAAAGCAGATAGAGTGTGAAAAATGAATTTCTGAGCTTTCT 1860
Db 1801 ATTCTGATTCATGAAGAAAGCAGATAGAGTGTGAAAAATGAATTTCTGAGCTTTCT 1860
QY 1861 CTTAGTGTAAAGAAAGAAAGACATCTTCATGAAATAGTACGTCGCGGAGAAATTT 1920
Db 1861 CTTAGTGTAAAGAAAGAAAGACATCTTCATGAAATAGTACGTCGCGGAGAAATTT 1920
QY 1921 GCCATGCTAAGACTGAGCTAGACACAAATGAACATCAGAGCCAGTAAAAAATTT 1980
Db 1921 GCCATGCTAAGACTGAGCTAGACACAAATGAACATCAGAGCCAGTAAAAAATTT 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 3

US-09-289-198-302
; Sequence 302, Application US/09289198
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

;; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
;; FILE REFERENCE: 210121.419C5
;; CURRENT APPLICATION NUMBER: US/09/289,198
;; EARLIER FILING DATE: 1999-04-09
;; EARLIER APPLICATION NUMBER: US 09/062,451
;; EARLIER FILING DATE: 1998-04-17
;; EARLIER APPLICATION NUMBER: US 08/991,789
;; EARLIER FILING DATE: 1997-12-11
;; EARLIER APPLICATION NUMBER: US 08/838,762
;; EARLIER FILING DATE: 1997-04-09
;; EARLIER APPLICATION NUMBER: PCT/US97/00485
;; EARLIER FILING DATE: 1997-01-10
;; EARLIER APPLICATION NUMBER: US 08/700,014
;; EARLIER FILING DATE: 1996-08-20
;; EARLIER APPLICATION NUMBER: US 08/585,392
;; EARLIER FILING DATE: 1996-01-01
;; NUMBER OF SEQ ID NOS: 312
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 302
;; LENGTH: 2000
;; TYPE: DNA
;; ORGANISM: Homo sapien
US-09-289-198-302
Query Match 100.0%; Score 2000; DB 16; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6,6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTGGTGAAGTGAATTCATAGCCGCGCTGCTCTGTAAGAAAGCCATTTGGTCTC 60
Db 1 ATGGTGGTGAAGTGAATTCATAGCCGCGCTGCTCTGTAAGAAAGCCATTTGGTCTC 60
QY 61 AGAGCAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
Db 61 AGAGCAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
QY 121 AGCAAGTGGGCACTTCTGAGACACGACGACTCTCTATGAAGACACTGACAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACACGACGACTCTCTATGAAGACACTGACAGAGCAAG 180
QY 181 ATGGGCAAGTGGGCGGCACTGCTCCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Db 181 ATGGGCAAGTGGGCGGCACTGCTCCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
QY 241 GCGGCTTCTGAGACACGACGACTCTCTATGAAGACACTGACAGCAAGATGGGCAAG 300
Db 241 GCGGCTTCTGAGACACGACGACTCTCTATGAAGACACTGACAGCAAGATGGGCAAG 300
QY 301 TGTGCTGCCACTGCTTCCCTGCTGCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
Db 301 TGTGCTGCCACTGCTTCCCTGCTGCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
QY 361 GGAGACTAGCATGACATGCTTCATGAGCCAGGTAACAGTCCCTGGAGAAATTTG 420
Db 361 GGAGACTAGCATGACATGCTTCATGAGCCAGGTAACAGTCCCTGGAGAAATTTG 420
QY 421 GACAGCTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 421 GACAGCTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 481 CTCAGGACACTGACGTCGTAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 540
Db 481 CTCAGGACACTGACGTCGTAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTGCTGCAAGAGATGCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTGCTGCAAGAGATGCAACTTAAT 600
QY 601 GTCTTCAACAAAAAGAGAGACGCTGTATAAAGCCCTTACATCCAGGAAGATGAA 660
Db 601 GTCTTCAACAAAAAGAGAGACGCTGTATAAAGCCCTTACATCCAGGAAGATGAA 660
QY 661 TGTGCGTTAATGTTGCTGAACATGGCATGATCCAAATATTCAGATGATGAAAT 720

|||||
Db 661 TGTGGTAAATGTCTGGAAACATGGCACTGATCCAAATATTCAGATGATGTAAT 720
Qy 721 ACCACTCTGCACATAGCTATCTATATGAAGATTAATTAATGCGCAAGCACTGCTTA 780
Db 721 ACCACTCTGCACATAGCTATCTATATGAAGATTAATTAATGCGCAAGCACTGCTTA 780
Qy 781 TATGTCGTGATATGTAATCAAAAAAACAAGCATGGGCTCACACCTGTTACTTGGTGA 840
Db 781 TATGTCGTGATATGTAATCAAAAAAACAAGCATGGGCTCACACCTGTTACTTGGTGA 840
Qy 841 CATGAGCAAAAAACAGCAAGTCTGAAATTTTATCAAAAAAAGCGAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTCTGAAATTTTATCAAAAAAAGCGAATTTAAATGCA 900
Qy 901 CTGGATAGATATGGAAGCACTGCTCATCTGATATGTTGGATCAGCAAGTATA 960
Db 901 CTGGATAGATATGGAAGCACTGCTCATCTGATATGTTGGATCAGCAAGTATA 960
Qy 961 GTACAGCTTCTACTGAGCAAAATATGATGATCTTCAGAGATCTATCTGGACAGC 1020
Db 961 GTACAGCTTCTACTGAGCAAAATATGATGATCTTCAGAGATCTATCTGGACAGC 1020
Qy 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGCGAGTACTTCTGCTAC 1080
Db 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGCGAGTACTTCTGCTAC 1080
Qy 1081 AAGAAAAACAGATCTTAAAAATCTCTCTGAAAAACAGCAATCCAGAACAGCTTAAAG 1140
Db 1081 AAGAAAAACAGATCTTAAAAATCTCTCTGAAAAACAGCAATCCAGAACAGCTTAAAG 1140
Qy 1141 CTGACATCGAGAGAGATCAAAAGTCAAAAGGAGGAGGAAATTAAGCAGCAGAGAA 1200
Db 1141 CTGACATCGAGAGAGATCAAAAGTCAAAAGGAGGAGGAAATTAAGCAGCAGAGAA 1200
Qy 1201 ATGTCTCAAGAACCAAAATTAATTAAGATGCTGATAGAGAGTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAAATTAATTAAGATGCTGATAGAGAGTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAGATTAATTAATGCTGATAGAGAGTGAAGAAATGAAG 1320
Db 1261 AAGCATGAAGATTAATTAATGCTGATAGAGAGTGAAGAAATGAAG 1320
Qy 1321 AATGATGAATGATTAATCTCAAAAGAGAGAGCAACCTGAAATATGCAATTT 1380
Db 1321 AATGATGAATGATTAATCTCAAAAGAGAGAGCAACCTGAAATATGCAATTT 1380
Qy 1381 CCTGACAAGAAAGTGAAGATATCAGAAATTTGGAATTTAGTTCTGACATCAAGAA 1440
Db 1381 CCTGACAAGAAAGTGAAGATATCAGAAATTTGGAATTTAGTTCTGACATCAAGAA 1440
Qy 1441 AAACAGATGCCAAATACTCTTCTGAAAAACAGCAACCCAGAACAGCTTAAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATACTCTTCTGAAAAACAGCAACCCAGAACAGCTTAAAGCTGACA 1500
Qy 1501 TCAGAGGAAGATCAAAAGGCTTGAAGGAGTGAAGAAAGGCGCAGAGTGAAGAAAT 1560
Db 1501 TCAGAGGAAGATCAAAAGGCTTGAAGGAGTGAAGAAAGGCGCAGAGTGAAGAAAT 1560
Qy 1561 TTTATGGCTATGGAAGAAATGAAGAGCAAGCAAGTACTCATGTCGATTTCCAGAAAC 1620
Db 1561 TTTATGGCTATGGAAGAAATGAAGAGCAAGCAAGTACTCATGTCGATTTCCAGAAAC 1620
Qy 1621 CTGACTAATGTCCTGCTGCTGCAATGCTGATGATGATTAATTTCTCAAGAAAGC 1680
Db 1621 CTGACTAATGTCCTGCTGCTGCAATGCTGATGATGATTAATTTCTCAAGAAAGC 1680
Qy 1681 AAGAACCTGAAGAGCAGCAATTTCTGACACTGAGAAATGAAGATATCAGCTGCGAA 1740
Db 1681 AAGAACCTGAAGAGCAGCAATTTCTGACACTGAGAAATGAAGATATCAGCTGCGAA 1740
Qy 1741 CAAATGATACTCAGAGCAATTTTGTGAAGAACAGAACCTGGAATATTACAGATGAG 1800
Db 1741 CAAATGATACTCAGAGCAATTTTGTGAAGAACAGAACCTGGAATATTACAGATGAG 1800

Db 1741 CAAATGATACTCAGAGCAATTTTGTGAAGAACAGAACCTGGAATATTACAGATGAG 1800
Qy 1801 ATTCGATTCATGAAGAAAGAGATAGAGGTTGAAGAAATGAATTCGAGCTTCT 1860
Db 1801 ATTCGATTCATGAAGAAAGAGATAGAGGTTGAAGAAATGAATTCGAGCTTCT 1860
Qy 1861 CTGATGTTGAAGAAAGAAAGACATCTTCTGAAATATGATGATGCTGGGGAAGAAAT 1920
Db 1861 CTGATGTTGAAGAAAGAAAGACATCTTCTGAAATATGATGATGCTGGGGAAGAAAT 1920
Qy 1921 GCCATGCTAAGACTGAGCTAGACACAAATGAATCAGAGCCAGCTAAAAA 1980
Db 1921 GCCATGCTAAGACTGAGCTAGACACAAATGAATCAGAGCCAGCTAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 4
US-09-429-755-302
; Sequence 302, Application US/09429755A
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-302

Query Match 100.0%; Score 2000; DB 18; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6,6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGATGTTGAGGTGATTCATGCGCGCTGCTTCTGTGAAGAGCAATTTGGTCTC 60
Db 1 ATGATGTTGAGGTGATTCATGCGCGCTGCTTCTGTGAAGAGCAATTTGGTCTC 60
Qy 61 AAGAGCAAGATGGCAAGTGGTGGCTGCTTCCCTGCTGCAAGGAGAGCGCAAG 120
Db 61 AAGAGCAAGATGGCAAGTGGTGGCTGCTTCCCTGCTGCAAGGAGAGCGCAAG 120
Qy 121 AAGACGTGGGCACTTCTGAGAACCCAGACGACTGCTATGAAGCACTCAGAGCAAG 180
Db 121 AAGACGTGGGCACTTCTGAGAACCCAGACGACTGCTATGAAGCACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGGTGGCGCACTGCTTCCCTGCTGAGGAGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGGTGGCGCACTGCTTCCCTGCTGAGGAGGAGTGGCAAGCAAGCTG 240
Qy 241 GGCCTTCTGAGAGCAGACGACATCTGCTATGAAGCACTCAGAGCAAGTGGCAAG 300
Db 241 GGCCTTCTGAGAGCAGACGACATCTGCTATGAAGCACTCAGAGCAAGTGGCAAG 300
Qy 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGAGGAGGCAAGCAAGTGGGCTTGG 360
Db 301 TGGTGTGCTGCACTGCTTCCCTGCTGCAAGGAGGAGGCAAGCAAGTGGGCTTGG 360
Qy 361 GGAGACTACAGATGAGAGTCCCTTCAATGAAGCCAGGATACAGCTCCGTGAGAAATCTG 420
Db 361 GGAGACTACAGATGAGAGTCCCTTCAATGAAGCCAGGATACAGCTCCGTGAGAAATCTG 420

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QY 421 GACAAGCTCCACAGAGCTGCTGGTGGGTTAAAGTCCCAAGAAAGATCTCATGTGATG 480
    |||||||
Db 421 GACAAGCTCCACAGAGCTGCTGGTGGGTTAAAGTCCCAAGAAAGATCTCATGTGATG 480
QY 481 CTCAGGACACTGACGTGAAACAGACAGACAAAAGAGGACTGCTTCATCTGACC 540
    |||||||
Db 481 CTCAGGACACTGACGTGAAACAGACAGACAAAAGAGGACTGCTTCATCTGACC 540
QY 541 TCTGCCAATGGAATTCAGAAATAGTAAATCTCTGCTGGACAGACGATGCACTTAAT 600
    |||||||
Db 541 TCTGCCAATGGAATTCAGAAATAGTAAATCTCTGCTGGACAGACGATGCACTTAAT 600
QY 601 GTCCCTGACAAACAAAAGAGAGAGCTGTGATAAAGCCCTGACAAATCCAGGAAGTAA 660
    |||||||
Db 601 GTCCCTGACAAACAAAAGAGAGAGCTGTGATAAAGCCCTGACAAATCCAGGAAGTAA 660
QY 661 TGTGCGCTTAATGTGCTGGGAAACATGGACATGATCCAAATATTCAGAGATGAAAT 720
    |||||||
Db 661 TGTGCGCTTAATGTGCTGGGAAACATGGACATGATCCAAATATTCAGAGATGAAAT 720
QY 721 ACCACTGTGACATGCTATCTATATGAAGATTAATGAGCAAGCAGCTGCTCTTA 780
    |||||||
Db 721 ACCACTGTGACATGCTATCTATATGAAGATTAATGAGCAAGCAGCTGCTCTTA 780
QY 781 TATGCTCTGATATGCAATCAAAAACAGCATGGCCTCACACCATGTTACTTGTTA 840
    |||||||
Db 781 TATGCTCTGATATGCAATCAAAAACAGCATGGCCTCACACCATGTTACTTGTTA 840
QY 841 CATGAGCAAAAACAGCAAGCTGTAATTTTATCAAGAAAAGGAATTTAAAGCA 900
    |||||||
Db 841 CATGAGCAAAAACAGCAAGCTGTAATTTTATCAAGAAAAGGAATTTAAAGCA 900
QY 901 CTGATGATGATGAGAGAGAGCTGCTCATCTGCTGATGCTGATGATGATGATGATG 960
    |||||||
Db 901 CTGATGATGATGAGAGAGAGCTGCTCATCTGCTGATGCTGATGATGATGATGATG 960
QY 961 GTACGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
    |||||||
Db 961 GTACGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAGAG 1020
QY 1021 GCCAGAGATGATGCTGTTCTAGTCATCATCATGATTTTCCGATCTTCTGATAC 1080
    |||||||
Db 1021 GCCAGAGATGATGCTGTTCTAGTCATCATCATGATTTTCCGATCTTCTGATAC 1080
QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGAAGAACAGCAATCCAGAAACAGATTAAG 1140
    |||||||
Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGAAGAACAGCAATCCAGAAACAGATTAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCAAAAAGGTTCAAAAGGAGTGAATTAAGCCAGAGAAA 1200
    |||||||
Db 1141 CTGACATCAGAGAGAGAGTCAAAAAGGTTCAAAAGGAGTGAATTAAGCCAGAGAAA 1200
QY 1201 ATGCTCAAGACAGCAAAATTAATAGATGATGATGATGATGATGATGATGATGATG 1260
    |||||||
Db 1201 ATGCTCAAGACAGCAAAATTAATAGATGATGATGATGATGATGATGATGATGATG 1260
QY 1261 AAGCATGAAGTAAATATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
    |||||||
Db 1261 AAGCATGAAGTAAATATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
QY 1321 AATGCTGATTAATGATTAATTTCTCAAGAGAGAGAGCAACCTGAAAATTCAGCAATTT 1380
    |||||||
Db 1321 AATGCTGATTAATGATTAATTTCTCAAGAGAGAGAGCAACCTGAAAATTCAGCAATTT 1380
QY 1381 CCTGACACAGCAAGAGTGAAGATATCAGAGATTTGGCAATTAATGTTTCTGATACAAAGAA 1440
    |||||||
Db 1381 CCTGACACAGCAAGAGTGAAGATATCAGAGATTTGGCAATTAATGTTTCTGATACAAAGAA 1440
QY 1441 AAACAGATGCAAAATCTCTTCTGAAAACAGCAACCCAGAAAGCACTTAAGAGCTGACA 1500
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Db 1441 AAACAGATGCAAAATCTCTTCTGAAAACAGCAACCCAGAAAGCACTTAAGAGCTGACA 1500

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QY 1501 TCAGAGGAGAGATCACAAGAGCTTGAAGGAGATGAAAAATGGCCAGCCAGATAGAAAAT 1560
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Db 1501 TCAGAGGAGAGATCACAAGAGCTTGAAGGAGATGAAAAATGGCCAGCCAGATAGAAAAT 1560
QY 1561 TTTATGGCTATCCGAAGAAATGAAGAAACAGAGAGTACTCATGTCGATTTCCAGAAAAC 1620
    |||||||
Db 1561 TTTATGGCTATCCGAAGAAATGAAGAAACAGAGAGTACTCATGTCGATTTCCAGAAAAC 1620
QY 1621 CTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
    |||||||
Db 1621 CTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
QY 1681 AGAACACCTGAAAGCCAGCAATTTCTGACACATGAGAAATGAAGATTCACAGTGAGAA 1740
    |||||||
Db 1681 AGAACACCTGAAAGCCAGCAATTTCTGACACATGAGAAATGAAGATTCACAGTGAGAA 1740
QY 1741 CAAAATGATATCTGAAAGCAATTTTGAAGAACAGAACTGGAATTAATACAGATGAG 1800
    |||||||
Db 1741 CAAAATGATATCTGAAAGCAATTTTGAAGAACAGAACTGGAATTAATACAGATGAG 1800
QY 1801 ATTCTGATTCATGAAAGAAAGCAGATGAAAGTGGTGAAGAAATGAATTCGAGCTTCT 1860
    |||||||
Db 1801 ATTCTGATTCATGAAAGAAAGCAGATGAAAGTGGTGAAGAAATGAATTCGAGCTTCT 1860
QY 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGACATGAAATTAATGATGCTGCGGAAAGAAAT 1920
    |||||||
Db 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGACATGAAATTAATGATGCTGCGGAAAGAAAT 1920
QY 1921 GCCATGCTAAGACTGAGAGCTAGACCAATGAATCAGAGCCAGCTTAAGAAAAA 1980
    |||||||
Db 1921 GCCATGCTAAGACTGAGAGCTAGACCAATGAATCAGAGCCAGCTTAAGAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
    |||||||
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

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RESULT 5
US-09-443-686-374
; Sequence 374, Application US/09443686
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9A
; CURRENT APPLICATION NUMBER: US/09/443,686
; NUMBER OF SEQ ID NOS: 551
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-443-686-374

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Query Match 100.0%; Score 2000; DB 18; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6,6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTGTGAGGTGATTCATATGCGGCTGCTCTGTAAGAAAGCATTTGGCTC 60
Db 1 ATGGTGTGAGGTGATTCATATGCGGCTGCTCTGTAAGAAAGCATTTGGCTC 60

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OY	61	AGSAGCAAGATGGGCAAGATGTCGTCGCTGCTCCCTGCTGCGAGGAGACGGGCAAG	120
Db	61	AGGAGCAAGATGGGCAAGATGTCGTCGCTGCTCCCTGCTGCGAGGAGAGGGCAAG	120
OY	121	AGCAACCTGGGCACTTCTTGAGACACAGCAGCACTGCTGATGACACACTGAGAGCAAG	180
Db	121	AGCAACTGGGCACTTCTGGAAGACACAGCACTGCTGATGAAACACTGAGAGCAAG	180
OY	181	ATGGGCAAGTGTGTCGGCCCACTGCTCCCTGCTGCGAGGGAGTGGCAAGAGCAAGTG	240
Db	181	ATGGGCAAGTGTGTCGGCCCACTGCTCCCTGCTGCGAGGGAGTGGCAAGAGCAAGTG	240
OY	241	GGCCCTTCTGGAAACCAACGACGACTGCTGATGAAAGACTGAGAAACAAGTGGCAAG	300
Db	241	GGCCCTTCTGGAAACCAACGACGACTGCTGATGAAAGACTGAGAAACAAGTGGCAAG	300
OY	301	TGGTGTGCCCACTGCTCCCTGCTGCAAGGGGAGGGCAAGCAAGTGGGGCTTGG	360
Db	301	TGGTGTGCCCACTGCTCCCTGCTGCAAGGGGAGGGCAAGCAAGTGGGGCTTGG	360
OY	361	GGAGACTAGCATGACAGTGGCTTTCATGGAGCCAGGTACCAAGTCCGCGAGAAAGATCTG	420
Db	361	GGAGACTAGCATGACAGTGGCTTTCATGGAGCCAGGTACCAAGTCCGCGAGAAAGATCTG	420
OY	421	GACACAGTCCACAGAGCTGCTGTGGGGTAAAGTCCCAAGAAAGATCTATGCTATG	480
Db	421	GACACAGTCCACAGAGCTGCTGTGGGGTAAAGTCCCAAGAAAGATCTATGCTATG	480
OY	481	CTCAGGACACTGACGTGAACAGAAGAGCAACAAAGAGACTGCTCATGCTGATG	540
Db	481	CTCAGGACACTGACGTGAACAGAAGAGCAACAAAGAGACTGCTCATGCTGATG	540
OY	541	TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGGACAGACGATGTCACATTAT	600
Db	541	TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGGACAGACGATGTCACATTAT	600
OY	601	GTCCTTACACAACAAAAGAGAGACGCTCTGATTAAGGCCGTGCAATGCCAGAGATGAA	660
Db	601	GTCCTTACACAACAAAAGAGAGACGCTCTGATTAAGGCCGTGCAATGCCAGAGATGAA	660
OY	661	TGTGCTGTAATGTTGCTGGAAACATGGCAGCTGATCCAAATATCCAGATGAGATGGAAAT	720
Db	661	TGTGCTGTAATGTTGCTGGAAACATGGCAGCTGATCCAAATATTCAGATGAGATGGAAAT	720
OY	721	ACCACTGTGACATACGCTATCTAATTAAGAAATTAATTAATGAGCCAAAGCACTGCTCTTA	780
Db	721	ACCACTGTGACATACGCTATCTAATTAAGAAATTAATTAATGAGCCAAAGCACTGCTCTTA	780
OY	781	TATGCTGCTGATATCGATCAATCAAAAACAGATGGCCTCACACCACTGTACTGGTGTA	840
Db	781	TATGCTGCTGATATCGATCAATCAAAAACAGATGGCCTCACACCACTGTACTGGTGTA	840
OY	841	CATAGGAAAAACAGCAAGTCGTGAATTTTAATCAAGAAAAAGCAATTTTAATCA	900
Db	841	CATAGGAAAAACAGCAAGTCGTGAATTTTAATCAAGAAAAAGCAATTTTAATCA	900
OY	901	CTGAGTAGATATGGAAGGACTGCTCTCATACTTGGTGTATGTTGGATCAGCAAGTATA	960
Db	901	CTGAGTAGATATGGAAGGACTGCTCTCATACTTGGTGTATGTTGGATCAGCAAGTATA	960
OY	961	GTCAGCCTTCTACTTGAGCAAAATATTTGATGTAATCTTCAAGATCTATCTGAGACAGG	1020
Db	961	GTCAGCCTTCTACTTGAGCAAAATATTTGATGTAATCTTCAAGATCTATCTGAGACAGG	1020
OY	1021	GCCAGAGATGCTGTTTCTAGTCATCATCATGTAATTTGCAAGTCTTCTGACTAC	1080
Db	1021	GCCAGAGATGCTGTTTCTAGTCATCATCATGTAATTTGCAAGTCTTCTGACTAC	1080
OY	1081	AAAGAAAAAAGATGCTAAAAATCTTTCTGAAAACAGCAATCCAGAAACAAAGACTTAAAG	1140
Db	1081	AAAGAAAAAAGATGCTAAAAATCTTTCTGAAAACAGCAATCCAGAAACAAAGACTTAAAG	1140
OY	1141	CTGACATCAGAGAAAGATCACAAAGGTTCAAGGCCATGTAATAATGCCACGACAGAGAA	1200

Db	1141	CTGACATACGAGGAAGAGCTCACAAAGGTTCAAAGGCAGTGAATAATAGCCACCCAGAGAA	1200
QY	1201	ATGTCTCAAGAACCCAGAAATAAATTAAGATGGTGATAGAGAGGTTGAAGAATAATGAAG	1260
Db	1201	ATGTCTCAAGAACCCAGAAATAAATTAAGATGGTGATAGAGAGGTTGAAGAATAATGAAG	1260
QY	1261	AAGCATGAAGAATAATTAATGTGGGATTACTAGAAAACCTGACTAATATGTGTCTACTGTGGC	1320
Db	1261	AAGCATGAAGAATAAATGTGGGATTACTAGAAAACCTGACTAATATGTGTCTACTGTGGC	1320
QY	1321	AATGGTGAATTAATGATTAATTCCTCAAGGAAGACACAAACCCTGAATAATCAGCAATTT	1380
Db	1321	AATGGTGAATTAATGATTAATTCCTCAAGGAAGACACAAACCCTGAATAATCAGCAATTT	1380
QY	1381	CCGTGACAACGAAAGTGAAGAGATACACAGAAATTTGCCAATTAGTTTCTGACTACAAAGAA	1440
Db	1381	CCTGACAACGAAAGTGAAGAGATACACAGAAATTTGCCAATTAGTTTCTGACTACAAAGAA	1440
QY	1441	AAACGATGCCAAATTAATCTTTCTGAAAAACGCAACCCAGAACAGACTTAAAGCTGACA	1500
Db	1441	AAACGATGCCCAAAATTAATCTTTCTGAAAAACGCAACCCAGAACAGACTTAAAGCTGACA	1500
QY	1501	TCAGAGGAAGAGTCAACAAGCCTTAGAGGCGAGTGAATATGGCCAGCCAGAGCTAGAAAT	1560
Db	1501	TCAGAGGAAGAGTCAACAAGCCTTAGAGGCGAGTGAATATGGCCAGCCAGAGCTAGAAAT	1560
QY	1561	TTTTATGGCTATCGAAGAAATGAAGAAGCAGGAAGTACTCATGTGCGATTCGCCAGAAAAC	1620
Db	1561	TTTTATGGCTATCGAAGAAATGAAGAAGCAGGAAGTACTCATGTGCGATTCGCCAGAAAAC	1620
QY	1621	CTGACTAATGTGTGCCACTGTCTGTGGCAATGTGTATGTGATTAATTTCTCTCCAAAGGAAGC	1680
Db	1621	CTGACTAATGTGTGCCACTGTCTGTGGCAATGTGTATGTGATTAATTTCTCTCCAAAGGAAGC	1680
QY	1681	AGAACACCGGAAGCAGACAATTTCTCTGCACATGTGAATGAAGATATCACAGTACGAA	1740
Db	1681	AGAACACCTGAAAGCAGCAATTTCTCTGCACATGTGAATGAAGATATCACAGTACGAA	1740
QY	1741	CAAAATGATACTCAGAACCAATTTTTGTGAAGAACGAACACTGGAATTTACACAGATGAG	1800
Db	1741	CAAAATGATACTCAGAACCAATTTTTGTGAAGAACGAACACTGGAATTTACACAGATGAG	1800
QY	1801	ATTCTGATTCATGAAGAAGAAAGCAGATAGAAGTGTGTTGAAAAAATAATTTCTGAGCTTCT	1860
Db	1801	ATTCTGATTCATGAAGAAGAAAGCAGATAGAAGTGTGTTGAAAAAATAATTTCTGAGCTTCT	1860
QY	1861	CTTAGTGTGAAGAAAGAAACACATCTTGCACTGAATAATAGTACCTTTCGGGAGCAATTT	1920
Db	1861	CTTAGTGTGAAGAAAGAAAGCAATCTTTCGCAATGAATAATAGTACCTTTCGGGAGCAATTT	1920
QY	1921	GCCATGCTTAAGACTGGAGCTAGACCAATGAANAATCATGAGGCCAGCTAAAAA	1980
Db	1921	GCCATGCTTAAGACTGGAGCTAGACCAATGAANAATCATGAGGCCAGCTAAAAA	1980
QY	1981	AAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAA 2000	

RESULT 6
US-09-483-672A-374
: Sequence 374, Application US/09483672A
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan Louise
: APPLICANT: Jiang Yuqi
: APPLICANT: Reed, Steven G.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Rafter, Marc W.

```

; APPLICANT: Solk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Wang, Aljun
; APPLICANT: Meagher, Madeleine
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.42711C11
; CURRENT APPLICATION NUMBER: US/09/483,672A
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-483-672A-374

Query Match      100.0%; Score 2000; DB 18; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6,6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGTGGTATTCATCCGCGCTCTCTGTGAAGAGCCATTGGCTC 60
DB 1 ATGGTGGTTGAGTGGTATTCATCCGCGCTCTCTGTGAAGAGCCATTGGCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGGCTGGCTTCCCTGCTGAGGAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGGTGGCTGGCTTCCCTGCTGAGGAGAGCGGCAAG 120
QY 121 AGCAAGCTGGGCACTTCTGTGAGACACGACACTCTGTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAAGCTGGGCACTTCTGTGAGACACGACACTCTGTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGGCGCCGCACTGCTTCCCTGCTGAGGAGGAGAGTGGCAAGAGTGTG 240
DB 181 ATGGGCAAGTGGGCGCCGCACTGCTTCCCTGCTGAGGAGGAGAGTGGCAAGAGTGTG 240
QY 241 GGGCCTTCTGGAGACACGACGACTGTCTATGAAGACACTCAGAGCAAGAGTGGCAAG 300
DB 241 GGGCCTTCTGGAGACACGACGACTGTCTATGAAGACACTCAGAGCAAGAGTGGCAAG 300
QY 301 TGTGCTGCTCCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGTGGCGCTTGG 360
DB 301 TGTGCTGCTCCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGTGGCGCTTGG 360
QY 361 GGAGACTACGATGACAGTGGCTTCCCTGCTGAGGAGGAGTACACGCTGCTGGAGAGATCTG 420
DB 361 GGAGACTACGATGACAGTGGCTTCCCTGCTGAGGAGGAGTACACGCTGCTGGAGAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTGGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATCTGATG 480
DB 421 GACAAGCTCCACAGAGCTGGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATCTGATG 480
QY 481 CTCAGGGACACTGACGTGAACAAAGAAAGACAAAGAAAGAGGACTGCTTCAACTGCGCC 540
DB 481 CTCAGGGACACTGACGTGAACAAAGAAAGACAAAGAAAGAGGACTGCTTCAACTGCGCC 540
QY 541 TCTGCAATGGAATTCAGAAAGTAAAGTCTGCTGGAGAGAGATGCAACTTAAT 600
DB 541 TCTGCAATGGAATTCAGAAAGTAAAGTCTGCTGGAGAGAGATGCAACTTAAT 600
QY 601 GTCCCTTGAACAACAAAAGAGAGACAGCTCTGTATTAAGGCGCTTACATCCAGGAAGATGAA 660
DB 601 GTCCCTTGAACAACAAAAGAGAGACAGCTCTGTATTAAGGCGCTTACATCCAGGAAGATGAA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGCGACTGATCCAAATATTCAGATGAGTATGAAAT 720
DB 661 TGTGCGTTAATGTTGCTGGAACATGCGACTGATCCAAATATTCAGATGAGTATGAAAT 720
QY 721 AACACCTGACATACGCTATCTATTAAGAGATTAATTAATGGCCAAAGCACTGCTCTTA 780
DB 721 AACACCTGACATACGCTATCTATTAAGAGATTAATTAATGGCCAAAGCACTGCTCTTA 780
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QY 781 TATGCTGCTGATATCGAATCAAAAACAGAGATGGCTCACACCACCTTACTTGGTGA 840
DB 781 TATGCTGCTGATATCGAATCAAAAACAGAGATGGCTCACACCACCTTACTTGGTGA 840
QY 841 CATAGCAAAAACAGCAAGCTGTAATTTTATTAACAAGAAAAAGGAATTTAAATGCA 900
DB 841 CATAGCAAAAACAGCAAGCTGTAATTTTATTAACAAGAAAAAGGAATTTAAATGCA 900
QY 901 CTGATAGATATGAGAGAGAGCTGCTCATATCTGCTGTATGTTGGATGACGAAATATA 960
DB 901 CTGATAGATATGAGAGAGAGCTGCTCATATCTGCTGTATGTTGGATGACGAAATATA 960
QY 961 GTCAGCCTTCTACTTGAAGCAAAATATTAATTAATCTTCAAGATCTATCTGACAGACG 1020
DB 961 GTCAGCCTTCTACTTGAAGCAAAATATTAATTAATCTTCAAGATCTATCTGACAGACG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATATTAATTTGCCAGTTACTTTCGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATATTAATTTGCCAGTTACTTTCGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAATAATCTTCTGAAAACAGCAATCCAGAAAGAACTTAAG 1140
DB 1081 AAAGAAAAACAGATGCTAAATAATCTTCTGAAAACAGCAATCCAGAAAGAACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGTACAAAAGGTTCAAAAGCAGTGAATAATAGCCAGCCAGAGAAA 1200
DB 1141 CTGACATCAGAGAGAGTACAAAAGGTTCAAAAGCAGTGAATAATAGCCAGCCAGAGAAA 1200
QY 1201 ATGCTCTAAGACACGAAATTAATTAAGATGTGATATGAAGAGTTGAAGAAATTAAG 1260
DB 1201 ATGCTCTAAGACACGAAATTAATTAAGATGTGATATGAAGAGTTGAAGAAATTAAG 1260
QY 1261 AAGCATGAAGTATATATGTTGGGATTAAGTAAAGCTGCTATGTTGGTACAGTGGC 1320
DB 1261 AAGCATGAAGTATATATGTTGGGATTAAGTAAAGCTGCTATGTTGGTACAGTGGC 1320
QY 1321 AATGCTATATATGATTAATTTCTCAAAAGAGAGCAGAAACCTGTAATAATTCAGCAATTT 1380
DB 1321 AATGCTATATATGATTAATTTCTCAAAAGAGAGCAGAAACCTGTAATAATTCAGCAATTT 1380
QY 1381 CTTGACACAGCAAGTGAAGAGTATCACGAATTTGCCAATTAATTTGCTGACTCAAAAGAA 1440
DB 1381 CTTGACACAGCAAGTGAAGAGTATCACGAATTTGCCAATTAATTTGCTGACTCAAAAGAA 1440
QY 1441 AAACAGATGCCAAATATCTCTTCTGAAAACAGCAACCCAGAAACAGCACTTAAGCTGACA 1500
DB 1441 AAACAGATGCCAAATATCTCTTCTGAAAACAGCAACCCAGAAACAGCACTTAAGCTGACA 1500
QY 1501 TCAGAGGAAGAGTCCAAAAGGCTTGAAGGCAAGTGAATAATGGCCAGCCAGAGCTAGAAAAT 1560
DB 1501 TCAGAGGAAGAGTCCAAAAGGCTTGAAGGCAAGTGAATAATGGCCAGCCAGAGCTAGAAAAT 1560
QY 1561 TTTATGGCTATCCGAAGAAATGAAGAGACAGGAAGTACTATGTGCGATTTCCAGAAAAC 1620
DB 1561 TTTATGGCTATCCGAAGAAATGAAGAGACAGGAAGTACTATGTGCGATTTCCAGAAAAC 1620
QY 1621 CTGACTAATGATGGTCCACTGCTGGCAATGTGATGATGATTAATTTCTCCAGAGAGAGC 1680
DB 1621 CTGACTAATGATGGTCCACTGCTGGCAATGTGATGATGATTAATTTCTCCAGAGAGAGC 1680
QY 1681 AGAAGACCTGAAAAGCCAGCAATTTCTGACACTGAGAATGAAGATATCACTGACGAA 1740
DB 1681 AGAAGACCTGAAAAGCCAGCAATTTCTGACACTGAGAATGAAGATATCACTGACGAA 1740
QY 1741 CAAAATGATATCTAGAAAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACAGATGAG 1800
DB 1741 CAAAATGATATCTAGAAAGCAATTTTGTGAAGAACAGAACCTGGAATATTAACAGATGAG 1800
QY 1801 ATTCTGATTCATGAAGAAAGCAGATGAGTGGTTGAATAATTAATTTGAGCTTTC 1860
DB 1801 ATTCTGATTCATGAAGAAAGCAGATGAGTGGTTGAATAATTAATTTGAGCTTTC 1860
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Db 1561 TTATGCTATCGAAGAAATGAAGACGAGAGTACTCATGTGCTGATGCCAGAAAAC 1620
QY 1621 CTGACTAATGGTGCACCTGCTGCAATGGTATGATGATTAATTCCTCAAGAAAGAGC 1680
Db 1621 CTGACTAATGGTGCACCTGCTGCAATGGTATGATGATTAATTCCTCAAGAAAGAGC 1680
QY 1661 AGAACACCTGAAGACGACCAATTTCTGACACTGAGAAATGAAGATACAGTGCAGAA 1740
Db 1661 AGAACACCTGAAGACGACCAATTTCTGACACTGAGAAATGAAGATACAGTGCAGAA 1740
QY 1741 CAAATATGATCTGAGAACCAATTTTGTGAAGACGAAACACTGGAATTTACAGATAG 1800
Db 1741 CAAATATGATCTGAGAACCAATTTTGTGAAGACGAAACACTGGAATTTACAGATAG 1800
QY 1801 ATTCTGATTCATGAAGAAACAGATAGAAAGTGTGAAAAATTAATTCGAGCTTTCT 1860
Db 1801 ATTCTGATTCATGAAGAAACAGATAGAAAGTGTGAAAAATTAATTCGAGCTTTCT 1860
QY 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGATGAAAAATAGTACGTTGCGGGAAGAAAT 1920
Db 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGATGAAAAATAGTACGTTGCGGGAAGAAAT 1920
QY 1921 GCCATGCTAAGACCTGAGACTGACACATGAAACATCGAGCCAGCTAAAAAAGAAAA 1980
Db 1921 GCCATGCTAAGACCTGAGACTGACACATGAAACATCGAGCCAGCTAAAAAAGAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 8
US-09-536-857-374

; Sequence 374, Application us/09536857

GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuhui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kelos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.42712C12
; CURRENT APPLICATION NUMBER: US/09/536, 857
; NUMBER OF SEQ ID NOS: 592
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-536-857-374

Query Match 100.0%; Score 2000; DB 20; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6, 6e-726;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTTGAGTTGATTCATCCGCGCTGCTCTCTGTAAGAACCATTTGGTCTC 60
Db 1 ATGTGTTGAGTTGATTCATCCGCGCTGCTCTCTCTGTAAGAACCATTTGGTCTC 60
QY 61 AGAGCAAGATGGCAAGTGGTGGCTGCTGCTCCCTCTCAGGAGAGCGGCAAG 120
Db 61 AGAGCAAGATGGCAAGTGGTGGCTGCTGCTCCCTCTCAGGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGGAGACGACGACCTCTGTATGAAGACACTAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGGAGACGACGACCTCTGTATGAAGACACTAGAGCAAG 180

Db 121 AGCAAGTGGGCACTTCTGGAGACGACGACCTCTGTATGAAGACACTAGAGCAAG 180
QY 181 ATGGCAAGTGGTGGCGGCACTGCTCCCTGCTGACAGGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGCAAGTGGTGGCGGCACTGCTCCCTGCTGACAGGGGAGTGGCAAGCAAGCTG 240
QY 241 GGGCTTCTGAGAGACACGACGACTCTGCTATGAAGACACTCAGGAACAGATGGGCAAG 300
Db 241 GGGCTTCTGAGAGACACGACGACTCTGCTATGAAGACACTCAGGAACAGATGGGCAAG 300
QY 301 TGGTGTCCCACTGCTTCCCTGCTGACAGGGGAGCGGCAAGAGTGGGCTTGG 360
Db 301 TGGTGTCCCACTGCTTCCCTGCTGACAGGGGAGCGGCAAGAGTGGGCTTGG 360
QY 361 GGAGACTGATGACAGTGGCTTCAATGAGGCGGAGTCCAGTCCGCTGGAGAGATCTG 420
Db 361 GGAGACTGATGACAGTGGCTTCAATGAGGCGGAGTCCAGTCCGCTGGAGAGATCTG 420
QY 421 GACAAAGCTCCACAGAGCTGCTGGTGGGTAAGTCCCAAGAAAGATCTCATGCTATG 480
Db 421 GACAAAGCTCCACAGAGCTGCTGGTGGGTAAGTCCCAAGAAAGATCTCATGCTATG 480
QY 481 CTCAGGCACTGACGTGATACAGAAGGACAGCAAGAAAGAGACTGCTCATCTGGCC 540
Db 481 CTCAGGCACTGACGTGATACAGAAGGACAGCAAGAAAGAGACTGCTCATCTGGCC 540
QY 541 TCTGCAATGGGAATTCAGAGTATGAATACTCGCTGACAGAGTGTCAACTTAAT 600
Db 541 TCTGCAATGGGAATTCAGAGTATGAATACTCGCTGACAGAGTGTCAACTTAAT 600
QY 601 GTCTTGAACAACAAAAGAGGACAGCTGTGATAAAGGCCGTACAAATGCGAAGATGAA 660
Db 601 GTCTTGAACAACAAAAGAGGACAGCTGTGATAAAGGCCGTACAAATGCGAAGATGAA 660
QY 661 TGTGCGTAAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGAGTATGAGAAAT 720
Db 661 TGTGCGTAAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGAGTATGAGAAAT 720
QY 721 ACCACTGCACTACGCTATCTATATGAAGTAAATTAATGGCCAAAGCACTGCTGTA 780
Db 721 ACCACTGCACTACGCTATCTATATGAAGTAAATTAATGGCCAAAGCACTGCTGTA 780
QY 781 TATGCTGTATATGAAATCAAAAACAGATGGCTCACACCACTGTACTGTGCTGA 840
Db 781 TATGCTGTATATGAAATCAAAAACAGATGGCTCACACCACTGTACTGTGCTGA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAATCAAGAAAAAGCAATTAATGAACA 900
Db 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAATCAAGAAAAAGCAATTAATGAACA 900
QY 901 CTGATAGATATGGAAGAGCTGCTCATACTGCTGATGTTGGTGCAGCAAGTATA 960
Db 901 CTGATAGATATGGAAGAGCTGCTCATACTGCTGATGTTGGTGCAGCAAGTATA 960
QY 961 GTCAAGCTTCTACTTGAACAAAATATGATGATCTCTCAAGATCTATCTGACAGAGC 1020
Db 961 GTCAAGCTTCTACTTGAACAAAATATGATGATCTCTCAAGATCTATCTGACAGAGC 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATATGATTAATTTGCCAGTTACTTGACACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATATGATTAATTTGCCAGTTACTTGACACTAC 1080
QY 1081 AAGAAAAACAGATGCTTAAATATCTCTTCTGAAGAACAGCAATCCAGAAACAGACTTAAG 1140
Db 1081 AAGAAAAACAGATGCTTAAATATCTCTTCTGAAGAACAGCAATCCAGAAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGTCAAAAAGTTCAAAAGGCTGAAGAAATATACAGCCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGTCAAAAAGTTCAAAAGGCTGAAGAAATATACAGCCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGCTATAGAGAGTTGAAGAAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGCTATAGAGAGTTGAAGAAAGAAATGAAG 1260

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QY 1261 AAGCATGAAGTAAATATGTGGATTACTAGAAAACCTGACTAATGTGTCTACTGTGC 1320
    |||||
Db 1261 AAGCATGAAGTAAATATGTGGATTACTAGAAAACCTGACTAATGTGTCTACTGTGC 1320
QY 1321 AATGTGTATATGATTAATTCCTCAAGAGAGACAGAACCTGAAAATCAGCAATTT 1380
    |||||
Db 1321 AATGTGTATATGATTAATTCCTCAAGAGAGACAGAACCTGAAAATCAGCAATTT 1380
QY 1381 CCTGACACGAAAGTGAAGAGATACACAGAAATTTGCGAATTTGTTTCTGACTACAAAGAA 1440
    |||||
Db 1381 CCTGACACGAAAGTGAAGAGATACACAGAAATTTGCGAATTTGTTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAATACTCTCTGAAAACAGCAACCCAGACAAGACTTAAGCTGACA 1500
    |||||
Db 1441 AAACAGATGCCAAATACTCTCTGAAAACAGCAACCCAGACAAGACTTAAGCTGACA 1500
QY 1501 TCAGAGGAAGACTCACAAAGCCTTGAGGGCAGTGAATAATGCCAGCCAGAGCTAGAAAAT 1560
    |||||
Db 1501 TCAGAGGAAGACTCACAAAGCCTTGAGGGCAGTGAATAATGCCAGCCAGAGCTAGAAAAT 1560
QY 1561 TTTATGGCTATGAGAAATGAAGAAGCAAGCAAGTACTCATGTGGATTTCCAGAAAAC 1620
    |||||
Db 1561 TTTATGGCTATGAGAAATGAAGAAGCAAGCAAGTACTCATGTGGATTTCCAGAAAAC 1620
QY 1621 CTGACTAATGTGCTCCACTGCTGGCAATGTGATGATTAATTCCTCCAGAAAAGC 1680
    |||||
Db 1621 CTGACTAATGTGCTCCACTGCTGGCAATGTGATGATTAATTCCTCCAGAAAAGC 1680
QY 1681 AGACACCTGAAAGCCAGCAATTTCTTGACACTGGAATGAAGAGTATCACAGTACGAA 1740
    |||||
Db 1681 AGACACCTGAAAGCCAGCAATTTCTTGACACTGGAATGAAGAGTATCACAGTACGAA 1740
QY 1741 CAAATGATACCTCAAGCAATTTGTGAAGAACAGACCTGGAAATATTAACAGTGG 1800
    |||||
Db 1741 CAAATGATACCTCAAGCAATTTGTGAAGAACAGACCTGGAAATATTAACAGTGG 1800
QY 1801 ATTCTGATTCATGAGAAAGAGATAGAAAGTGTGAAAATAATGAATCTGAGCTTTT 1860
    |||||
Db 1801 ATTCTGATTCATGAGAAAGAGATAGAAAGTGTGAAAATAATGAATCTGAGCTTTT 1860
QY 1861 CTTACTTGTAGAAAAGAAAGACATCTTGCATGAAATAGTACGTTGCGGGAAGAAAT 1920
    |||||
Db 1861 CTTACTTGTAGAAAAGAAAGACATCTTGCATGAAATAGTACGTTGCGGGAAGAAAT 1920
QY 1921 GCCATGCTAAAGCTGAGCTAGACACATGAACATCAGAGCAGCTTAAAAA 1980
    |||||
Db 1921 GCCATGCTAAAGCTGAGCTAGACACATGAACATCAGAGCAGCTTAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAA 2000
    |||||
Db 1981 AAAAAAAAAAAAAAAAAA 2000
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RESULT 9
US-09-568-100A-374
Sequence 374, Application US/09568100A
GENERAL INFORMATION:

```
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
```

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APPLICANT: Skelky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.42713c13
CURRENT FILING DATE: 2000-05-09
NUMBER OF SEQ ID NOS: 701
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-568-100A-374

Query Match      100.0%  Score 2000:  DB 22:  Length 2000:
Best Local Similarity 100.0%:  Pred. No. 6.6e-226;
Matches 2000:  Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATGTGTGTTGAGTTGATTCATGCGCGCTGCTCTTCTGTGAAGAGCCATTTGTC 60
    |||||
Db 1 AATGTGTGTTGAGTTGATTCATGCGCGCTGCTCTTCTGTGAAGAGCCATTTGTC 60
QY 61 AGGACCAAGATGGCGAAGTGTGCTGCTTCCCTGCTGCAAGGAGCGCAAG 120
    |||||
Db 61 AGGACCAAGATGGCGAAGTGTGCTGCTTCCCTGCTGCAAGGAGCGCGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGGAACACGACGACTGCTGATGAAGCACTAGAGCAAG 180
    |||||
Db 121 AGCAAGTGGGCACTTCTGGAACACGACGACTGCTGATGAAGCACTAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGCGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGACGTG 240
    |||||
Db 181 ATGGGCAAGTGTGCGCGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGACGTG 240
QY 241 GCGGCTTCTGAGACACGACGACTGCTGATGAAGACACTGAGAACAGATGGGCAAG 300
    |||||
Db 241 GCGGCTTCTGAGACACGACGACTGCTGATGAAGACACTGAGAACAGATGGGCAAG 300
QY 301 TGGTCTGCTGCACTGCTTCCCTGCTGAGGGGAGCGCAAGAGTGGGCGCTTG 360
    |||||
Db 301 TGGTCTGCTGCACTGCTTCCCTGCTGAGGGGAGCGCAAGAGTGGGCGCTTG 360
QY 361 GGAGACTACGATGACAGTCTTCAATGAGCCAGGTACAGCTGCTGGAGAAGTCTG 420
    |||||
Db 361 GGAGACTACGATGACAGTCTTCAATGAGCCAGGTACAGCTGCTGGAGAAGTCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGTTGGGGTAAAGTCCCGAAGAGATCTCATGTCATG 480
    |||||
Db 421 GACAAGCTCCACAGAGCTGCTGTTGGGGTAAAGTCCCGAAGAGATCTCATGTCATG 480
QY 481 CTCAGGGACACGACGCTGAACAAAGAGCAAGCAAGAGAGACCTTACATCTGGCC 540
    |||||
Db 481 CTCAGGGACACGACGCTGAACAAAGAGCAAGCAAGAGAGACCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGGACAGAGATGCAACTTAAT 600
    |||||
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGGACAGAGATGCAACTTAAT 600
QY 601 GTCTTTGACACAAAAGAGACAGCTGTGATTAAGGCGCTGCAATGCCAGAGATGAA 660
    |||||
Db 601 GTCTTTGACACAAAAGAGAGACAGCTGTGATTAAGGCGCTGCAATGCCAGAGATGAA 660
QY 661 TGTGCTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATAGTGAAT 720
    |||||
Db 661 TGTGCTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATAGTGAAT 720
QY 721 ACCACTCTGCACTAGCCTTCTATATGAAGATTAATTAATGGCCAAAGCACTGCTTA 780
    |||||
Db 721 ACCACTCTGCACTAGCCTTCTATATGAAGATTAATTAATGGCCAAAGCACTGCTTA 780
QY 781 TATGCTGTGATGATGAATCAAAAAGCAAGCATGGCTCACACCACTGTTACTGTGTGA 840
    |||||
Db 781 TATGCTGTGATGATGAATCAAAAAGCAAGCATGGCTCACACCACTGTTACTGTGTGA 840
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Oy 541 TCTGCCAATGGGAATTCAGAAAGTACTAAAACCTCTGCTGAGACAGATGTCACCTTAAT 600
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Db 541 TCTGCCAATGGGAATTCAGAAAGTACTAAAACCTCTGCTGAGACAGATGTCACCTTAAT 600
Oy 601 GTCTTGACCAACAAAAAGAGACAGCTCTGATMAAGGCCGTACAAATGCCAGGAAGATGAA 660
    |||||
Db 601 GTCTTGACCAACAAAAAGAGACAGCTCTGATMAAGGCCGTACAAATGCCAGGAAGATGAA 660
Oy 661 TGTGGGTAAATGTCTGAGACATGGCAGCTGATCCAAATATTCCAGATGAGATATGAAAT 720
    |||||
Db 661 TGTGGGTAAATGTCTGAGACATGGCAGCTGATCCAAATATTCCAGATGAGATATGAAAT 720
Oy 721 AACCACTGCACTAGCTATCTATATGAAATTAATTAATGAGCCAAAGCACTGCTTTA 780
    |||||
Db 721 AACCACTGCACTAGCTATCTATATGAAATTAATTAATGAGCCAAAGCACTGCTTTA 780
Oy 781 TATGTTGCTGATATGAAATCAAAAAACAAGCATGGCCTCACACACTGTTACTTGGTGA 840
    |||||
Db 781 TATGTTGCTGATATGAAATCAAAAAACAAGCATGGCCTCACACACTGTTACTTGGTGA 840
Oy 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAACCAATTTAAATGCA 900
    |||||
Db 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAACCAATTTAAATGCA 900
Oy 901 CTGGATAGTATGAAAGAGCTGCTCATCTGCTGATGTTGATGATGATGATGATGATGAT 960
    |||||
Db 901 CTGGATAGTATGAAAGAGCTGCTCATCTGCTGATGTTGATGATGATGATGATGATGAT 960
Oy 961 GTACACCTTCTACTTGAGCAAAATATGATGATGATGATGATGATGATGATGATGATGAT 1020
    |||||
Db 961 GTACACCTTCTACTTGAGCAAAATATGATGATGATGATGATGATGATGATGATGATGAT 1020
Oy 1021 GCCAAGAGTATGCTGTTTCTAAGTATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
    |||||
Db 1021 GCCAAGAGTATGCTGTTTCTAAGTATCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
Oy 1081 AAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGATCCCAAGAACAACTTAAG 1140
    |||||
Db 1081 AAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGATCCCAAGAACAACTTAAG 1140
Oy 1141 CTGACATCAGAGAAAGAGTCAACAAAGTTCAAAAGCAGTGAATAATAGCCAGCAGAGAA 1200
    |||||
Db 1141 CTGACATCAGAGAAAGAGTCAACAAAGTTCAAAAGCAGTGAATAATAGCCAGCAGAGAA 1200
Oy 1201 ATGTCTCAAGAACCAAAATTAATTAAGATGATGATGATGATGATGATGATGATGATG 1260
    |||||
Db 1201 ATGTCTCAAGAACCAAAATTAATTAAGATGATGATGATGATGATGATGATGATGATG 1260
Oy 1261 AAGCATGAAAGTAAATATGTGGGATTTACTAGAAAACTGACTAAATGTTCACTGCTGGC 1320
    |||||
Db 1261 AAGCATGAAAGTAAATATGTGGGATTTACTAGAAAACTGACTAAATGTTCACTGCTGGC 1320
Oy 1321 AATGGTGAATGAATTAATTCCTCAAGAGAGACAGAAACCTGAAATACAGCAATTT 1380
    |||||
Db 1321 AATGGTGAATGAATTAATTCCTCAAGAGAGAGACAGAAACCTGAAATACAGCAATTT 1380
Oy 1381 CCTGCAACGAAAGTGAAGAGATATCAGAAATTTGGAATTTGTTCTGACTACAAAGAA 1440
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Db 1381 CCTGCAACGAAAGTGAAGAGATATCAGAAATTTGGAATTTGTTCTGACTACAAAGAA 1440
Oy 1441 AAAGAGATGCCAAATTAATCTCTGAAAAACAGCAACCCAGAAACAAAGACTTAAGCTGAA 1500
    |||||
Db 1441 AAAGAGATGCCAAATTAATCTCTGAAAAACAGCAACCCAGAAACAAAGACTTAAGCTGAA 1500
Oy 1501 TCAGAGAGAAAGTCAACAAAGCCTTGAGGCACTGAAATAGCCAGCAGAGAGCTAGAAAT 1560
    |||||
Db 1501 TCAGAGAGAAAGTCAACAAAGCCTTGAGGCACTGAAATAGCCAGCAGAGAGCTAGAAAT 1560
Oy 1561 TTTATGGCTATGAAAGAAATGAAGAAGCAGCAAGTACTCATGTGGATTTCCAGAGAAAT 1620
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Db 1561 TTTATGGCTATGAAAGAAATGAAGAAGCAGCAAGTACTCATGTGGATTTCCAGAGAAAT 1620

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Oy 1621 CTGACTAAATGATGTCACAGCTGTCGCAATGATGATGATGATTAATTCCTCCAAAGAGAGC 1680
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Db 1621 CTGACTAAATGATGTCACAGCTGTCGCAATGATGATGATGATTAATTCCTCCAAAGAGAGC 1680
Oy 1681 AGAACACCTGAAAGCCAGCAATTTCTTGACACTGAGATGAAGATACACAGTACAGAA 1740
    |||||
Db 1681 AGAACACCTGAAAGCCAGCAATTTCTTGACACTGAGATGAAGATACACAGTACAGAA 1740
Oy 1741 CAAATGATACACAGCAATTTGATGAAGAACAGAACACTGGAATATTAACAGATGAG 1800
    |||||
Db 1741 CAAATGATACACAGCAATTTGATGAAGAACAGAACACTGGAATATTAACAGATGAG 1800
Oy 1801 ATTCTGATTCATGAAGAAAGCAGATAGAAAGTGTGAAAAATGAATTCAGCTTTCT 1860
    |||||
Db 1801 ATTCTGATTCATGAAGAAAGCAGATAGAAAGTGTGAAAAATGAATTCAGCTTTCT 1860
Oy 1861 CTTAAGTGTGAAGAAAGAAAGACATCTTGATGAAATATGATGATGATGATGATGATGAT 1920
    |||||
Db 1861 CTTAAGTGTGAAGAAAGAAAGACATCTTGATGAAATATGATGATGATGATGATGATGAT 1920
Oy 1921 GCCATGCTTAAGCTGAGCTAGACACATGAACATCAGAGCCAGCTAAAAAAGAGAG 1980
    |||||
Db 1921 GCCATGCTTAAGCTGAGCTAGACACATGAACATCAGAGCCAGCTAAAAAAGAGAG 1980
Oy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
    |||||
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

```

```

RESULT 11
US-09-590-583-302
; Sequence 302: Application US/09590583
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, David C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C9
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-590-583-302

Query Match      100.0%; Score 2000; DB 22; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6,6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```


QY	241	GGCGCTTCTGGAGACCCACGACGACTGCTGTATGAGACACTCAGAGACAGATGGGCGAAG	300
Dd	241	GGCGCTTCTGGAGACCCACGACGACTGCTGTATGAGACACTCAGAGACAGATGGGCGAAG	300
QY	301	TGGTGTGCGCCACTCTTCCCTCTGTGAGGGGAGGGGCAAGGCAAGGTGGGGCTTGG	360
Dd	301	TGGTGTGCGCCACTCTTCCCTCTGTGAGGGGAGGGGCAAGGCAAGGTGGGGCTTGG	360
QY	361	GGAGACTACGATGACAGTGCCTTTCATGAGGCCAGGTACACGTCCTGTGAGAGAAATCTG	420
Dd	361	GGAGACTACGATGACAGTGCCTTTCATGAGGCCAGGTACACGTCCTGTGAGAGAAATCTG	420
QY	421	GACAAAGCTCCACAGAGTGGCTGGTGGGGTAAAGTCCCCAGAAAGATCTCATGCTCATG	480
Dd	421	GACAAAGCTCCACAGAGTGGCTGGTGGGGTAAAGTCCCCAGAAAGATCTCATGCTCATG	480
QY	481	CTCAGGGACACTGACGTGAACAGAAAGAGCAACCAAAAGAGACTGCTACATGTGGCC	540
Dd	481	CTCAGGGAGCACTGACGTGAACAGAAAGAGCAACCAAAAGAGACTGCTACATGTGGCC	540
QY	541	TCTGCCAATGGGAATTCAGAAATGTAATACTCTGCTGGACAGACGATGTCACTTAAT	600
Dd	541	TCTGCCAATGGGAATTCAGAAATGTAATACTCTGCTGGACAGACGATGTCACTTAAT	600
QY	601	GTCCTTGACAACAAAAAGAGAGACGCTGTATAAAGCCGTCAATGCCAGGAATATAA	660
Dd	601	GTCCTTGACAACAAAAAGAGAGACGCTGTATAAAGCCGTCAATGCCAGGAATATAA	660
QY	661	TGTGCGTTAATGTTGCTGGGAACATGGCACTGATCCAAATATTCAGATAGTATGGAAT	720
Dd	661	TGTGCGTTAATGTTGCTGGGAACATGGCACTGATCCAAATATTCAGATAGTATGGAAT	720
QY	721	ACCACTGCACTGACGTACTCTATCTAATGAAGATAATTAATGGCCAAAGCACTGCTCTTA	780
Dd	721	ACCACTGCACTGACGTACTCTATCTAATGAAGATAATTAATGGCCAAAGCACTGCTCTTA	780
QY	781	TATGGTGTGATATCGAATCAAAAAACAAGCATAGGCTCACACACTGTTACTTGCTGTA	840
Dd	781	TATGGTGTGATATCGAATCAAAAAACAAGCATAGGCTCACACACTGTTACTTGCTGTA	840
QY	841	CATGACAAAAACAGCAAGTCGTGAATTTTATATCAAGAAAAAAGCGAATTTAAATGCA	900
Dd	841	CATGACAAAAACAGCAAGTCGTGAATTTTATATCAAGAAAAAAGCGAATTTAAATGCA	900
QY	901	CTGGATGATATGGAAGGACTGCTCTCATCTGCTGATGTTGTGGATCAGCAAGTATA	960
Dd	901	CTGGATGATATGGAAGGACTGCTCTCATCTGCTGATGTTGTGGATCAGCAAGTATA	960
QY	961	GTCAGCCTTACTCTTGAGCAAAATATTTGATGTCTTCTCAAGATCTATCTGGACAGAG	1020
Dd	961	GTCAGCCTTACTCTTGAGCAAAATATTTGATGTCTTCTCAAGATCTATCTGGACAGAG	1020
QY	1021	GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTCGACTAC	1080
Dd	1021	GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTCGACTAC	1080
QY	1081	AAAGAAAAACGATGCTAAAAAATCTCTTGAAACAGCAATCCAGAAACAGACTTAAG	1140
Dd	1081	AAAGAAAAACGATGCTAAAAAATCTCTTGAAACAGCAATCCAGAAACAGACTTAAG	1140
QY	1141	CTGACATCAGAGAAAGATCACAAGGTTCCAAAGGCAAGCAATAAGCCAGGCAGAGAAA	1200
Dd	1141	CTGACATCAGAGAAAGATCACAAGGTTCCAAAGGCAAGCAATAAGCCAGGCAGAGAAA	1200
QY	1201	ATGTCTCAAGAACCAAGAAATTAATTAAGGATGCTGATAGAGAGGTTGAAGACAATTAAG	1260
Dd	1201	ATGTCTCAAGAACCAAGAAATTAATTAAGGATGCTGATAGAGAGGTTGAAGACAATTAAG	1260
QY	1261	AAGCATGAAGATTAATATGTTGGATTAATAGAAAAACCTGACATAATAGTGTACCTGCTGGC	1320
Dd	1261	AAGCATGAAGATTAATATGTTGGATTAATAGAAAAACCTGACATAATAGTGTACCTGCTGGC	1320

OY	1331	AAAGTGATTAATGATTAATTCCTCCAAAGGAAGACAGAAACCCGAAAATCAGCAATTT	1380
OY	1331	AAAGTGATTAATGATTAATTCCTCCAAAGGAAGACAGAAACCCGAAAATCAGCAATTT	1380
Db	1321	AATGGTGATTAATGATTAATTCCTCCAAAGGAAGACAGAAACCCGAAAATCAGCAATTT	1380
OY	1381	CCTGACAAACGAAGATGAAAGATATCACAGAAATTTGGCAATTAAGTTCTGACTACAAAGA	1440
Db	1381	CCTGACAAACGAAGATGAAAGATATCACAGAAATTTGGCAATTAAGTTCTGACTACAAAGA	1440
OY	1441	AAACGATGCCAAATATCTCTTGAAAACAGCAACCCAGAACACAGACTTAAAGCTGACA	1500
OY	1441	AAACGATGCCAAATATCTCTTGAAAACAGCAACCCAGAACACAGACTTAAAGCTGACA	1500
Db	1501	TCGAGGGAAGGTCCAAAGGCTTGAGGGGAGTGGAAAATGGCCAGCCAGAGCTGAAAAT	1560
OY	1561	TTTATGGCTATCGAAGAAATGAAGAAGACAGCAAGTACTCATGTGCGATTTCCAGAAAAC	1620
Db	1561	TTTATGGCTATCGAAGAAATGAAGAAGACAGCAAGTACTCATGTGCGATTTCCAGAAAAC	1620
OY	1621	CTGACTAATGGTGCCACTGCTGGCAATGCTGATGATGATTAATTCCTCCAGGAAGAGC	1680
OY	1681	AGAACACCTGGAACCCAGCAATTTCCCTGCACCTGAGAAATGAAGAGATACAGTGGACAA	1740
Db	1681	AGAACACCTGGAACCCAGCAATTTCCCTGCACCTGAGAAATGAAGAGATACAGTGGACAA	1740
OY	1741	CAAAATGATCTCGAAGCAATTTTGTGAAAGAACAGACACTGGAATATTAACAGCATAG	1800
Db	1741	CAAAATGATCTCGAAGCAATTTTGTGAAAGAACAGACACTGGAATATTAACAGCATAG	1800
OY	1801	ATTCGTATTCATGAGAAAACAGATAGAAAGTGGTGA AAAAATGAATTCGACCTTCT	1860
Db	1801	ATTCGTATTCATGAGAAAACAGATAGAAAGTGGTGA AAAAATGAATTCGACCTTCT	1860
OY	1861	CTTAGTGTAGAAAGAAAAGCAATCTTGCAATGAAATAGTACGTCGGGGAAGAATTT	1920
Db	1861	CTTAGTGTAGAAAGAAAAGCAATCTTGCAATGAAATAGTACGTCGGGGAAGAATTT	1920
OY	1921	GCCATGCTAAGACGTGAGCTAGACACATGTAACATCAGAGCCAGCTAAAAA	1980
Db	1921	GCCATGCTAAGACGTGAGCTAGACACATGTAACATCAGAGCCAGCTAAAAA	1980
OY	1981	AAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAA 2000	
RESULT 12			
US-09-593-793A-374			
: Sequence 374, Application US/09593793A			
: GENERAL INFORMATION:			
: APPLICANT: Xu, Jiangchun			
: APPLICANT: Dillon, Davin C.			
: APPLICANT: Mitcham, Jennifer L.			
: APPLICANT: Harlocker, Susan L.			
: APPLICANT: Jiang, Yuyu			
: APPLICANT: Reed, Steven D.			
: APPLICANT: Kelos, Michael D.			
: APPLICANT: Fanger, Gary R.			
: APPLICANT: Retler, Marc W.			
: APPLICANT: Stolk, John A.			
: APPLICANT: Day, Craig H.			
: APPLICANT: Vedvick, Thomas S.			
: APPLICANT: Carter, Darrick			
: APPLICANT: Li, Samuel			
: APPLICANT: Wang, Aijun			
: APPLICANT: Skeiky, Yasir A.W.			
: APPLICANT: Helper, William			
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND			
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER			
: FILE REFERENCE: 210121.42715015			

/ CURRENT APPLICATION NUMBER: US/09/593,793A
/ CURRENT FILING DATE: 2000-06-13
/ NUMBER OF SEQ ID NOS: 814
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 374
/ LENGTH: 2000
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-593-793A-374

Query Match 100.0%; Score 2000; DB 22; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6,6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGGTGTGAGGTGATTCATGCCGGCTCTTGTGTAAGAAAGCATTTGGTCTC 60
DB 1 ATGGTGTGAGGTGATTCATGCCGGCTCTTGTGTAAGAAAGCATTTGGTCTC 60
OY 61 AGGAGCAGATGGGCAAGTGTGCTCCGTTGCTTCCCTGCTGCAGGGAGACGGCAAG 120
DB 61 AGGAGCAGATGGGCAAGTGTGCTCCGTTGCTTCCCTGCTGCAGGGAGACGGCAAG 120
OY 121 AGCAAGCTGGGCACTTCTGAGACACGACGACTGTCTATGAAGACTCAGAGCAAG 180
DB 121 AGCAAGCTGGGCACTTCTGAGACACGACGACTGTCTATGAAGACTCAGAGCAAG 180
OY 181 ATGGGCAAGTGGTGGCCGCTCTTCCCTGCTGCAGGGGAGTGGCAAGCAACGTG 240
DB 181 ATGGGCAAGTGGTGGCCGCTCTTCCCTGCTGCAGGGGAGTGGCAAGCAACGTG 240
OY 241 GGGCTTCTGAGACACGACGACTGTCTATGAAGACTCAGAGCAAGTGGGCAAG 300
DB 241 GGGCTTCTGAGACACGACGACTGTCTATGAAGACTCAGAGCAAGTGGGCAAG 300
OY 301 TGGTGTGGCACTGCTTCCCTGCTCAGGGGAGCGGCAAGCAAGTGGGCTTGG 360
DB 301 TGGTGTGGCACTGCTTCCCTGCTCAGGGGAGCGGCAAGCAAGTGGGCTTGG 360
OY 361 GGAGACTAGATGACAGTCCCTTCATGAGACCAGGTACACAGTCCCTGAGAGAACTG 420
DB 361 GGAGACTAGATGACAGTCCCTTCATGAGACCAGGTACACAGTCCCTGAGAGAACTG 420
OY 421 GACAAAGCTCCACAGAGCTCTGTGGGTAAAGTCCCGAAGAAAGATCTCATGTCATG 480
DB 421 GACAAAGCTCCACAGAGCTCTGTGGGTAAAGTCCCGAAGAAAGATCTCATGTCATG 480
OY 481 CTCAGGAGACCTGACCTGAAACAAGAGACAAAGAAAGAGCTCTCTACATCTGGCC 540
DB 481 CTCAGGAGACCTGACCTGAAACAAGAGAGACAAAGAAAGAGCTCTCTACATCTGGCC 540
OY 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTCTGTGACAGAGATGTCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTCTGTGACAGAGATGTCAACTTAAT 600
OY 601 GTCTCTTGACACAAAAGAGACAGCTGTGATTAAGGCGGTACAAATGCCAGAAATGAA 660
DB 601 GTCTCTTGACACAAAAGAGAGACAGCTGTGATTAAGGCGGTACAAATGCCAGAAATGAA 660
OY 661 TGTGGCTTATGTGTGTGAAACATGGCAGTCCAAATATTCACAATGATGTGAAT 720
DB 661 TGTGGCTTATGTGTGTGAAACATGGCAGTCCAAATATTCACAATGATGTGAAT 720
OY 721 ACCACTCTGACCTAGCTATCTATATGAAGATTAATTAATGAGCAAGACTGCTTA 780
DB 721 ACCACTCTGACCTAGCTATCTATATGAAGATTAATTAATGAGCAAGACTGCTTA 780
OY 781 TATGTGCTGATATGCAATCAAAAAAAGCATGGCTCACACACTGTTACTTGGTGA 840
DB 781 TATGTGCTGATATGCAATCAAAAAAAGCATGGCTCACACACTGTTACTTGGTGA 840
OY 841 CATGAGCAAAAAAGCAAGTCTGTAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
DB 841 CATGAGCAAAAAAGCAAGTCTGTAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900

OY 901 CTGATAGATATGAAGAGACTGCTCATACTTGTGTAAGTGTGATCAGCAACTATA 960
DB 901 CTGATAGATATGAAGAGAGCTGCTCATACTTGTGTAAGTGTGATCAGCAACTATA 960
OY 961 GTCAGCCTTCTACTTGAGCAAAATATGATGTATCTTCAAGATCATCTGACAGAG 1020
DB 961 GTCAGCCTTCTACTTGAGCAAAATATGATGTATCTTCAAGATCATCTGACAGAG 1020
OY 1021 GCCAGAGATATGCTTTTCTAGTCAATCATATGTAATTTGCCAGTTACTTTTGACTAC 1080
DB 1021 GCCAGAGATATGCTTTTCTAGTCAATCATATGTAATTTGCCAGTTACTTTTGACTAC 1080
OY 1081 AAGAAAGAAACAGATGCTAAAAATCTCTTGAAAGAACAGCAATCCAGAACACTTAAG 1140
DB 1081 AAGAAAGAAACAGATGCTAAAAATCTCTTGAAAGAACAGCAATCCAGAACACTTAAG 1140
OY 1141 CTGACATCAGAGAGAGTACAAAGGTTCAAGGCAAGTGAATAAGCCAGCCAGAGAA 1200
DB 1141 CTGACATCAGAGAGAGTACAAAGGTTCAAGGCAAGTGAATAAGCCAGCCAGAGAA 1200
OY 1201 ATGTCTCAAGAACCAAAATTAATTAAGATGGTATGAGAGGTTAAGAAAGATGAAG 1260
DB 1201 ATGTCTCAAGAACCAAAATTAATTAAGATGGTATGAGAGGTTAAGAAAGATGAAG 1260
OY 1261 AAGCATGAAGATATATGTTGGGATTAAGTAAGAAACCTGACTAATGCTGCACTGGG 1320
DB 1261 AAGCATGAAGATATATGTTGGGATTAAGTAAGAAACCTGACTAATGCTGCACTGGG 1320
OY 1321 AATGATGAATATGATTAATTCCTCAAGAGAGAGCAACACCTGAAAAATCGCAATTT 1380
DB 1321 AATGATGAATATGATTAATTCCTCAAGAGAGAGCAACACCTGAAAAATCGCAATTT 1380
OY 1381 CCTGACAAAGAAAGTGAAGATTCACAGAAATTTGGCAATTAATTTCTGACTCAAAAGA 1440
DB 1381 CCTGACAAAGAAAGTGAAGATTCACAGAAATTTGGCAATTAATTTCTGACTCAAAAGA 1440
OY 1441 AAACAGATGCCAAATATCTTCTGAAAGACAGCAACCCAGAAACAACTTAAGTGTACA 1500
DB 1441 AAACAGATGCCAAATATCTTCTGAAAGACAGCAACCCAGAAACAACTTAAGTGTACA 1500
OY 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGGCAGTGAAGAAATGCGCAGAGCTAAGAAAT 1560
DB 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGGCAGTGAAGAAATGCGCAGAGCTAAGAAAT 1560
OY 1561 TTTATGCTATGCAAAATTAAGAAAGCAAGGATCTCATGTCGGATTTCCAGAAAC 1620
DB 1561 TTTATGCTATGCAAAATTAAGAAAGCAAGGATCTCATGTCGGATTTCCAGAAAC 1620
OY 1621 CTGACTAATGGTCCCACTGCTGCAATGGTATGATGATTAATTTCTCCCAAGAGAGC 1680
DB 1621 CTGACTAATGGTCCCACTGCTGCAATGGTATGATGATTAATTTCTCCCAAGAGAGC 1680
OY 1681 AGAACACTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAGATATACACAGTGAAG 1740
DB 1681 AGAACACTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAGATATACACAGTGAAG 1740
OY 1741 CAAATGATATCTGAAAGCAATTTTGTGAAGAACAAACACTGGAATATTTACCGATGAG 1800
DB 1741 CAAATGATATCTGAAAGCAATTTTGTGAAGAACAAACACTGGAATATTTACCGATGAG 1800
OY 1801 ATTCTGATTCATGAAAGAAAGCAGATAGAAAGTGTGAAGAAATTAATCTGAGCTTTC 1860
DB 1801 ATTCTGATTCATGAAAGAAAGCAGATAGAAAGTGTGAAGAAATTAATCTGAGCTTTC 1860
OY 1861 CTTAGTTGTGAAGAAAGAAAGACATCTTGCAATGAATAATGATGTTGGGGGAAGAAAT 1920
DB 1861 CTTAGTTGTGAAGAAAGAAAGACATCTTGCAATGAATAATGATGTTGGGGGAAGAAAT 1920
OY 1921 GCCATGCTAAGATGAGAGTACAAATGAAGCAATCAGACCAAGTAAAGAAAAA 1980
DB 1921 GCCATGCTAAGATGAGAGTACAAATGAAGCAATCAGACCAAGTAAAGAAAAA 1980

QY 1981 AAAAAAAAAAAAAAAAAA 2000
 Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 13

US-09-605-783A-374
 ; Sequence 374, Application US/09605783A
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yuqi
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darick
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skelky, Yasir A.W.
 ; APPLICANT: Hepler, William
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.427C16
 ; CURRENT APPLICATION NUMBER: US/09/605,783A
 ; NUMBER OF FILING DATE: 2000-06-27
 ; NUMBER OF SEQ ID NOS: 835
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 374
 ; LENGTH: 2000
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; US-09-605-783A-374

Query Match 100.0%; Score 2000; DB 23; Length 2000;
 Best Local Similarity 100.0%; Pred. No. 6.6e-226;
 Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTGAAGTGAATCCATGCGCGCTCCCTCTTCTGTGAAGAACCATTTGCTC 60
 Db 1 ATGGTGGTGAAGTGAATCCATGCGCGCTCCCTCTTCTGTGAAGAACCATTTGCTC 60
 QY 61 AGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTTCCCTGCTCAGGAGAGCGGCAAG 120
 Db 61 AGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTTCCCTGCTCAGGAGAGCGGCAAG 120
 QY 121 AGCAAGCGGCGACCTTCTGGAGACACAGACGACTCTGCTATGAAGACACTAGGAGCAAG 180
 Db 121 AGCAAGCGGCGACCTTCTGGAGACACAGACGACTCTGCTATGAAGACACTAGGAGCAAG 180
 QY 181 ATGGGCAAGTGTGCTGCCGCTGCTCCCTGCTGTGACAGGGGAGTGGCAAGACGCTG 240
 Db 181 ATGGGCAAGTGTGCTGCCGCTGCTCCCTGCTGTGACAGGGGAGTGGCAAGACGCTG 240
 QY 241 GGGCCTTCTGGAGACACAGACGACTCTGCTATGAAGACACTAGGAGCAAGTGGCAAG 300
 Db 241 GGGCCTTCTGGAGACACAGACGACTCTGCTATGAAGACACTAGGAGCAAGTGGCAAG 300
 QY 301 TGGTGGTGGCAAGTGTGCTGCCGCTGCTGACAGGGGAGCGGCAAGAGTGGGCGCTGG 360
 Db 301 TGGTGGTGGCAAGTGTGCTGCCGCTGCTGACAGGGGAGCGGCAAGAGTGGGCGCTGG 360
 QY 361 GGAGACTACGATGACAGTGCCTTCTGATGAGAGCCAGTACCAAGTCCGCTGAGAGATCTG 420
 Db 361 GGAGACTACGATGACAGTGCCTTCTGATGAGAGCCAGTACCAAGTCCGCTGAGAGATCTG 420
 QY 421 GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
 Db 421 GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480

Db 421 GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCAAGAAAGATCTCATGCTCATG 480
 QY 481 CTCAGGACACTGACGTGACAGAGACAGCAAGCAAGAGAGAGTGTCTACATCTGCCC 540
 Db 481 CTCAGGACACTGACGTGACAGAGACAGCAAGCAAGAGAGAGTGTCTACATCTGCCC 540
 QY 541 TCTGCCAATGGGAATTCGAAGTGAATAACTCCTGCTGACAGACGATGTCACCTTAAT 600
 Db 541 TCTGCCAATGGGAATTCGAAGTGAATAACTCCTGCTGACAGACGATGTCACCTTAAT 600
 QY 601 GTCCCTGACACAAAGAGAGACAGCTGTGATTAAGGCCGTACAAATGCCAGAGATGAA 660
 Db 601 GTCCCTGACACAAAGAGAGACAGCTGTGATTAAGGCCGTACAAATGCCAGAGATGAA 660
 QY 661 TGTCCGTTAATGTTGCTGGAACATGCGACTATCCAAATATTCAGATGATGAAAT 720
 Db 661 TGTCCGTTAATGTTGCTGGAACATGCGACTATCCAAATATTCAGATGATGAAAT 720
 QY 721 ACCACTGACACTACGCTATCTATTAATGAAGATTAATTAATGSCCAAGCACTGCTTA 780
 Db 721 ACCACTGACACTACGCTATCTATTAATGAAGATTAATTAATGSCCAAGCACTGCTTA 780
 QY 781 TATGCTGCTGATATGCAATCAAAAAACAGATGCGCTCACACCACTTACTGTGCTA 840
 Db 781 TATGCTGCTGATATGCAATCAAAAAACAGATGCGCTCACACCACTTACTGTGCTA 840
 QY 841 CATGAGCAAAACAGCAAGTGTGAATTTTAATCAAGAAAGCAATTAATTAATGCA 900
 Db 841 CATGAGCAAAACAGCAAGTGTGAATTTTAATCAAGAAAGCAATTAATTAATGCA 900
 QY 901 CTGATAGATATGAAGAGAGCTGCTCATCTGCTGTATGTTGATGATGCAAGATTA 960
 Db 901 CTGATAGATATGAAGAGAGCTGCTCATCTGCTGTATGTTGATGATGCAAGATTA 960
 QY 961 GTCAAGCTTCTACTTGAACAAATATGATGATCTCTCAAGATCTATCTGACAGACG 1020
 Db 961 GTCAAGCTTCTACTTGAACAAATATGATGATCTCTCAAGATCTATCTGACAGACG 1020
 QY 1021 GCCAGAGATATGCTGTTTCTAGTCAATCATGATTAATTTCCAGATCTTCTGACTAC 1080
 Db 1021 GCCAGAGATATGCTGTTTCTAGTCAATCATGATTAATTTCCAGATCTTCTGACTAC 1080
 QY 1081 AAAGAAAAACAGATGCTAAAAATCTTTCTGAAAAACAGCAATCCAGAACAACTTAAAG 1140
 Db 1081 AAAGAAAAACAGATGCTAAAAATCTTTCTGAAAAACAGCAATCCAGAACAACTTAAAG 1140
 QY 1141 CTGACATGAGAGAGAGTCAAAAGTTCAAAGGCAAGTGAATTAATGACCCAGAGAAA 1200
 Db 1141 CTGACATGAGAGAGAGTCAAAAGTTCAAAGGCAAGTGAATTAATGACCCAGAGAAA 1200
 QY 1201 ATGCTCTAAGAACAGAAATTAATGAAGATGATAGAGAGAGTGAAGAAATGAAG 1260
 Db 1201 ATGCTCTAAGAACAGAAATTAATGAAGATGATAGAGAGAGTGAAGAAATGAAG 1260
 QY 1261 AAGCATGAAATTAATGATGAGATTAATGAAAACTGACTAATGCTGCTGAGC 1320
 Db 1261 AAGCATGAAATTAATGATGAGATTAATGAAAACTGACTAATGCTGCTGAGC 1320
 QY 1321 AATGCTGATTAATGATTAATCTCTCAAGAGAGAGCAAGAACCTGAAATACAGCAATTT 1380
 Db 1321 AATGCTGATTAATGATTAATCTCTCAAGAGAGAGCAAGAACCTGAAATACAGCAATTT 1380
 QY 1381 CCTGACAAAGAAATGAAGATTAATGAAATTTGCGAATTTGCTGACTACAAAGAA 1440
 Db 1381 CCTGACAAAGAAATGAAGATTAATGAAATTTGCGAATTTGCTGACTACAAAGAA 1440
 QY 1441 AAACAGATGCCAAATACTCTTCTGAAAAACAGAACCCAGAACCAAGCTTAAGCTGACA 1500
 Db 1441 AAACAGATGCCAAATACTCTTCTGAAAAACAGAACCCAGAACCAAGCTTAAGCTGACA 1500
 QY 1501 TCAGAGAGAGAGTACAAAGGCTTGAAGGCAAGTGAATAATGCGCAGAGAGCTGAAGAAAT 1560
 Db 1501 TCAGAGAGAGAGTACAAAGGCTTGAAGGCAAGTGAATAATGCGCAGAGAGCTGAAGAAAT 1560

QY 1561 TTTATGGCTATCGAAGAAATGAAGAAGACGAGTACTCATGTGGATTCCAGAAAC 1620
|||||
Db 1561 TTTATGGCTATCGAAGAAATGAAGAAGACGAGTACTCATGTGGATTCCAGAAAC 1620
QY 1621 CTGACTAATAGTGGCCACTGCTGGCAATGATGATGATTAATTCCTCCAAAGAAAGC 1680
|||||
Db 1621 CTGACTAATAGTGGCCACTGCTGGCAATGATGATGATTAATTCCTCCAAAGAAAGC 1680
QY 1681 AGAACAACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAGAATATACAGTACGAA 1740
|||||
Db 1681 AGAACAACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAGAATATACAGTACGAA 1740
QY 1741 CAAATGATACCTAGAGCAATTTGTGAAGAAAGCAAGCAATATTTACACGTGAG 1800
|||||
Db 1741 CAAATGATACCTAGAGCAATTTGTGAAGAAAGCAAGCAATATTTACACGTGAG 1800
QY 1801 AATCTGATTCATGAAGAAAGCAGATAGAAGTGGTTGAAGAAATGAATTCGAGCTTCT 1860
|||||
Db 1801 AATCTGATTCATGAAGAAAGCAGATAGAAGTGGTTGAAGAAATGAATTCGAGCTTCT 1860
QY 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGCAATGAATAATGACGTTGGGGAAGAAAT 1920
|||||
Db 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGCAATGAATAATGACGTTGGGGAAGAAAT 1920
QY 1921 GCCATGCTAGAGCTGAGCTAGACACATGAACATCAGAGCGCTAAAGAAAAA 1980
|||||
Db 1921 GCCATGCTAGAGCTGAGCTAGACACATGAACATCAGAGCGCTAAAGAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAA 2000
|||||
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 14
US-09-636-215-374
; Sequence 374, Application US/09636215
; GENERAL INFORMATION:

; APPLICANT: Xu, Jlangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jlang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-636-215-374

Query Match 100.0%; Score 2000; DB 24; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6,6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGTGTGAGGTGATTCATGCCGCTGCTTCTGTGAAGAAAGCAATTTGGTCTC 60

Db 1 ATGGTGTGAGGTGATTCATGCCGCTGCTTCTGTGTGAAGAAAGCAATTTGGTCTC 60
|||||
QY 61 AGAGCAAGATGGGCAAGTGTGTGCTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
|||||
Db 61 AGAGCAAGATGGGCAAGTGTGTGCTGCTTCCCTGCTGCAAGGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGACCAAGCAAGCAAGTGTGTGAAGCACTGAGAGCAAG 180
|||||
Db 121 AGCAACGTGGGCACTTCTGAGACCAAGCAAGCAAGTGTGTGAAGCACTGAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGTGCAAGCAAG 240
|||||
Db 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGTGCAAGCAAG 240
QY 241 GGGGCTTGTGAGACCAAGCAAGCAAGTGTGTGAAGCACTGAGAGCAAGTGTGCAAG 300
|||||
Db 241 GGGGCTTGTGAGACCAAGCAAGCAAGTGTGTGAAGCACTGAGAGCAAGTGTGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGGAGGAGCAAGCAAGTGTGCAAG 360
|||||
Db 301 TGGTGTGCACTGCTTCCCTGCTGCAAGGAGGAGGAGCAAGCAAGTGTGCAAG 360
QY 361 GGAGACTAGATGACAGTGTGCTTCCCTGCTGCAAGGAGGAGGAGTGTGCAAG 420
|||||
Db 361 GGAGACTAGATGACAGTGTGCTTCCCTGCTGCAAGGAGGAGGAGTGTGCAAG 420
QY 421 GACAGCTTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
|||||
Db 421 GACAGCTTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 CTCAGGACACTGAGCTGTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
|||||
Db 481 CTCAGGACACTGAGCTGTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
QY 541 TCTGCCAATGGGAATTCAGAAATGTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 600
|||||
Db 541 TCTGCCAATGGGAATTCAGAAATGTAAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 GTCTTGTGACACAAAAGAGGAGACGCTGTGATTAAGCCGCTGACATGCCAGAAATG 660
|||||
Db 601 GTCTTGTGACACAAAAGAGGAGACGCTGTGATTAAGCCGCTGACATGCCAGAAATG 660
QY 661 TGTGCTTAATGTGTGTAAGCAATGACATGCAATATTCAGATGATGATGATG 720
|||||
Db 661 TGTGCTTAATGTGTGTAAGCAATGACATGCAATATTCAGATGATGATGATGATG 720
QY 721 ACCACTGCTACAGCTATCTATATGAAGATTAATGAAGCAAGCAAGCAAGCAAG 780
|||||
Db 721 ACCACTGCTACAGCTATCTATATGAAGATTAATGAAGCAAGCAAGCAAGCAAG 780
QY 781 TATGTGTGATATGCAATCAAAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 840
|||||
Db 781 TATGTGTGATATGCAATCAAAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 840
QY 841 CATGAGCAAAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 900
|||||
Db 841 CATGAGCAAAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 900
QY 901 CTGAGATAGTATGAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 960
|||||
Db 901 CTGAGATAGTATGAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 960
QY 961 GTGAGCTTCTACTGAGCAAAAATGATGATGATGATGATGATGATGATGATGAT 1020
|||||
Db 961 GTGAGCTTCTACTGAGCAAAAATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1021 GCCAGAGTATGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATG 1080
|||||
Db 1021 GCCAGAGTATGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATG 1080
QY 1081 AAGGAAAGCAAGTGTGAAGTCTGCTGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1140
|||||

Db 1081 AAAGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
 QY 1141 CTGACATCAGAGAGAGATGTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCCAGAGAAA 1200
 Db 1141 CTGACATCAGAGAGAGATGTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCCAGAGAAA 1200
 QY 1201 ATGTCTCAAGAACCCAGAAATTAATTAAGATGCTGATAGAGAGGTTGAAGAAATGAG 1260
 Db 1201 ATGTCTCAAGAACCCAGAAATTAATTAAGATGCTGATAGAGAGGTTGAAGAAATGAG 1260
 QY 1261 AAGCATTAAGTATTAATGTGGGATTAAGTAAAGAACCTGACTAATGCTGCTGCTGCTG 1320
 Db 1261 AAGCATTAAGTATTAATGTGGGATTAAGTAAAGAACCTGACTAATGCTGCTGCTGCTG 1320
 QY 1321 AATGATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1380
 Db 1321 AATGATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1380
 QY 1381 CTTGACACAGCAAGAGTGAAGATATCACAGAAATTTGCAATTTAGTTTCTGACTACAAAGAA 1440
 Db 1381 CTTGACACAGCAAGAGTGAAGATATCACAGAAATTTGCAATTTAGTTTCTGACTACAAAGAA 1440
 QY 1441 AAACAGATGCCAAATATCTCTTCTGAAACAGCAACCCAGACAAAGACTTAAGACTGACA 1500
 Db 1441 AAACAGATGCCAAATATCTCTTCTGAAACAGCAACCCAGACAAAGACTTAAGACTGACA 1500
 QY 1501 TCAGAGAGAGAGTGCACAAAGGCTTGAGGCGAGTGAATAATGGCCAGCAGAGCTGAAAT 1560
 Db 1501 TCAGAGAGAGAGTGCACAAAGGCTTGAGGCGAGTGAATAATGGCCAGCAGAGCTGAAAT 1560
 QY 1561 TTTATGGCTATCGAAGAAATGAAGACACGGAAGTACTCATGCTGCTGCTGCTGCTGCTG 1620
 Db 1561 TTTATGGCTATCGAAGAAATGAAGACACGGAAGTACTCATGCTGCTGCTGCTGCTGCTG 1620
 QY 1621 CTGACTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
 Db 1621 CTGACTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
 QY 1681 AGAAGACCTGAAGCCAGCAATTTCTGACACTGAGATGAAGATGAAGATGAAGATGAAG 1740
 Db 1681 AGAAGACCTGAAGCCAGCAATTTCTGACACTGAGATGAAGATGAAGATGAAGATGAAG 1740
 QY 1741 CAAATATATCTCAGAAAGCAATTTTGTGAAGAACAGAACTGGAATTTACAGATGAG 1800
 Db 1741 CAAATATATCTCAGAAAGCAATTTTGTGAAGAACAGAACTGGAATTTACAGATGAG 1800
 QY 1801 ATTCTGATGATGAAGAAAGCAGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1860
 Db 1801 ATTCTGATGATGAAGAAAGCAGATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1860
 QY 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGACATGAATAATGATGCTGCGGGAAGAAAT 1920
 Db 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGACATGAATAATGATGCTGCGGGAAGAAAT 1920
 QY 1921 GGCATGCTAAGAGCTGAGAGCTGAGACAAATGAACATCAGAGCCAGCTTAAAAA 1980
 Db 1921 GGCATGCTAAGAGCTGAGAGCTGAGACAAATGAACATCAGAGCCAGCTTAAAAA 1980
 QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
 Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 15

US-09-651-236-374

Sequence 374, Application US/09651236

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Devin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yugu

APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darick
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Aljun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE REFERENCE: 210121.42718C18
 ; CURRENT APPLICATION NUMBER: US/09/651,236
 ; NUMBER OF SEQ. ID NOS: 865
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ. ID NO 374
 ; LENGTH: 2000
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; US-09-651-236-374

Query Match 100.0%; Score 2000; DB 25; Length 2000;
 Best Local Similarity 100.0%; Pred. No. 6,6e-226;
 Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTTGATAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60
 Db 1 ATGTGTTGATAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 60
 QY 61 AGAGCAAGATGAGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
 Db 61 AGAGCAAGATGAGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
 QY 121 AGCAAGTGGGCACTTGTGAGACACAGACACTGCTATGAAGACACTGAGAGCAAG 180
 Db 121 AGCAAGTGGGCACTTGTGAGACACAGACACTGCTATGAAGACACTGAGAGCAAG 180
 QY 181 ATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
 Db 181 ATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 240
 QY 241 GGCCTCTGAGAGACACAGACACTGCTATGAAGACACTGAGAGCAAGATGGCAAG 300
 Db 241 GGCCTCTGAGAGACACAGACACTGCTATGAAGACACTGAGAGCAAGATGGCAAG 300
 QY 301 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
 Db 301 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
 QY 361 GGAGACTAGCATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 Db 361 GGAGACTAGCATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
 QY 421 GACAGCTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 Db 421 GACAGCTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 QY 481 CTCAGGACACTGACGTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 Db 481 CTCAGGACACTGACGTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 QY 541 TCTGCAATGGGAATTCAGAAATGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
 Db 541 TCTGCAATGGGAATTCAGAAATGTAATTAATTAATTAATTAATTAATTAATTAATTAAT 600
 QY 601 GTCTTGACAAACAAAG 660
 Db 601 GTCTTGACAAACAAAG 660
 QY 661 TGTGCTTAAATGTTGCTGGAACATGCACTGATCCAAATATTCAGATGATGATGAAT 720

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|||||
Db 661 TGTGGTTATATGTCTGGAAACATGGCACTGATCCAAATATTCAGATGATGAAAT 720
OY 721 ACCACTGCGACTAGCTATCTATATATGAAGATTAATTAATGCGCAACACTGCTCTTA 780
Db 722 ACCACTGCGACTAGCTATCTATATGAAGATTAATTAATGCGCAACACTGCTCTTA 780
OY 781 TATGGTGTGATATGAATCAAAAAACAAGCATGGCCCTCACACACTGTACTGGTGA 840
Db 781 TATGGTGTGATATGAATCAAAAAACAAGCATGGCCCTCACACACTGTACTGGTGA 840
OY 841 CATGAGCAAAAAACAGCAAGTGTGAAATTTTAAATCAGAAAAAAGCGAATTTAAATGA 900
Db 841 CATGAGCAAAAAACAGCAAGTGTGAAATTTTAAATCAGAAAAAAGCGAATTTAAATGA 900
OY 901 CTGGAATAGATATGAAGAGCTGCTCATCTGCTGATGTTGGATCAGCAAGTATA 960
Db 901 CTGGAATAGATATGAAGAGCTGCTCATCTGCTGATGTTGGATCAGCAAGTATA 960
OY 961 GTACAGCTTCTACTTGAGCAAAATATGATGATCTTTCAGAGATCTATCGACAGAG 1020
Db 961 GTACAGCTTCTACTTGAGCAAAATATGATGATCTTTCAGAGATCTATCGACAGAG 1020
OY 1021 GCCAAGAGTATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAAGAGTATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
OY 1081 AAGAGAAAAACATGCTAAATAATCTCTGTAAGAACAGCAATCCAGAAACAGCTTAAG 1140
Db 1081 AAGAGAAAAACATGCTAAATAATCTCTGTAAGAACAGCAATCCAGAAACAGCTTAAG 1140
OY 1141 CTGACATCAGAGAGAGTACACAAAGGTTCAAGAGCAGTGAATAATGGCCAGCAGAAA 1200
Db 1141 CTGACATCAGAGAGAGTACACAAAGGTTCAAGAGCAGTGAATAATGGCCAGCAGAAA 1200
OY 1201 ATGTCTCAAGAACCAAGAAATAAATAGATGATAGAGAGTTGAAGAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAGAAATAAATAGATGATAGAGAGTTGAAGAGAAATGAAG 1260
OY 1261 AAGCAAGAAATTAATGCTGGATTAATCTAGAAACCTACTAATGCTGCTGCTG 1320
Db 1261 AAGCAAGAAATTAATGCTGGATTAATCTAGAAACCTACTAATGCTGCTGCTG 1320
OY 1321 AATGGTGAATATGATTAATCTCTCAAGAGAGAGCAAGCACTGAAATAGCAATTT 1380
Db 1321 AATGGTGAATATGATTAATCTCTCAAGAGAGAGCAAGCACTGAAATAGCAATTT 1380
OY 1381 CCTGACAAAGAAAGTGAAGATATCACAGAAATTTGGAAATTTGCTGACTACAAAGAA 1440
Db 1381 CCTGACAAAGAAAGTGAAGATATCACAGAAATTTGGAAATTTGCTGACTACAAAGAA 1440
OY 1441 AAACAGATGCCAAATACTCTTCTGAAAACAGCAACCCAGAAACAGACTTAAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATACTCTTCTGAAAACAGCAACCCAGAAACAGACTTAAAGCTGACA 1500
OY 1501 TCAGAGAGAGTACCAAAAGGCTTGAGGCGAGTGAATAATGGCCAGCAGAGTGAAGAAAT 1560
Db 1501 TCAGAGAGAGTACCAAAAGGCTTGAGGCGAGTGAATAATGGCCAGCAGAGTGAAGAAAT 1560
OY 1561 TTTATGCTATATGAAAGAAATGAAGACAGCAAGTACTCATGTGGATTTCCAGAAAAAC 1620
Db 1561 TTTATGCTATATGAAAGAAATGAAGACAGCAAGTACTCATGTGGATTTCCAGAAAAAC 1620
OY 1621 CTGATATATGCTGCCACTGCTGCAATGCTGATGATTAATTTCTTCAAGGAAAGAGC 1680
Db 1621 CTGATATATGCTGCCACTGCTGCAATGCTGATGATTAATTTCTTCAAGGAAAGAGC 1680
OY 1681 AGAAGACCTGAAAGCAGCAATTTCTCTGACACTGAGAAATGAAGAGATACAGAGTGCAGAA 1740
Db 1681 AGAAGACCTGAAAGCAGCAATTTCTCTGACACTGAGAAATGAAGAGATACAGAGTGCAGAA 1740
OY 1741 CAAAATGATACTCAGAGCAATTTTGTGAAGAACAGAACTGGAATATTACAGATGAG 1800
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Db 1741 CAAAATGATACTCAGAGCAATTTTGTGAAGAACAGAACTGGAATATTACAGATGAG 1800
OY 1801 ATTTCGATTCATGAAGAAAGCAAGATAGAAAGTGTGAAGAAATGAATCTGAGCTTCT 1860
Db 1801 ATTTCGATTCATGAAGAAAGCAAGATAGAAAGTGTGAAGAAATGAATCTGAGCTTCT 1860
OY 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGATGAAATATGATACGTTGGGGAGAAATTT 1920
Db 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGATGAAATATGATACGTTGGGGAGAAATTT 1920
OY 1921 GCCATGCTAAGACTGAGCTAGACACAAATGAACATCAGAGCCAGCTAAAAAAGAAAA 1980
Db 1921 GCCATGCTAAGACTGAGCTAGACACAAATGAACATCAGAGCCAGCTAAAAAAGAAAA 1980
OY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

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RESULT 16

us-09-657-279-374

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; Sequence 374, Application US/09657279
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqun
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedyick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C19
; CURRENT APPLICATION NUMBER: US/09/657, 279
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 877
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-657-279-374

```

Query Match 100.0%; Score 2000; DB 25; Length 2000;

Best local similarity 100.0%; Pred. No. 6.6e-226;

Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 ATGTTGTTGAGTTGATTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGGTCTC 60
Db 1 ATGTTGTTGAGTTGATTCATGCGGCTGCTCTTCTGTGAAGAGCAATTTGGTCTC 60
OY 61 AAGAGCAATATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
Db 61 AAGAGCAATATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
OY 121 AGCAAGTGGGCACTTCTGAGACACAGAGACTGTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACACAGAGACTGTATGAAGACACTCAGAGCAAG 180
OY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAACGTG 240
Db 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGAGAGTGGCAAGCAACGTG 240

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Oy	241	GGCCCTTCTGGAGCCACGACGACTCGGTATGAAGACACTCAGAACAAAGTGGGCAAG	300
Db	241	GGCCCTTCTGGAGCCACGACGACTCGGTATGAAGACACTCAGAACAAAGTGGGCAAG	300
Oy	301	TGATGCTGCCACTGCTCCCTCTGCTCAGGGGGAGCGGCAAGAGCAAGTGGGCGCTTGG	360
Db	301	TGATGCTGCCACTGCTCCCTCTGCTCAGGGGGAGCGGCAAGAGCAAGTGGGCGCTTGG	360
Oy	361	GGAACTACAGTATGACACTGCTTCATGAGAGCCCGGTACCAAGTCCGGAGAAAGATCTG	420
Db	361	GGAACTACAGTATGACACTGCTTCATGAGAGCCCGGTACCAAGTCCGGAGAAAGATCTG	420
Oy	421	GACAAGCTCCACAGAGCTGCTGGTGGGGGAAAAGTCCCGAAGAAAGATCTCATGTCATG	480
Db	421	GACAAGCTCCACAGAGCTGCTGGTGGGGGAAAAGTCCCGAAGAAAGATCTCATGTCATG	480
Oy	481	CTCAGGGACACTGACGTGAACAAGAGGACCAAGCAAAAGAGACGTCTACATATCGCC	540
Db	481	CTCAGGGACACTGACGTGAACAAGAGGACCAAGCAAAAGAGACGTCTACATATCGCC	540
Oy	541	TCCTGCCAATGGGAATTCAGAAATGTAATAATCTCTGCTGGACAGACGATGTCAACTTAAT	600
Db	541	TCCTGCCAATGGGAATTCAGAAATGTAATAATCTCTGCTGGACAGACGATGTCAACTTAAT	600
Oy	601	GTCCTTGACAACAAAAGAGACAGCTCGATTAAGCCGCTACATATGCGCAGGAAGATAA	660
Db	601	GTCCTTGACAACAAAAGAGACAGCTCGATTAAGCCGCTACATATGCGCAGGAAGATAA	660
Oy	661	TGTGCGTTAATGTTGCTGCGAACAATGGCAGCTGATCCAAATATTCAGATAGATGAAT	720
Db	661	TGTGCGTTAATGTTGCTGCGAACAATGGCAGCTGATCCAAATATTCAGATAGATGAAT	720
Oy	721	ACCACTCTGCACCTACGCTATCTTAATGAAGATAAATTAATGCGCAAGACACTGCTTTA	780
Db	721	ACCACTCTGCACCTACGCTATCTTAATGAAGATAAATTAATGCGCAAGACACTGCTTTA	780
Oy	781	TATGTCGTGATATCGAATGAAAAACAAGCATGGCGTCACACCACTGTTACTGGTGTA	840
Db	781	TATGTCGTGATATCGAATGAAAAACAAGCATGGCGTCACACCACTGTTACTGGTGTA	840
Oy	841	CATGAGCAAAAAACAGCAAGTCGTGAATTTTTTAATCAAGAAAAAAGCGAATTTAATGCA	900
Db	841	CATGAGCAAAAAACAGCAAGTCGTGAATTTTTTAATCAAGAAAAAAGCGAATTTAATGCA	900
Oy	901	CTGGATATGATATGGAAAGAGCTGCTCTCATATCTTGTCTGATATGTTGGATCAGCAATYA	960
Db	901	CTGGATATGATATGGAAAGAGCTGCTCTCATATCTTGTCTGATATGTTGGATCAGCAATYA	960
Oy	961	GTCAGCCTTACTTATGAGCAAAATATTTGATGTAATCTTCAAGATCTATCTGGACAGCG	1020
Db	961	GTCAGCCTTACTTATGAGCAAAATATTTGATGTAATCTTCAAGATCTATCTGGACAGCG	1020
Oy	1021	GCCAGAGATATGCTGTTTCTAGTCAATCATATGTAATTTGGCAGTATCTTCTGACATAC	1080
Db	1021	GCCAGAGATATGCTGTTTCTAGTCAATCATATGTAATTTGGCAGTATCTTCTGACATAC	1080
Oy	1081	AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAAACAAAGACTTAAG	1140
Db	1081	AAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAAACAAAGACTTAAG	1140
Oy	1141	CTGACATATCAGAGGAAGAGTCAACAAGTTCAAAAGCAGTGAATAATAGCCAGCAGAGAAA	1200
Db	1141	CTGACATATCAGAGGAAGAGTCAACAAGTTCAAAAGCAGTGAATAATAGCCAGCAGAGAAA	1200
Oy	1201	ATGCTCTAAGAACACGAAATTAATTAAGATGGTATAGAGAGGTGAAGAAAGAAATGAG	1260
Db	1201	ATGCTCTAAGAACACGAAATTAATTAAGATGGTATAGAGAGGTGAAGAAAGAAATGAG	1260
Oy	1261	AAGCATAAAGTAAATATATGTGGGATTAATAGAAAACCTGACTAAATAGTGTCACTGTCGC	1320
Db	1261	AAGCATAAAGTAAATATATGTGGGATTAATAGAAAACCTGACTAAATAGTGTCACTGTCGC	1320
Oy	1321	AATGCTGATTAATGATTAATTTCTCAAGGAAGACGAGAACCTGAAATTCAGCAATTT	1380

Db	1321	AAATGCTATATATGATTAAATTCCTCAAGAGAGACAGACACCTGGAAATATACCAATTT	1380
Qy	1381	CTTGACACAGAAAGTGAAGATATCAACAGAAATTTGGCAATTAGTTCTGACTACAAAAGAA	1440
Db	1381	CCTGACACAGAAAGTGAAGATATCAACAGAAATTTGGCAATTAGTTCTGACTACAAAAGAA	1440
Qy	1441	AAACAGATGCCAAATATCTCTCTGAAAACACCAACCCAGAACCAAGACTTAAACCTGACA	1500
Db	1441	AAACAGATGCCAAATATCTCTCTGAAAACACCAACCCAGAACCAAGACTTAAACCTGACA	1500
Qy	1501	TCACAGAGAAGAGTCCACAAAGGCTTGAGGGCAGTGAATAATGGCCACACAGACTTGAAAT	1560
Db	1501	TCACAGAGAAGAGTCCACAAAGGCTTGAGGGCAGTGAATAATGGCCACACAGACTTGAAAT	1560
Qy	1561	TTTTATGGCTATCGAAGAAATGAAGAAGCAGGAAAGTACTCATGTGCGATTTCCAGAAAAC	1620
Db	1561	TTTTATGGCTATCGAAGAAATGAAGAAGCAGGAAAGTACTCATGTGCGATTTCCAGAAAAC	1620
Qy	1621	CTGACTATATGGTGGCCTGCTGGCCATTTGGTATGATGGATTTAAATTCCTCCAAAGAAAGCC	1680
Db	1621	CTGACTATATGGTGGCCTGCTGGCCATTTGGTATGATGGATTTAAATTCCTCCAAAGAAAGCC	1680
Qy	1681	AGAACACCTGAAAGGCCAGCAATTTCTGACACTGGAATGAAGATATCACAGTAGACAA	1740
Db	1681	AGAACACCTGAAAGGCCAGCAATTTCTGACACTGGAATGAAGATATCACAGTAGACAA	1740
Qy	1741	CAAAATGATACTCAGAAAGCAATTTTGTGAAAGAACAGAACACTGTGAATTTACACGATGAG	1800
Db	1741	CAAAATGATACTCAGAAAGCAATTTTGTGAAAGAACAGAACACTGTGAATTTACACGATGAG	1800
Qy	1801	ATTTGTGATTCATGAAGAAAGCAGATAGAAAGTGTTGAAAAAATGAATTTGACACTTTC	1860
Db	1801	ATTTGTGATTCATGAAGAAAGCAGATAGAAAGTGTTGAAAAAATGAATTTGACACTTTC	1860
Qy	1861	CTTAGTGTGAAGAAAGAAAGACATCTTGATGAAATAATAGTACTTCCGGGAAGAAAT	1920
Db	1861	CTTAGTGTGAAGAAAGAAAGACATCTTGATGAAATAATAGTACTTCCGGGAAGAAAT	1920
Qy	1921	GCCATGCTAAGACTGGAGCTAGACACAAATGAAGAAATCATCAGAGCCAGCTTAAAAA	1980
Db	1921	GCCATGCTAAGACTGGAGCTAGACACAAATGAAGAAATCATCAGAGCCAGCTTAAAAA	1980
Qy	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAAA 2000	

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RESULT 17
US-09-679-272-374
; Sequence 374, Application US/09679272
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Skeiky, Yasir
; APPLICANT: Reed, Steven G.
; APPLICANT: Cheever, Martin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534
; CURRENT APPLICATION NUMBER: US/09/679,272
; CURRENT FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 476
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-679-272-374

```

Query Match	100.0%;	Score 2000;	DB 26;	Length 2000;
Best Local Similarity	100.0%;	Pred. No. 6.6e-226;		
Matches 2000; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C20
CURRENT APPLICATION NUMBER: us/09/679,426
CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 895
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-679-426-374

Query Match 100.0%; Score 2000; DB 26; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6,6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTAGGTTGATTCATCCCGGCTGCTTCTGTGAAGAACCACTTTGGTCTC 60
Db 1 ATGGTGGTTAGGTTGATTCATCCCGGCTGCTTCTGTGAAGAACCACTTTGGTCTC 60
QY 61 AGAGCAAGATGAGCAAGTGTGCTGCGCTTCCCTGCTCAGAGAGAGCGGCAAG 120
Db 61 AGAGCAAGATGAGCAAGTGTGCTGCGCTTCCCTGCTCAGAGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGAGACAGACACTCTCTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTGAGAGACAGACACTCTCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGCCCACTGCTTCCCTGCTCAGAGAGAGAGTGGCAAGACTG 240
Db 181 ATGGGCAAGTGTGCGCCCACTGCTTCCCTGCTCAGAGAGAGAGTGGCAAGACTG 240
QY 241 GCGCCTTCTGAGACACGACACTGTCTATGAAGACACTCAGAGCAAGAGTGGCAAG 300
Db 241 GCGCCTTCTGAGACACGACACTGTCTATGAAGACACTCAGAGCAAGAGTGGCAAG 300
QY 301 TGGTGGTCCACTGCTTCCCTGCTCAGAGAGAGCGGCAAGAGAGTGGCGCTTGG 360
Db 301 TGGTGGTCCACTGCTTCCCTGCTCAGAGAGAGCGGCAAGAGAGTGGCGCTTGG 360
QY 361 GAGACACTACATGACACTGCTTCTCATGAGACCCAGGTAACAGCTCCCTGGAGAACTG 420
Db 361 GAGACACTACATGACACTGCTTCTCATGAGACCCAGGTAACAGCTCCCTGGAGAACTG 420
QY 421 GACAAGCTCCACAGAGTGTGCTGGTGGGTAAAGTCCCGAGAAAGATGTCATGTCATG 480
Db 421 GACAAGCTCCACAGAGTGTGCTGGTGGGTAAAGTCCCGAGAAAGATGTCATGTCATG 480
QY 481 CTCAGGAGACACTGACGTGAACAAGAGAGCAAGCAAAAGAGACTGCTACATCTGGCC 540
Db 481 CTCAGGAGACACTGACGTGAACAAGAGAGCAAGCAAAAGAGACTGCTACATCTGGCC 540
QY 541 TCTGCGCAATGGGAATTAAGAACTCTGCTGAGACAGATGTCATTAAT 600
Db 541 TCTGCGCAATGGGAATTAAGAACTCTGCTGAGACAGATGTCATTAAT 600
QY 601 GTCTTGAACAACAAG 660
Db 601 GTCTTGAACAACAAG 660

QY 661 TGGCGTTAATGTTGCTGGAACATGACATGATCCAAATATTCAGATGATGAAAT 720
Db 661 TGGCGTTAATGTTGCTGGAACATGACATGATCCAAATATTCAGATGATGAAAT 720
QY 721 ACCACTGTGACACTGCTATCTATTAAGATTAATTAATGCGCAAGACGCTCTTA 780
Db 721 ACCACTGTGACACTGCTATCTATTAAGATTAATTAATGCGCAAGACGCTCTTA 780
QY 781 TATGTCGTGATATGATCAAAAAAAGACATGCGCTCACACCACTGTTACTGTGTA 840
Db 781 TATGTCGTGATATGATCAAAAAAAGACATGCGCTCACACCACTGTTACTGTGTA 840
QY 841 CATGAGCAAAAAACAGCAAGTGTGAAAATTTTAAATCAAGAAAAAGCAATTAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTGTGAAAATTTTAAATCAAGAAAAAGCAATTAATGCA 900
QY 901 CTGATATGATATGAGAGAGAGCTGCTATCTCTGATGTTGATGATGATGATGATG 960
Db 901 CTGATATGATATGAGAGAGAGAGCTGCTATCTCTGATGTTGATGATGATGATGATG 960
QY 961 GTGACCTTCTACTTGAAGCAAAATATGATGATCTCTCAAGATCTATCTGACAGAG 1020
Db 961 GTGACCTTCTACTTGAAGCAAAATATGATGATCTCTCAAGATCTATCTGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTATCATCATGTAATTTGCCAGTTACTTGTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTATCATCATGTAATTTGCCAGTTACTTGTGACTAC 1080
QY 1081 AAAAAAAGCAATGCTAAAAATCTCTGAAAACAGCAATCCAGAAACAAAGACTTAAAG 1140
Db 1081 AAAAAAAGCAATGCTAAAAATCTCTGAAAACAGCAATCCAGAAACAAAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCAAAAGGTTCAAAAGCGTGAATAATACCCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGAGTCAAAAGGTTCAAAAGCGTGAATAATACCCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACAGAAATTAATAGAGTGTATAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACAGAAATTAATAGAGTGTATAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGTATTAATGAGGATTTACTGAAAACCTGATGATGATGATGATGATG 1320
Db 1261 AAGCATGAAGTATTAATGAGGATTTACTGAAAACCTGATGATGATGATGATGATG 1320
QY 1321 AATGATATATGATTAATTTCTCAAGAGAGAGCAACCTGAAATACAGCAATTT 1380
Db 1321 AATGATATATGATTAATTTCTCAAGAGAGAGCAACCTGAAATACAGCAATTT 1380
QY 1381 CTTGACAAAGAGAGTATACAGAAATTTGCAATTTAGTTTCTGACTACAAAGAA 1440
Db 1381 CTTGACAAAGAGAGTATACAGAAATTTGCAATTTAGTTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCAAAATCTCTGAAAACAGCAACCCAGAAACAGCAATTAAGCTGACA 1500
Db 1441 AAACAGATGCAAAATCTCTGAAAACAGCAACCCAGAAACAGCAATTAAGCTGACA 1500
QY 1501 TCAAGAGAGAGAGTCAAAAGGCTTGAAGGCAAGTGAATGGCCAGCCAGAGCTGAAAT 1560
Db 1501 TCAAGAGAGAGAGTCAAAAGGCTTGAAGGCAAGTGAATGGCCAGCCAGAGCTGAAAT 1560
QY 1561 TTTATGCTATCGAAGAAATGAGAGACACGAAATGCTATGTCGATTCAGAAAC 1620
Db 1561 TTTATGCTATCGAAGAAATGAGAGACACGAAATGCTATGTCGATTCAGAAAC 1620
QY 1621 CTGACTAATGCTGCACTGCTGCAAGGATGATGATGATTAATTTCTCCAGAGAGAGC 1680
Db 1621 CTGACTAATGCTGCACTGCTGCAAGGATGATGATGATTAATTTCTCCAGAGAGAGC 1680
QY 1681 AGAAGACCTGAG 1740
Db 1681 AGAAGACCTGAG 1740
QY 1741 CAAATATGATCTAGAGAGCAATTTTGTGAAGAACAGAACTGGAATTTTACAGATGAG 1800


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Db 1741 CAAAATGATCTCAGAACATTTTGTGAAGACAGAACTGGAAATTTACAGATGAG 1800
Qy 1801 ATTCGATCTCATGAAGAAAGACAGATAGAACTGGTTGAAAAAATGATTCGAGCTTTCT 1860
Db 1801 ATTCGATCTCATGAAGAAAGACAGATAGAACTGGTTGAAAAAATGATTCGAGCTTTCT 1860
Qy 1861 CTGAGTTGTAGAAAGAAAGACATCTTGCAATGAAATAGTACGTGCGGGAAGAAAT 1920
Db 1861 CTGAGTTGTAGAAAGAAAGACATCTTGCAATGAAATAGTACGTGCGGGAAGAAAT 1920
Qy 1921 GCCATGCTAAGACCTGAGACCTAGACAAATGAAACATCAGACGACCTAAAAA 1980
Db 1921 GCCATGCTAAGACCTGAGACCTAGACAAATGAAACATCAGACGACCTAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
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RESULT 19

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US-09-685-166-374
: Sequence 374, Application US/09685166
: GENERAL INFORMATION:
: APPLICANT: Xu, Jlangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yuqi
: APPLICANT: Henderson, Robert A.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darlick
: APPLICANT: Li, Samuel
: APPLICANT: Wang, Aijun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: FILE REFERENCE: 210121.427C21
: CURRENT APPLICATION NUMBER: US/09/685.166
: NUMBER OF SEQ ID NOS: 898
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 374
: LENGTH: 2000
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-685-166-374
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Query Match 100.0%; Score 2000; DB 27; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6,6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 ATGCTGTTGAGTGTATTCATGCGGCTGCCTCTTCTGTGAAGACCAATTTGGTCTC 60
Db 1 ATGCTGTTGAGTGTATTCATGCGGCTGCCTCTTCTGTGAAGACCAATTTGGTCTC 60
Qy 61 AGGAGCAAGATGGGCAATGGTGGCTGCTCCCTGCTGAGGAGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGGCAATGGTGGCTGCTCCCTGCTGAGGAGAGCGGCAAG 120
Qy 121 AGCAAGCTGGGCACTTCTGAGACAGACGACTGCTGATGAACACTCAGAGCAAG 180
Db 121 AGCAAGCTGGGCACTTCTGAGACAGACGACTGCTGATGAACACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGGTGGCCGCACTGCTCCCTGCTGACAGGGGAGTGGCAAGAGCAAGCTG 240
Db 181 ATGGGCAAGTGGTGGCCGCACTGCTCCCTGCTGACAGGGGAGTGGCAAGAGCAAGCTG 240
```

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Qy 241 GGCGCTTCGGAGACACAGACACTCTGCTATGAAGACACTCAGGAAAGATGGGCAAG 300
Db 241 GGCGCTTCGGAGACACAGACACTCTGCTATGAAGACACTCAGGAAAGATGGGCAAG 300
Qy 301 TGTGCTCCCACTGCTCCCTGCTGTCAGGGGGAGCGGCAAGAGCAAGGTGGCGCTTGG 360
Db 301 TGTGCTCCCACTGCTCCCTGCTGTCAGGGGGAGCGGCAAGAGCAAGGTGGCGCTTGG 360
Qy 361 GGAGACTACGATGACAGTGCCTTTCATGAGCCAGGTCACACGTCCTGAGAGATCTG 420
Db 361 GGAGACTACGATGACAGTGCCTTTCATGAGCCAGGTCACACGTCCTGAGAGATCTG 420
Qy 421 GACAGCTCCACAGAGCTGCCGTGGGGTAAAGTCCCGAAGAGATCTCATCTGTCATG 480
Db 421 GACAGCTCCACAGAGCTGCCGTGGGGTAAAGTCCCGAAGAGATCTCATCTGTCATG 480
Qy 481 CTCAGGACACTGACGTGACCAAGAGACAAAGAGAGACTGCTCTACATCTGGCC 540
Db 481 CTCAGGACACTGACGTGACCAAGAGACAAAGAGAGACTGCTCTACATCTGGCC 540
Qy 541 TCTGCCAATGGGAATTCAGAACTACTTAAACTCTGCTGAGACAGCATGTCACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAACTACTTAAACTCTGCTGAGACAGCATGTCACTTAAT 600
Qy 601 GTCCCTTGACAAACAAAAGAGGACAGCTGATAAAGGCGGTCAATGGCAGGAATGAA 660
Db 601 GTCCCTTGACAAACAAAAGAGGACAGCTGATAAAGGCGGTCAATGGCAGGAATGAA 660
Qy 661 TGTGCGTTAATGTTGCTGGAACTGCACTGATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACTGCACTGATCCAAATATTCAGATGATGGAAT 720
Qy 721 ACCACTCTGCACTACGCTATCTATATGAGATTAATTAATGAGCCAAAGCACTGCTTA 780
Db 721 ACCACTCTGCACTACGCTATCTATATGAGATTAATTAATGAGCCAAAGCACTGCTTA 780
Qy 781 TATGCTGCTGATATGATGATCAAAAACAAAGCATGGGCTCACACGCTGTACTTGGTGA 840
Db 781 TATGCTGCTGATATGATGATCAAAAACAAAGCATGGGCTCACACGCTGTACTTGGTGA 840
Qy 841 CATGAGCAAAAACACAGAGCTGTAATTTTAATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAACACAGAGCTGTAATTTTAATCAAGAAAAAGCAATTTAAATGCA 900
Qy 901 CTGATATGATATGAGAGAGCTGCTCATACTGCTGATATGTTGGATCAGCAAGTATA 960
Db 901 CTGATATGATATGAGAGAGCTGCTCATACTGCTGATATGTTGGATCAGCAAGTATA 960
Qy 961 GTACAGCTTCTACCTTACGACAAAATTTGATGATCTTCCAGATCTATCTGAGACAGG 1020
Db 961 GTACAGCTTCTACCTTACGACAAAATTTGATGATCTTCCAGATCTATCTGAGACAGG 1020
Qy 1021 GCCAGAGATATGCTGTTTCTAGTATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTATCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Qy 1081 AAAAGAAAAACAGATCTTAAAAATCTTCTGAAAACAGCAATCCAGAACAGACTTAAG 1140
Db 1081 AAAAGAAAAACAGATCTTAAAAATCTTCTGAAAACAGCAATCCAGAACAGACTTAAG 1140
Qy 1141 CTGACATCAGAGAGAGATGCAAAAGTTCAAGAGCAGTGAATAATGACGACAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGATGCAAAAGTTCAAGAGCAGTGAATAATGACGACAGAGAAA 1200
Qy 1201 ATGCTCAAGAACCAAGAAATTAATTAAGATGGTGTAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGCTCAAGAACCAAGAAATTAATTAAGATGGTGTAGAGAGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAAGTAATTAATGTTGGATTAATAGAAAACCTGACTAATGTTGCTCACTGCGC 1320
Db 1261 AAGCATGAAAGTAATTAATGTTGGATTAATAGAAAACCTGACTAATGTTGCTCACTGCGC 1320
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QY	1321	AATGCTGATTAATGATTAATCTCTCAAGAGAGAGAAACCTGAAATACGAATTT	1380
Db	1321	AATGCTGATTAATGATTAATCTCTCAAGAGAGAGAAACCTGAAATACGAATTT	1380
QY	1381	CTGACACAGAAAGTGAAGATATCAAGATTTGGCAATTGATTCTTGACTACAAAGAA	1440
Db	1381	CTGACACAGAAAGTGAAGATATCAAGATTTGGCAATTGATTCTTGACTACAAAGAA	1440
QY	1441	AAACAGATGCCAAATATCTTTTGAAAAACAGCACCCGAAACAAGACTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAATATCTTTTGAAAAACAGCACCCGAAACAAGACTTAAAGCTGACA	1500
QY	1501	TCAGAGAAAGTGCACAAAGGCTTGAGGGCAGTGGAAAAATGGCCACCGAGCTGAAAT	1560
Db	1501	TCAGAGAAAGTGCACAAAGGCTTGAGGGCAGTGGAAAAATGGCCACCGAGCTGAAAT	1560
QY	1561	TTTATGGCTATCCAGAAATAATGAAGACAGCAAGTACTGATGTGGATTTCCACAGAAAC	1620
Db	1561	TTTATGGCTATCCAGAAATAATGAAGACAGCAAGTACTGATGTGGATTTCCACAGAAAC	1620
QY	1621	CTGACTAATGGTGCACCTGCTGGCAATGGTATGATGATTAATTCTCCAGAAAGAGC	1680
Db	1621	CTGACTAATGGTGCACCTGCTGGCAATGGTATGATGATTAATTCTCCAGAAAGAGC	1680
QY	1681	AGAACACCTTAAAGCCACGCAATTTCTTGACACTGAGATGAAGATATCACAGTACGAA	1740
Db	1681	AGAACACCTTAAAGCCACGCAATTTCTTGACACTGAGATGAAGATATCACAGTACGAA	1740
QY	1741	CAAAATGATACCTCAGAAAGCAATTTTGTGAAGAAACAGACACTGGAATTTACACATGAG	1800
Db	1741	CAAAATGATACCTCAGAAAGCAATTTTGTGAAGAAACAGACACTGGAATTTACACATGAG	1800
QY	1801	ATTCTGATTCATGAGAAAGACAGATAGAAAGTGTGAAAAAATGAATTCGAGCTTTCT	1860
Db	1801	ATTCTGATTCATGAGAAAGACAGATAGAAAGTGTGAAAAAATGAATTCGAGCTTTCT	1860
QY	1861	CTTAGTGTGAAGAAAGAAAAAGCATCTTGATGAAAAATGATACCTTCGCGGAAAGAAATT	1920
Db	1861	CTTAGTGTGAAGAAAGAAAAAGCATCTTGATGAAAAATGATACCTTCGCGGAAAGAAATT	1920
QY	1921	GCCATGCTAAGACTGGAGCTAGACACATGAAGAAACATCAGAGCCACTTAAAAA	1980
Db	1921	GCCATGCTAAGACTGGAGCTAGACACATGAAGAAACATCAGAGCCACTTAAAAA	1980
QY	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
RESULT 20			
US-09-685-166A-374			
: Sequence 374, Application US/09685166A			
: GENERAL INFORMATION:			
: APPLICANT: Xu, Jiangchun			
: APPLICANT: Dillon, Davlin C.			
: APPLICANT: Mitcham, Jennifer L.			
: APPLICANT: Harlocker, Susan L.			
: APPLICANT: Jiang, Yugu.			
: APPLICANT: Henderson, Robert A.			
: APPLICANT: Kalos, Michael D.			
: APPLICANT: Fanger, Gary R.			
: APPLICANT: Retter, Marc W.			
: APPLICANT: Day, Craig H.			
: APPLICANT: Vedvick, Thomas S.			
: APPLICANT: Carter, Darrick			
: APPLICANT: Li, Samuel			
: APPLICANT: Wang, Aijun			
: APPLICANT: Skeiky, Yasir A.W.			
: APPLICANT: Hepler, William			
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER			
FILE REFERENCE: 210121.427C21			

		CURRENT APPLICATION NUMBER: US/09/685,166A			
		CURRENT FILING DATE: 2000-10-10			
		NUMBER OF SEQ ID NOS: 898			
		SOFTWARE: FASTSEQ for Windows Version 3.0			
		SEQ ID NO 374			
		LENGTH: 2000			
		TYPE: DNA			
		ORGANISM: Homo sapien			
		US-09-685-166A-374			
		Query Match		100.0%; Score 2000; DB 27; Length 2000;	
		Best Local Similarity		100.0%; Pred. No. 6.6e-226;	
		Matches 2000; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	ATGCGTGTGAGGTGATTCATGCGCGCTGCTCTTCTGTGAGAGAGCCATTGGCTCTC	60		
DB	1	ATGGGTGTGAGGTGATTCATGCGCGCTGCTCTTCTGTGAGAGAGCCATTGGCTCTC	60		
QY	61	AGGAGCAAGATGGCAAGTGGTGGTCCGCTTCCCTGCTGCAGAGGAGAGCGGCAAG	120		
DB	61	AGGAGCAAGATGGCAAGTGGTGGTCCGCTTCCCTGCTGCAGAGGAGAGCGGCAAG	120		
QY	121	AGCAACGTGGGCACTTCTGGAGACCAGCAGCACTGCTATGAAGACACTCAGAGCAAG	180		
DB	121	AGCAACGTGGGCACTTCTGGAGACCAGCAGCACTGCTATGAAGACACTCAGAGCAAG	180		
QY	181	ATGGGCAAGTGGTGGCGGCACACTGCTTCCCTGCTCAGGGGGAGTGGCAAGCAACGTG	240		
DB	181	ATGGGCAAGTGGTGGCGGCACACTGCTTCCCTGCTCAGGGGGAGTGGCAAGCAACGTG	240		
QY	241	GGCGCTTCTGGAGACCAGCAGCACTCTGCTATGAAGACACTCAGAGCAAGTGGGCAAG	300		
DB	241	GGCGCTTCTGGAGACCAGCAGCACTCTGCTATGAAGACACTCAGAGCAAGTGGGCAAG	300		
QY	301	TGGTGCCTGCACCTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGTGGCGCTTGG	360		
DB	301	TGGTGCCTGCACCTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGTGGCGCTTGG	360		
QY	361	GGAGACTACGATGACAGTGGCTTCTCATGTGAGAGCCAGGTACACAGCTCCGTGGAGAGATCTG	420		
DB	361	GGAGACTACGATGACAGTGGCTTCTCATGTGAGAGCCAGGTACACAGCTCCGTGGAGAGATCTG	420		
QY	421	GACAACTCCACAGAGCTGCTGCTGGGGTAAAGTCCCAAGAAAGATCTCATCTGCTATG	480		
DB	421	GACAACTCCACAGAGCTGCTGCTGGGGTAAAGTCCCAAGAAAGATCTCATCTGCTATG	480		
QY	481	CTCAGGGGACACTGCAGCTGTAACAAGAGGACAAAGAAAGAGGACATGCTTACATCTGGCC	540		
DB	481	CTCAGGGGACACTGCAGCTGTAACAAGAGGACAAAGAAAGAGGACATGCTTACATCTGGCC	540		
QY	541	TCTGCAATGGGAATTCAAGAGTAGTAATAAATCCTGCTGTGAGACAGACGATGTCACTTAAT	600		
DB	541	TCTGCAATGGGAATTCAAGAGTAGTAATAAATCCTGCTGTGAGACAGACGATGTCACTTAAT	600		
QY	601	GTCCTTGACAAACAAAGAGGACAGCTCTGATTAAGGCCGTGCAATGCCAGAGATGAA	660		
DB	601	GTCCTTGACAAACAAAGAGGACAGCTCTGATTAAGGCCGTGCAATGCCAGAGATGAA	660		
QY	661	TGTGGCTTAAGTGGTGGTGGACATGGGCACTGATCCAAATATTCAGATGAGTATGGAAAT	720		
DB	661	TGTGGCTTAAGTGGTGGTGGACATGGGCACTGATCCAAATATTCAGATGAGTATGGAAAT	720		
QY	721	ACCACTCTGCACACTACGCTATCTAATTAAGTAAATTAATGGCCAAAGCACTGCTCTTA	780		
DB	721	ACCACTCTGCACACTACGCTATCTAATTAAGTAAATTAATGGCCAAAGCACTGCTCTTA	780		
QY	781	TATGGTGTGATATCGAATCAAAAAAACAAGATGGGCTCACACCACTGTACTTGGTGTGA	840		
DB	781	TATGGTGTGATATCGAATCAAAAAAACAAGATGGGCTCACACCACTGTACTTGGTGTGA	840		
QY	841	CATGAGCAAAAAACAGCAAGTGTGAAATTTTTTAATCAAGAAAAAAGCAATTTAAATGCA	900		
DB	841	CATGAGCAAAAAACAGCAAGTGTGAAATTTTTTAATCAAGAAAAAAGCAATTTAAATGCA	900		

D	541	TCGCCAATGGGAATTTCAGAAAGTATGTTAAAACTCCTCTGTGGACAGACGATGTCACCTTAAT	600
Q	601	GTCTTGACAACAAAAGAGGACAGCTCTGATTAAGGCGGTATCAATGCCAGGAAGATAA	660
D	601	GTCCCTTACAAACAAAAGAGACAGCTGTGATTAAGGCGGTATCAATGCCAGGAACATGAA	660
Q	661	TGTGCGTTAATGTTGTCGGAAACAAATGGCCACTGATCCAAATATTCAGATGACGATGGAAT	720
D	661	TGTGCGTTAATGTTGTCGGAAACATGGCCACTGATCCAAATATTCAGATGACGATGGAAT	720
Q	721	ACCACCTGTGCACCTACGCTATCTAATTAAGAAGATTAATTAATGGCCAAAGCACTGCTCTTA	780
D	721	ACCACCTGTGCACCTACGCTATCTAATTAAGAAGATTAATTAATGGCCAAAGCACTGCTCTTA	780
Q	781	TATGTGCTGATATATCGAATCAAAAACCAAGCATGGCCCTCACACCACTGTTACTTGGTGTA	840
D	781	TATGTGCTGATATATCGAATCAAAAACCAAGCATGGCCCTCACACCACTGTTACTTGGTGTA	840
Q	841	CATGACGAAAAACGCAAGCTGTGAAATTTTATATCAAAAAAGCGAATTTAAATGCA	900
D	841	CATGACGAAAAACGCAAGCTGTGAAATTTTATATCAAAAAAGCGAATTTAAATGCA	900
Q	901	CTGGATAGATATGGAAGAGACTGCTCATCTGCTATGTTGGATCAGCAGATATA	960
D	901	CTGGATAGATATGGAAGAGACTGCTCATCTGCTATGTTGGATCAGCAGATATA	960
Q	961	GTCAGCCTTACTTGTGAGCAAAATATTGATGATCTTCAAGATCTATCTGGACAGAG	1020
D	961	GTCAGCCTTACTTGTGAGCAAAATATTGATGATCTTCAAGATCTATCTGGACAGAG	1020
Q	1021	GCCAGACAGTATGCTGTTTCTACTCATCATATGTAATTTGGCAGTTACTTCTCATAC	1080
D	1021	GCCAGACAGTATGCTGTTTCTACTCATCATATGTAATTTGGCAGTTACTTCTCATAC	1080
Q	1081	AAAAAAAACAGATGCTAAAAATCTCTTGAAACACGCAATCCAGAACACTTAAG	1140
D	1081	AAAAAAAACAGATGCTAAAAATCTCTTGAAACACGCAATCCAGAACACTTAAG	1140
Q	1141	CTGACATCAGAGAAAGTACAAAAGGTTCAAGGCAGTGAATAATAGCCAGCCAGAGAA	1200
D	1141	CTGACATCAGAGAAAGTACAAAAGGTTCAAGGCAGTGAATAATAGCCAGCCAGAGAA	1200
Q	1201	ATGTCTCAAGAACCAAGATTAATTAAGGATGGTATAGAGAGTTGAAAGAGAAATGAAG	1260
D	1201	ATGTCTCAAGAACCAAGATTAATTAAGGATGGTATAGAGAGTTGAAAGAGAAATGAAG	1260
Q	1261	AAGCATGAAGTATATGTGGGATTACTATGAAACCTGACTAATAGTGCTCATCTGTGCG	1320
D	1261	AAGCATGAAGTATATGTGGGATTACTATGAAACCTGACTAATAGTGCTCATCTGTGCG	1320
Q	1321	AATGGTGATTAATGATTAAATTCCTCAAGGAAAGCAGACAACTGAAAAATGACGAATTT	1380
D	1321	AATGGTGATTAATGATTAAATTCCTCAAGGAAAGCAGACAACTGAAAAATGACGAATTT	1380
Q	1381	CCTGACCAACGAAGTGAAGGTTACACAGAAATTTGCGAATTAAGTTTCTGACTACAAAGA	1440
D	1381	CCTGACCAACGAAGTGAAGGTTACACAGAAATTTGCGAATTAAGTTTCTGACTACAAAGA	1440
Q	1441	AAACAGATGCCAAAATCTCTTGAAAAACAGCAACCCAGAACCAAGACTTAAGCTGACA	1500
D	1441	AAACAGATGCCAAAATCTCTTGAAAAACAGCAACCCAGAACCAAGACTTAAGCTGACA	1500
Q	1501	TCAGAGAAAGAGTACAAAAGGTTGAGGGCAGTGAATAATGGCCAGCAGAGCTAACAAT	1560
D	1501	TCAGAGAAAGAGTACAAAAGGTTGAGGGCAGTGAATAATGGCCAGCAGAGCTAACAAT	1560
Q	1561	TTTATGGCTATCGAAGAATGAAGAAGCAGCAAGTACTCATGTGCGATTTCCAGAAAAC	1620
D	1561	TTTATGGCTATCGAAGAATGAAGAAGCAGCAAGTACTCATGTGCGATTTCCAGAAAAC	1620
Q	1621	CTGACTAATGGTGCACACTGCTGGCAATGGTATGATGATTAATTTCTTCCAGAAAGAGC	1680
D	1621	CTGACTAATGGTGCACACTGCTGGCAATGGTATGATGATTAATTTCTTCCAGAAAGAGC	1680

QY	1681	AAGAACCCGGAAGCAGCAATTTCTCGTACGTGGAAATGAGAATGCAGTCACGTA	1740
Db	1681	AAAAAAAAAAAAAAAAAAAAA	1740
QY	1741	CAAAATGATACACAGAACCAATTTTTGTGAAGAACAGAACACATCATATATTACACATGAG	1800
Db	1741	CAAAATGATACACAGAACCAATTTTTGTGAAGAACAGAACACATCATATATTACACATGAG	1800
QY	1801	ATTCTGATTTCATGAGAAAAAGCAGATAGAAATGTTGAAAAAATGAAATTTCTAGCTTTCT	1860
Db	1801	ATTCTGATTTCATGAGAAAAAGCAGATAGAAATGTTGAAAAAATGAAATTTCTAGCTTTCT	1860
QY	1861	CTTAGTGTTGAAGAAAAAGAAACAATCTTGCAATGAAATAGTACGTTGGGGAGAAATT	1920
Db	1861	CTTAGTGTTGAAGAAAAAGAAACAATCTTGCAATGAAATAGTACGTTGGGGAGAAATT	1920
QY	1921	GCCATGCTTAAGACTGGAGCTAGACACAATGAAACATCAGAGGCCAGCTATAAAAAAAAAA	1980
Db	1921	GCCATGCTTAAGACTGGAGCTAGACACAATGAAACATCAGAGGCCAGCTATAAAAAAAAAA	1980
QY	1981	AAAAAAAAAAAAAAAAAAAAA	2000
Db	1981	AAAAAAAAAAAAAAAAAAAAA	2000
 RESULT 22 US-09-709-729-374 ; Sequence 374, Application US/09709729 ; GENERAL INFORMATION: ; APPLICANT : Xu, Jiangchun ; APPLICANT : Dillon, Davin C. ; APPLICANT : Mitcham, Jennifer L. ; APPLICANT : Harlocker, Susan Louise ; APPLICANT : JIANG YUQU ; APPLICANT : Reed, Steven G. ; APPLICANT : Kalos, Michael ; APPLICANT : Fanger, Gary ; APPLICANT : Retter, Mark ; APPLICANT : SOLK, John ; APPLICANT : Day, Craig ; APPLICANT : Skelky, Yasir A.W. ; APPLICANT : Wang, Aljun ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND ; FILE REFERENCE: 210121.427C22 ; CURRENT APPLICATION NUMBER: US/09/709,729 ; CURRENT FILING DATE: 2000-11-09 ; NUMBER OF SEQ ID NOS: 551 ; SOFTWARE: FastSeq for Windows Version 3.0 ; SEQ ID NO: 374 ; LENGTH: 2000 ; TYPE: DNA ; ORGANISM: Homo sapien US-09-709-729-374			
 Query Match 100.0%; Score 2000; DB 28; Length 2000; Best Local Similarity 100.0%; Pred. No. 6,6e-226; Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	ATGGTGTTGAGGTTGATTCATGCGCGGCTGCTCTTCTGTGAAGAACCATTTGGTCTC	60
Db	1	ATGGTGTTGAGGTTGATTCATGCGCGGCTGCTCTTCTGTGAAGAACCATTTGGTCTC	60
QY	61	AGGACGACATGGGCAAGTGGTGTGCGCTTTCCTGCTGCAGGAGAGCGGCAAG	120
Db	61	AGGACGACATGGGCAAGTGGTGTGCGCTTTCCTGCTGCAGGAGAGCGGCAAG	120
QY	121	ACCAACGTGGGCACTTCTGAGACACAGACGACTCGTATGAAGACACTCAGAGCAAG	180
Db	121	ACCAACGTGGGCACTTCTGAGACACAGACGACTCGTATGAAGACACTCAGAGCAAG	180
QY	181	ATGGGCAAGTGTGCGCACACTGCTTCCCCTCTGCAGGGGGAGTGGCAAGACAAGTG	240

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Db 181 ATGGGCAAGTGGTCCGCGACATGCTTCCCTCTGACAGGGGAGTGGCAAGAGCAACGCG 240
Oy 241 GCGCGTTCTGAGACACAGACGACCTCTGATGAAAGACACTAGAACAAAGTGGGCAAG 300
Db 241 GCGCGTTCTGAGACACAGACGACCTCTGATGAAAGACACTAGAACAAAGTGGGCAAG 300
Oy 301 TGGTCTCCACTGCTCCCTGCTGACAGGGGAGCGGCAAGAGAGTGGGCGCTTGG 360
Db 301 TGGTCTCCACTGCTCCCTGCTGACAGGGGAGCGGCAAGAGAGTGGGCGCTTGG 360
Oy 361 GGAGACTACGATGACAGTGGCTTCTGAGAGCCAGGTACACAGTCCGTGGAGAGATCG 420
Db 361 GGAGACTACGATGACAGTGGCTTCTGAGAGCCAGGTACACAGTCCGTGGAGAGATCG 420
Oy 421 GACAGCTCCACAGAGCTGCTGGTGGGTTAAAGTCCCGAGAAAGATCTCATCTCATG 480
Db 421 GACAGCTCCACAGAGCTGCTGGTGGGTTAAAGTCCCGAGAAAGATCTCATCTCATG 480
Oy 481 CTCAGGACACTGACGCTGAACAGAGAGCAAGCAAAAGAGAGCTGCTTACATCTGGCC 540
Db 481 CTCAGGACACTGACGCTGAACAGAGAGCAAGCAAAAGAGAGCTGCTTACATCTGGCC 540
Oy 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGGACAGAGATGTCACTTAAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGGACAGAGATGTCACTTAAAT 600
Oy 601 GTCTTGGACACAAAAGAGACAGCTGTGATAAAGCCGTCATTCAGAGAGATGAA 660
Db 601 GTCTTGGACACAAAAGAGAGACAGCTGTGATAAAGCCGTCATTCAGAGAGATGAA 660
Oy 661 TGTGGCTTAATGTGTGGAAACATGGGACCTGATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGGCTTAATGTGTGGAAACATGGGACCTGATCCAAATATTCAGATGATGGAAT 720
Oy 721 ACCACTGTGACCTAGCTATCTATATGAAGATTAATGATGCAAAAGCTGCTTAA 780
Db 721 ACCACTGTGACCTAGCTATCTATATGAAGATTAATGATGCAAAAGCTGCTTAA 780
Oy 781 TATGTTGCTGATATGAAATCAAAAAGAGAGCTGCTGATGATGATGATGATGAT 840
Db 781 TATGTTGCTGATATGAAATCAAAAAGAGAGCTGCTGATGATGATGATGATGAT 840
Oy 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTAATGCA 900
Oy 901 CTGATATGATATGAAGAGCTGCTGATCTGATGATGATGATGATGATGATGATGAT 960
Db 901 CTGATATGATATGAAGAGCTGCTGATCTGATGATGATGATGATGATGATGATGAT 960
Oy 961 GTACACCTTCTATCTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAG 1020
Db 961 GTACACCTTCTATCTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAG 1020
Oy 1021 GCCAGAGATATGCTTTCTATGATCATCATGATTAATGATGATGATGATGATGAT 1080
Db 1021 GCCAGAGATATGCTTTCTATGATCATCATGATTAATGATGATGATGATGATGAT 1080
Oy 1081 AAAGAAAAACAGATCTAAAAATCTTCTGAAAAACAGCAATCCAGAACTTAAG 1140
Db 1081 AAAGAAAAACAGATCTAAAAATCTTCTGAAAAACAGCAATCCAGAACTTAAG 1140
Oy 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAAAGCAGTGAAGATGAGCCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAAAGCAGTGAAGATGAGCCAGAGAAA 1200
Oy 1201 ATGTCTCAAGAACCAAGATTAATGATGATGATGATGATGATGATGATGATGATG 1260
Db 1201 ATGTCTCAAGAACCAAGATTAATGATGATGATGATGATGATGATGATGATGATG 1260
Oy 1261 AAGCATGAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
Db 1261 AAGCATGAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1320

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Db 1261 AAGCATGAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
Oy 1321 AATGATGAATTAATGATTAATCTCAAGAGAGACAGACAGCAACGTAATATGCAATTT 1380
Db 1321 AATGATGAATTAATGATTAATCTCAAGAGAGAGACAGACAGCAACGTAATATGCAATTT 1380
Oy 1381 CCTGACAAACGAAAGTGAAGAGATATCAGAAATTTTCAATTAATGATGATGATGATG 1440
Db 1381 CCTGACAAACGAAAGTGAAGAGATATCAGAAATTTTCAATTAATGATGATGATGATG 1440
Oy 1441 AAACAGATCCAAATTAATCTTCTGAAAAACAGCAACCCAGAAACAGATTAAGCTGACA 1500
Db 1441 AAACAGATCCAAATTAATCTTCTGAAAAACAGCAACCCAGAAACAGATTAAGCTGACA 1500
Oy 1501 TCAGAGAGAGTCAACAAAGGCTTGAAGGAGTGAAGAGAGAGAGAGAGAGAGAGAG 1560
Db 1501 TCAGAGAGAGTCAACAAAGGCTTGAAGGAGTGAAGAGAGAGAGAGAGAGAGAGAG 1560
Oy 1561 TTTATGCTATGCAAGAAATGAAGAGACAGAGAGTACTCATGTGATGATGATGATGAT 1620
Db 1561 TTTATGCTATGCAAGAAATGAAGAGACAGAGAGTACTCATGTGATGATGATGATGAT 1620
Oy 1621 CTGACTAATGTCGCACTGCTGCAATGATGATGATGATGATGATGATGATGATGATG 1680
Db 1621 CTGACTAATGTCGCACTGCTGCAATGATGATGATGATGATGATGATGATGATGATG 1680
Oy 1681 AGAACACCTGAAAGCAGCAATTTCTGACACTGAGAAATGAAGAGATATCACAGTACGA 1740
Db 1681 AGAACACCTGAAAGCAGCAATTTCTGACACTGAGAAATGAAGAGATATCACAGTACGA 1740
Oy 1741 CAAATGATATCTCAGAGCAATTTTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
Db 1741 CAAATGATATCTCAGAGCAATTTTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
Oy 1801 AATGATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
Db 1801 AATGATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
Oy 1861 CTTAGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
Db 1861 CTTAGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
Oy 1921 GCCATGCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Db 1921 GCCATGCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Oy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 23
US-09-759-143-374
; Sequence 374, Application US/09759143
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitchem, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jjiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

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;; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
;; FILE REFERENCE: 210121.427C23
;; CURRENT APPLICATION NUMBER: US/09/759,143
;; CURRENT FILING DATE: 2001-01-12
;; NUMBER OF SEQ ID NOS: 934
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 374
;; LENGTH: 2000
;; TYPE: DNA
;; ORGANISM: Homo sapien
US-09-759-143-374

Query Match 100.0%; Score 2000; DB 29; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6,6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTGAAGTGAATTCATCCAGCGGCTCTCTGTGAAGAGCAATTTGGCTC 60
DB 1 ATGGTGGTGAAGTGAATTCATCCAGCGGCTCTCTGTGAAGAGCAATTTGGCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGGTGGCTGGCTTCCCTCTGTCAGGAGGAGCGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGGTGGCTGGCTTCCCTCTGTCAGGAGGAGCGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGACACGACGACTCTCTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTGAGACACGACGACTCTCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGGCGGCGGCTGCTCCCGCTGTCAGGGGGAGTGGCAAGAGCAAGT 240
DB 181 ATGGGCAAGTGGTGGGCGGCGGCTGCTCCCGCTGTCAGGGGGAGTGGCAAGAGCAAGT 240
QY 241 GGGCGCTTCTGAGACACGACGACTCTGTAAGACACTCAGAGCAAGAGTGGGCAAG 300
DB 241 GGGCGCTTCTGAGACACGACGACTCTGTAAGACACTCAGAGCAAGAGTGGGCAAG 300
QY 301 TGGTGGTGGGCACTCTTCCCTCTGTCAGGGGGAGGCGCAAGAGTGGGCGCTTGG 360
DB 301 TGGTGGTGGGCACTCTTCCCTCTGTCAGGGGGAGGCGCAAGAGTGGGCGCTTGG 360
QY 361 GGAAGACTGACATGACAGTGGCTTCTGAGAGCCAGTACCAAGTCCGCGGAGAGATCTG 420
DB 361 GGAAGACTGACATGACAGTGGCTTCTGAGAGCCAGTACCAAGTCCGCGGAGAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTGGCTGGTGGGTAAGTCCCAAGAAAGATCTCATGCTATG 480
DB 421 GACAAGCTCCACAGAGCTGGCTGGTGGGTAAGTCCCAAGAAAGATCTCATGCTATG 480
QY 481 CTCAGGGGCACTGACGTGAACAGAAAGAGCAAGAGAGTGGCTCTTCAATCTGACC 540
DB 481 CTCAGGGGCACTGACGTGAACAGAAAGAGCAAGAGAGTGGCTCTTCAATCTGACC 540
QY 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCTGCTGAGACAGCATGTCACACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAATAGTAAACTCTGCTGAGACAGCATGTCACACTTAAT 600
QY 601 GTCCCTGACAAACAAAAGAGAGAGCTGTGTAAGGCCGTAATCCAGTAAGATGAA 660
DB 601 GTCCCTGACAAACAAAAGAGAGAGCTGTGTAAGGCCGTAATCCAGTAAGATGAA 660
QY 661 TGTGCGCTTAATGTTGCTGGAAACATGGCACTGATCCAAATATTCAGATGATGAAAT 720
DB 661 TGTGCGCTTAATGTTGCTGGAAACATGGCACTGATCCAAATATTCAGATGATGAAAT 720
QY 721 ACCACTGTGACTACGTATCTATTAATGAATTAATTAATGGCAAGAGCTGCTTGA 780
DB 721 ACCACTGTGACTACGTATCTATTAATGAATTAATTAATGGCAAGAGCTGCTTGA 780
QY 781 TATGTCCTGATATCGAATCAAAAAACAGCATGGCTCAGACACGCTTACTTGGTGTGA 840
DB 781 TATGTCCTGATATCGAATCAAAAAACAGCATGGCTCAGACACGCTTACTTGGTGTGA 840
QY 841 CATGAGCAAAAAACGAAAGTGTGAAATTTTAAATCAAAAAAGCAATTTAAATGCA 900

DB 841 CATGAGCAAAAAACGAAAGTGTGAAATTTTAAATCAAAAAAGCAATTTAAATGCA 900
QY 901 CTGATATGATATGGAAGAGTGGCTCTCATCTTCTGATGTTGGATCAGCAAGTATA 960
DB 901 CTGATATGATATGGAAGAGTGGCTCTCATCTTCTGATGTTGGATCAGCAAGTATA 960
QY 961 GTGAGCTTCTACTTGAGCAAAATATGATATCTTCAAGATCTATCTGACAGAGC 1020
DB 961 GTGAGCTTCTACTTGAGCAAAATATGATATCTTCAAGATCTATCTGACAGAGC 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTCGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTTCGACTAC 1080
QY 1081 AAAAGAAAACGATGTAAATAATCTCTGAAAACGACATCCAGAACAGACTTAAG 1140
DB 1081 AAAAGAAAACGATGTAAATAATCTCTGAAAACGACATCCAGAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGTCACAAAGGTTCAAAAGGAGTGAATAATAGCCAGAGAAA 1200
DB 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAAAGGAGTGAATAATAGCCAGAGAAA 1200
QY 1201 ATGTCCTAAGAACCCAGAAATTAATTAAGATGATATGAGAGGTTGAAGAAATGAAG 1260
DB 1201 ATGTCCTAAGAACCCAGAAATTAATTAAGATGATATGAGAGGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
DB 1261 AAGCATGAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
QY 1321 AATGCTAATTAATGATTAATCTCTCAAAAGAGAGCAACACCTGAATAATCAGCAATTT 1380
DB 1321 AATGCTAATTAATGATTAATCTCTCAAAAGAGAGCAACACCTGAATAATCAGCAATTT 1380
QY 1381 CCTGACAAACGAAATGAAAGATATCACAGAAATTTGCCAATTAATGATGATGATGATGAT 1440
DB 1381 CCTGACAAACGAAATGAAAGATATCACAGAAATTTGCCAATTAATGATGATGATGATGAT 1440
QY 1441 AAACAGATGCCAAATATCTCTTGAAGAACGACAAACGACAAAGACTTAAGACTGACA 1500
DB 1441 AAACAGATGCCAAATATCTCTTGAAGAACGACAAACGACAAAGACTTAAGACTGACA 1500
QY 1501 TCAGAGGAGAGTCCAAAGAGCTTGAAGGAGTGAAGAAATGGCCAGCAGAGCTGAATAAT 1560
DB 1501 TCAGAGGAGAGTCCAAAGAGCTTGAAGGAGTGAAGAAATGGCCAGCAGAGCTGAATAAT 1560
QY 1561 TTTATGCTATCGAAGAAATGAAGACAGAGAGTACTCATGTCGATGATGATGATGATGATGAT 1620
DB 1561 TTTATGCTATCGAAGAAATGAAGACAGAGAGTACTCATGTCGATGATGATGATGATGATGAT 1620
QY 1621 CTGACTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
DB 1621 CTGACTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 1681 AGAAGACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAGATACAGAGTACAGAA 1740
DB 1681 AGAAGACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAGATACAGAGTACAGAA 1740
QY 1741 CAAAATATATCTCGAAGCAATTTTGTGAAGAACAGAACTGGAATTAATACAGATGAG 1800
DB 1741 CAAAATATATCTCGAAGCAATTTTGTGAAGAACAGAACTGGAATTAATACAGATGAG 1800
QY 1801 AATCTGATCATGAGAAAGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1860
DB 1801 AATCTGATCATGAGAAAGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 1860
QY 1861 CTTAGTGTGAAGAAAGAGAGATCTTGCATGAAATATGATGATGATGATGATGATGATGAT 1920
DB 1861 CTTAGTGTGAAGAAAGAGAGATCTTGCATGAAATATGATGATGATGATGATGATGATGAT 1920
QY 1921 GCCATGCTAAAGTGAAGTGAAGCAATGAATGATGATGATGATGATGATGATGATGATGAT 1980

Db 1921 GCCATGCTAAGACTGAGCTAGACACATGAATCAATCAGAGCCAGCTAATAAAAAAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 24
US-09-780-669-374
Sequence 374, Application US/09780669

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitchem, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darriick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hurst, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
NUMBER OF SEQ ID NOS: 2001-02-09
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-780-669-374

Query Match 100.0% Score 2000: DB 30: Length 2000:
Best Local Similarity 100.0%: Pred. No. 6.6e-226:
Matches 2000: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Qy 1 ATGCTGTTGAGTGTGATTCATGCGCGGCTGCTCTTCTGTGAAGAACCATTTGGTCTC 60
Db 1 ATGGTGTGAGTGTGATTCATGCGCGGCTGCTCTTCTGTGAAGAACCATTTGGTCTC 60
Qy 61 AGGACAGATGGCAAGTGTGCTGCGCTTCCCTGCTGCAGGAGAGCGGCAAG 120
Db 61 AGGACAGATGGCAAGTGTGCTGCGCTTCCCTGCTGCAGGAGAGCGGCAAG 120
Qy 121 AGCAAGTGGGCACTTCTGGAGACACGACGACTGCTGTATGAAGCACTCAGGAGCAAG 180
Db 121 AGCAAGTGGGCACTTCTGGAGACACGACGACTGCTGTATGAAGCACTCAGGAGCAAG 180
Qy 181 ATGGCAAGTGTGCGCGCACTGCTTCCCTGCTGCAGGAGAGTGGCAAGCAACTG 240
Db 181 ATGGCAAGTGTGCGCGCACTGCTTCCCTGCTGCAGGAGAGTGGCAAGCAACTG 240
Qy 241 GCGCGTTCTGGAGACACGACGACTGCTGTATGAAGCACTCAGGAGCAAGTGGCAAG 300
Db 241 GCGCGTTCTGGAGACACGACGACTGCTGTATGAAGCACTCAGGAGCAAGTGGCAAG 300
Qy 301 TGGTCTGCACTGCTTCCCTGCTGCAGGAGAGCGGCAAGCAAGTGGGCGCTTGG 360
Db 301 TGGTCTGCACTGCTTCCCTGCTGCAGGAGAGCGGCAAGCAAGTGGGCGCTTGG 360
Qy 361 GGAGACTAGATGACAGTGCCTTCTGAGAGCCAGGTACAGTCCGTCGTGAGAGATCTG 420

Db 361 GGAGACTAGATGACAGTGCCTTCTGAGAGCCAGGTACAGTCCGTCGTGAGAGATCTG 420
Qy 421 GACAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCGAAGAGATCTCATTCGTCATG 480
Db 421 GACAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCGAAGAGATCTCATTCGTCATG 480
Qy 481 CTCAGGACACTGAGCTGAACAAGACAAAGCAAGAGAGACTGCTTACATCTGGCC 540
Db 481 CTCAGGACACTGAGCTGAACAAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Qy 541 TCTGCCAATGGGAATTCAGAACTGTAACCTCTGCTGGAGACAGAGATGCACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAACTGTAACCTCTGCTGGAGACAGAGATGCACTTAAT 600
Qy 601 GTCTTGGACAAACAAAGAGGACAGCTGATTAAGAGCCGCTACATGCCAGAGATGAA 660
Db 601 GTCTTGGACAAACAAAGAGGACAGCTGATTAAGAGCCGCTACAAATGCCAGAGATGAA 660
Qy 661 TGTGGCTTAATGTGCTGGAACATGGCACTGATCCAAATATTCCAGATGATGGAAT 720
Db 661 TGTGGCTTAATGTGCTGGAACATGGCACTGATCCAAATATTCCAGATGATGGAAT 720
Qy 721 ACCACTCTGCACTAGCTATCTATATGAAGATTAATTAATGCGCAAGCACTGCTTA 780
Db 721 ACCACTCTGCACTAGCTATCTATATGAAGATTAATTAATGCGCAAGCACTGCTTA 780
Qy 781 TATGGTGTGATATGATCAATCAAAAGCAATGCGCTCACACACTGTTACTGGTGA 840
Db 781 TATGGTGTGATATGATCAATCAAAAGCAATGCGCTCACACACTGTTACTGGTGA 840
Qy 841 CATGAGCAAAACAGCAAGTGGAAATTTAATCAAGAAACGAATTTAATGA 900
Db 841 CATGAGCAAAACAGCAAGTGGAAATTTAATCAAGAAACGAATTTAATGA 900
Qy 901 CTGATATGATATGGAAGACTGCTCATACTGCTGATGTTGTTGATCAGCAACTATA 960
Db 901 CTGATATGATATGGAAGACTGCTCATACTGCTGATGTTGTTGATCAGCAACTATA 960
Qy 961 GTGAGCTTCTACTTGAAGCAAAATATTGATGATCTTCAAGATCTATCTGAGCAGAG 1020
Db 961 GTGAGCTTCTACTTGAAGCAAAATATTGATGATCTTCAAGATCTATCTGAGCAGAG 1020
Qy 1021 GCGAGAGTATGCTGTTCTAGTCAATCATGTAATTTGCGAGTACTTCTGCTAC 1080
Db 1021 GCGAGAGTATGCTGTTCTAGTCAATCATGTAATTTGCGAGTACTTCTGCTAC 1080
Qy 1081 AAGAAACAGATGCTAATAATCTTCTGAAACAGCAATCCAGAACAGACTTAAG 1140
Db 1081 AAGAAACAGATGCTAATAATCTTCTGAAACAGCAATCCAGAACAGACTTAAG 1140
Qy 1141 CTGACATCAGAGAGAGTGCACAAAGGTTCAAGAGCAATTAATGCGCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTGCACAAAGGTTCAAGAGCAATTAATGCGCAGAGAA 1200
Qy 1201 ATGTCCTCAAGAACAGAAATTAATAGATGGATGATGAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGTCCTCAAGAACAGAAATTAATAGATGGATGATGAGAGGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAAGTAATTAATGTTGATTAAGAAACCTGACTAATGTTCACTGCTGAC 1320
Db 1261 AAGCATGAAAGTAATTAATGTTGATTAAGAAACCTGACTAATGTTCACTGCTGAC 1320
Qy 1321 AATGCTGATTAATGATTAATCTCTCAAGAGAGAGCAACCTGAAATATGCAATTT 1380
Db 1321 AATGCTGATTAATGATTAATCTCTCAAGAGAGAGCAACCTGAAATATGCAATTT 1380
Qy 1381 CCTGACAAAGAAAGTAAGATATCACAAATTTGGAATTTAGTTCTGACTACAAAGAA 1440
Db 1381 CCTGACAAAGAAAGTAAGATATCACAAATTTGGAATTTAGTTCTGACTACAAAGAA 1440
Qy 1441 AAACAGATGCCAAATTAATCTTCTGAAACAGCAACCCAGAAACAGACTTAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATTAATCTTCTGAAACAGCAACCCAGAAACAGACTTAAGCTGACA 1500

Db	1441	AAACAGATGCCAAATATCTCTTCTTGAAAACACGACACCCAGAACAAAGACTTAAAGCTGACA	1500
Qy	1501	TCAGAGAGAGAGTCACAAAGGCTTGGAGGCGAGTGAAATATGGCCAGCCAGAGCTAGAAAT	1560
Db	1501	TCAGAGGAAGAAGTCACAAAGGCTTGGAGGCGAGTAAATATGGCCAGCCAGAGCTAGAAAT	1560
Qy	1561	TTTATGGCTATCCAGAAATGAGAAGACACGGAAGTACTCATGTGGGATTCGCCAGAAAC	1620
Db	1561	TTTTATGGCTATCCAGAAATGAGAAGACACGGAAGTACTCATGTGGGATTCGCCAGAAAC	1620
Qy	1621	CTGACTATATGGTGCCACTGCTGGCAATGGTATGATGATGATTATATCTCCCAAGAAAGAC	1680
Db	1621	CTGACTATATGGTGCCACTGCTGGCAATGGTATGATGATGATTATATCTCCCAAGAAAGAC	1680
Qy	1681	AGAACACCTGAAAGCCAGCAATTTCTGTGACACTGAGAAATGAAGAGTATCACAGTGACAA	1740
Db	1681	AGAACACCTGAAAGCCAGCAATTTCTGTGACACTGAGAAATGAAGAGTATCACAGTGACAA	1740
Qy	1741	CAAAATGATACTCAGAAAGCAATTTTGTGAAGACAGACACTGGAAATATTACAGATGAG	1800
Db	1741	CAAAATGATACTCAGAAAGCAATTTTGTGAAGACAGACACTGGAAATATTACAGATGAG	1800
Qy	1801	ATTCGTGATTCATGAGAAAGACGATATGAAAGTGGTGAAGAAATGAATTCAGCTTCT	1860
Db	1801	ATTCGTGATTCATGAGAAAGACGATATGAAAGTGGTGAAGAAATGAATTCAGCTTCT	1860
Qy	1861	CTTAGTGTATGAAGAAAGAAAGACATCTTGCAATGAAATATGATACGTTGGCGGAGAAAT	1920
Db	1861	CTTAGTGTATGAAGAAAGAAAGACATCTTGCAATGAAATATGATACGTTGGCGGAGAAAT	1920
Qy	1921	GCCATGCTAAGACTGGAGCTAGACACACATGAAACATCAGAGCCAGCTAAAAA	1980
Db	1921	GCCATGCTAAGACTGGAGCTAGACACACATGAAACATCAGAGCCAGCTAAAAA	1980
Qy	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAAA 2000	

```

RESULT 25
US-09-810-936-302
Sequence 302, Application US/09810936
GENERAL INFORMATION:
APPLICANT: Fridakis, Tony N.
APPLICANT: Reed, Steven G.
APPLICANT: Smith, John M.
APPLICANT: Misher, Linda E.
APPLICANT: Dillon, Davin C.
APPLICANT: Retter, Marc W.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Harlocker, Susan L.
APPLICANT: Day, Craig H.
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C11
CURRENT APPLICATION NUMBER: US/09/810,936
CURRENT FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 334
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 302
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-810-936-302

```

Query Match	100.0%	Score 2000	DB 31	Length 2000
Best Local Similarity	100.0%	Pred. No. 6.6e-226		
Matches 2000	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	ATGTGCTTGAGCTTGATTCATGCGCGCTGCTCTTCTGTGAAGAGCCATTGGTCTTC	60	
bb	1	ATGGTGGTGTAGCTTGATTCATGCGCGCTGCTCTTCTGTGAAGAGCCATTGGTCTTC	60	

OY	61	AGGAGCAGATGGGCAGTGTGTCTGTGCTTCCCTGCTGCGAGGGAGAGCGGCAG	120
Db	61	AGGAGCAGATGGGCAGTGTGTCTGTGCTTCCCTGCTGCGAGGGAGAGCGGCAG	120
OY	121	AGCAACGTGGGCATTTGTGGAGACCAAGCAGACTGTGCTATGACACACTCAGAGCAG	180
Db	121	AGCAACGTGGGCATTTGTGGAGACCAAGCAGACTGTGCTATGACACACTCAGAGCAG	180
OY	181	ATGGGCAAGTGTGTCCGCCACTGTCCCTGCTGTGAGGGGAGTGGCAAGCAGCTG	240
Db	181	ATGGGCAAGTGTGTCCGCCACTGTCCCTGCTGTGAGGGGAGTGGCAAGCAGCTG	240
OY	241	GGCCCTTCTGGAGCCACGACGACTGTGCTATGAACACTCAGGAAACAGTGGGCAG	300
Db	241	GGCCCTTCTGGAGCCACGACGACTGTGCTATGAACACTCAGGAAACAGTGGGCAG	300
OY	301	TGTGTCTGCACCTGCTTCCCTGCTGCGAGGGGAGCGGCAGAGCAGAGTGGGCGTTGG	360
Db	301	TGTGTCTGCACCTGCTTCCCTGCTGCGAGGGGAGCGGCAGAGCAGAGTGGGCGTTGG	360
OY	361	GGAGACTACGATGTGACACTGTGCTTCAATGAGGCCAGGTACACAGTCCGATGGAGAACTGTG	420
Db	361	GGAGACTACGATGTGACACTGTGCTTCAATGAGGCCAGGTACACAGTCCGATGGAGAACTGTG	420
OY	421	GACAAAGCTCCACAGAGCTGCGTGGTGGGGTAAAGTCCCGAAGAAAGATCTCATCGTCATG	480
Db	421	GACAAAGCTCCACAGAGCTGCGTGGTGGGGTAAAGTCCCGAAGAAAGATCTCATCGTCATG	480
OY	481	CTCAGGAGCAGCTGACGCTGAGAACAAAGAGACCAAGCAAAAGAGACATGCTACATCTGGCC	540
Db	481	CTCAGGAGCAGCTGACGCTGAGAACAAAGAGACCAAGCAAAAGAGACATGCTACATCTGGCC	540
OY	541	TCTGCCAATGGGAATTCAGAAAGTAAAGTAAACTCTCTGACAGACGATGTCAACTTAT	600
Db	541	TCTGCCAATGGGAATTCAGAAAGTAAAGTAAACTCTCTGACAGACGATGTCAACTTAT	600
OY	601	GTCCTTGACAAACAAAAGAGAGACGCTCTGATTAAGGCCGTACATGCCAGAGATGA	660
Db	601	GTCCTTGACAAACAAAAGAGAGACGCTCTGATTAAGGCCGTACATGCCAGAGATGA	660
OY	661	TGTGGTAAATGTGTGTGGAAACATGGGACTGATCCAAATATTCCAGATAGATGAAT	720
Db	661	TGTGGTAAATGTGTGTGGAAACATGGGACTGATCCAAATATTCCAGATAGATGAAT	720
OY	721	ACCACTCTGCACCTACGCTATCTATTAATGAAGATAAATTAATGGCCAAAGCAGCTGCTT	780
Db	721	ACCACTCTGCACCTACGCTATCTATTAATGAAGATAAATTAATGGCCAAAGCAGCTGCTT	780
OY	781	TATGTGCTGTATATTCGAATCAAAAACAGCAGTGGCTCACACACTGTACTTGTGTTA	840
Db	781	TATGTGCTGTATATTCGAATCAAAAACAGCAGTGGCTCACACACTGTACTTGTGTTA	840
OY	841	CATGAGCAAAAACAGCAAGCTGTGAATTTTTTATCAAGAAAAAGCGAATTTAAATCA	900
Db	841	CATGAGCAAAAACAGCAAGCTGTGAATTTTTTATCAAGAAAAAGCGAATTTAAATCA	900
OY	901	CTGATATGATATGGAAGAGCTGCTTCATCTTGGCTGTATGTGTGGATCCACAAGTATA	960
Db	901	CTGATATGATATGGAAGAGCTGCTTCATCTTGGCTGTATGTGTGGATCCACAAGTATA	960
OY	961	GTCAGCCTTCTACTTGGAGCAAAATATTGAATGATCTTCCAGAGATCTATGAGCAGAG	1020
Db	961	GTCAGCCTTCTACTTGGAGCAAAATATTGAATGATCTTCCAGAGATCTATGAGCAGAG	1020
OY	1021	GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC	1080
Db	1021	GCCAGAGATATGCTGTTTCTAGTCATCATCATGTAATTTGCCAGTTACTTCTGACTAC	1080
OY	1081	AAAGAAAAACGATGCTAAAAATCTCTCGAAAACAGCAATCCAGAAACAGACTTAAAG	1140
Db	1081	AAAGAAAAACGATGCTAAAAATCTCTCGAAAACAGCAATCCAGAAACAGACTTAAAG	1140


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Qy 1141 CTGACATCAGAGAGAGTACAAAGTTCAAAAGCCAGTGAATAATAGCCAGCCAGAGAAA 1200
    |||||||
Db 1141 CTGACATCAGAGAGAGTACAAAGTTCAAAAGCCAGTGAATAATAGCCAGCCAGAGAAA 1200
Qy 1201 ATGTCTCAAGAACCGAAATTAATAGATGTGTATAGAGAGTTGAGAGAGAAATGAAG 1260
    |||||||
Db 1201 ATGTCTCAAGAACCGAAATTAATAGATGTGTATAGAGAGTTGAGAGAGAAATGAAG 1260
Qy 1261 AAGCATGAAGATTAATATGTGGATTACTAGAAAACCTGACTAATAGTGTCTCCTGTGCG 1320
    |||||||
Db 1261 AAGCATGAAGATTAATATGTGGATTACTAGAAAACCTGACTAATAGTGTGTCTCCTGTGCG 1320
Qy 1321 AATGTTGATTAATGATTAATCTTCAAAAGAGAGAGAGAACCTGAAAATAGCAATTT 1380
    |||||||
Db 1321 AATGTTGATTAATGATTAATCTTCAAAAGAGAGAGAGAACCTGAAAATAGCAATTT 1380
Qy 1381 CCTGACAAACGAAAGTGAAGAGTATCAGAGAAATTTGGGAATTTGTTTCTGACTACAAAGAA 1440
    |||||||
Db 1381 CCTGACAAACGAAAGTGAAGAGTATCAGAGAAATTTGGGAATTTGTTTCTGACTACAAAGAA 1440
Qy 1441 AAACGATGCCAAATTAATCTTCTGAAAACAGCAACCCGAAACAGACTTAAGAGTGACA 1500
    |||||||
Db 1441 AAACGATGCCAAATTAATCTTCTGAAAACAGCAACCCGAAACAGACTTAAGAGTGACA 1500
Qy 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGGCAGTGAATAATGGCCAGGACAGAGCTAGAAAAT 1560
    |||||||
Db 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGGCAGTGAATAATGGCCAGGACAGAGCTAGAAAAT 1560
Qy 1561 TTTATGCTATGGAAGAAATGAAGAACGACGAGTACTCATGTGGGATTTCCAGAAAAC 1620
    |||||||
Db 1561 TTTATGCTATGGAAGAAATGAAGAACGACGAGTACTCATGTGGGATTTCCAGAAAAC 1620
Qy 1621 CTGACTAATGTTGGTCCACTGCTGGCAATGGTGTATGATGATTAATTCCTCCAGAGAAAGAC 1680
    |||||||
Db 1621 CTGACTAATGTTGGTCCACTGCTGGCAATGGTGTATGATGATTAATTCCTCCAGAGAAAGAC 1680
Qy 1681 AGAACACCTGAAAGCCAGCAATTTCTCTGACACTGAGAAATGAGAGATATACAGTGACGAA 1740
    |||||||
Db 1681 AGAACACCTGAAAGCCAGCAATTTCTCTGACACTGAGAAATGAGAGATATACAGTGACGAA 1740
Qy 1741 CAAATGATCTCAGAGCAATTTTGTGAAGAACAGACACTGGAATTTTACACGATGAG 1800
    |||||||
Db 1741 CAAATGATCTCAGAGCAATTTTGTGAAGAACAGACACTGGAATTTTACACGATGAG 1800
Qy 1801 ATTCTGATTCATGAGAAAGAGAGATAGAAAGTGTGAATAATGAATCTGAGCTTCT 1860
    |||||||
Db 1801 ATTCTGATTCATGAGAAAGAGAGATAGAAAGTGTGTGAATAATGAATCTGAGCTTCT 1860
Qy 1861 CTTAGTTGTAGAGAAAGAGACATCTTGATGAATAATAGTACGTTGGGGAGAAATTT 1920
    |||||||
Db 1861 CTTAGTTGTAGAGAAAGAGACATCTTGATGAATAATAGTACGTTGGGGAGAAATTT 1920
Qy 1921 GCCATGCTTAAGCTGAGCTAGACACATGAATGAATGAGCAGCTTAAGAGAGAGAGAG 1980
    |||||||
Db 1921 GCCATGCTTAAGCTGAGCTAGACACATGAATGAGCAGCTTAAGAGAGAGAGAG 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
    |||||||
Db 1981 AAAAAAAAAAAAAAAAAA 2000
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RESULT 26
US-09-822-827-374
: Sequence 374, Application US/09822827
: GENERAL INFORMATION:
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: APPLICANT: Xu, Jiangchun
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: FILE REFERENCE: 210121.534C1
: CURRENT APPLICATION NUMBER: US/09/822,827
: CURRENT FILING DATE: 2001-03-28
: NUMBER OF SEQ ID NOS: 982
: SOFTWARE: FastSeq for Windows Version 3.0
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: SEQ ID NO 374
: LENGTH: 2000
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-822-827-374
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Query Match          100.0%; Score 2000; DB 31; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6,6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 ATGTGCTTGAGGTGATTCATGCCGCTGCTTCTGTGAAGAGCAATTTGGTCTC 60
    |||||||
Db 1 ATGTGCTTGAGGTGATTCATGCCGCTGCTTCTGTGAAGAGCAATTTGGTCTC 60
Qy 61 AGAGAGCAATGAGGCAAGTGTGCTGCTGCTTCCCTGCTGAGGAGAGGCGCAAG 120
    |||||||
Db 61 AGAGAGCAATGAGGCAAGTGTGCTGCTGCTTCCCTGCTGAGGAGAGGCGCAAG 120
Qy 121 AGCAAGTGGGCACTTCTGAGACACGACGACTGCTATGAAGACACTCAGAGCAAG 180
    |||||||
Db 121 AGCAAGTGGGCACTTCTGAGACACGACGACTGCTATGAAGACACTCAGAGCAAG 180
Qy 181 ATGGGCAATGTTGCCGCTGCTTCCCTGCTGAGGAGAGTGGCAAGCAAGCTG 240
    |||||||
Db 181 ATGGGCAATGTTGCCGCTGCTTCCCTGCTGAGGAGAGTGGCAAGCAAGCTG 240
Qy 241 GGGCGTTCTGGAGACACGACGACTGCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
    |||||||
Db 241 GGGCGTTCTGGAGACACGACGACTGCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
Qy 301 TGGTGTGCTGCACTGCTTCCCTGCTGAGGAGGAGCGCAAGCAAGTGGGCGCTTG 360
    |||||||
Db 301 TGGTGTGCTGCACTGCTTCCCTGCTGAGGAGGAGCGCAAGCAAGTGGGCGCTTG 360
Qy 361 GGAAGCTACGATGACAGTCCCTTATGAGAGCCAGTACACAGTCCGTGGAGAAATCTG 420
    |||||||
Db 361 GGAAGCTACGATGACAGTCCCTTATGAGAGCCAGTACACAGTCCGTGGAGAAATCTG 420
Qy 421 GAAAGCTCAGAGAGCTGCTGAGTGAAGTCCCAAGAAAGATGTCATCGCATG 480
    |||||||
Db 421 GAAAGCTCAGAGAGCTGCTGAGTGAAGTCCCAAGAAAGATGTCATCGCATG 480
Qy 481 CTCAGGAGACCTGACCTGTAACAAAGAGCAAGCAAGAGCACTGCTACATCTGGCC 540
    |||||||
Db 481 CTCAGGAGACCTGACCTGTAACAAAGAGCAAGCAAGAGCACTGCTACATCTGGCC 540
Qy 541 TCTGCCAATGGGAATTCAGAGATGTAATACTCTGCTGACAGAGATGCACTTAAT 600
    |||||||
Db 541 TCTGCCAATGGGAATTCAGAGATGTAATACTCTGCTGACAGAGATGCACTTAAT 600
Qy 601 GTGCGTTGATGTTGCTGGAACATGGCACTGATCCAAATATTCACAGATGATGGAAT 720
    |||||||
Db 601 GTGCGTTGATGTTGCTGGAACATGGCACTGATCCAAATATTCACAGATGATGGAAT 720
Qy 721 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCACAGATGATGGAAT 780
    |||||||
Db 721 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCACAGATGATGGAAT 780
Qy 781 TATGTTGCTGATATGAATCAAAAAACAAGCATGGCTCACACCACTGTTACTGTGTA 840
    |||||||
Db 781 TATGTTGCTGATATGAATCAAAAAACAAGCATGGCTCACACCACTGTTACTGTGTA 840
Qy 841 CATGACCAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
    |||||||
Db 841 CATGACCAAAAACAGCAAGTGGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Qy 901 CTGATGATGATGGAAGAGCTGCTCATACTGCTGTAATGTTGTGATCAGCAAGTATA 960
    |||||||
Db 901 CTGATGATGATGGAAGAGCTGCTCATACTGCTGTAATGTTGTGATCAGCAAGTATA 960
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QY 961 GTCAGCCTTCTACTTGAGCAAAATATTGATATCTTCTCAAGATCTATCTGACAGACG 1020
    |||||||
Db 961 GTCAGCCTTCTACTTGAGCAAAATATTGATATCTTCTCAAGATCTATCTGACAGACG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATTAATTTGCCGTTACTTTCGTACTAC 1080
    |||||||
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATTAATTTGCCGTTACTTTCGTACTAC 1080
QY 1081 AAAGAAAAACGATGCTAAATAATCTCTTCGAAAAACGCAATCCAGAAACAACTTAAG 1140
    |||||||
Db 1081 AAAGAAAAACGATGCTAAATAATCTCTTCGAAAAACGCAATCCAGAAACAACTTAAG 1140
QY 1141 CTGACATCAGAGAAAGATCACAAGGCTTCAAGAGCAGTGAATAATAGCCAGAGAAA 1200
    |||||||
Db 1141 CTGACATCAGAGAAAGATCACAAGGCTTCAAGAGCAGTGAATAATAGCCAGAGAAA 1200
QY 1201 ATGCTCTAAGAACCAAGAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAATGAG 1260
    |||||||
Db 1201 ATGCTCTAAGAACCAAGAAATTAATTAAGATGCTGATAGAGAGTTGAAGAAATGAG 1260
QY 1261 AAGCATGAAGTATATATGTTGGATTAAGTAAACCTGACTATGTTGCTACTGCTGCG 1320
    |||||||
Db 1261 AAGCATGAAGTATATATGTTGGATTAAGTAAACCTGACTATGTTGCTACTGCTGCG 1320
QY 1321 AATGCTATATGATGATTAATTTCTCAAGAGAAAGCAGAACACCTGAAATCAGCAATTT 1380
    |||||||
Db 1321 AATGCTATATGATGATTAATTTCTCAAGAGAAAGCAGAACACCTGAAATCAGCAATTT 1380
QY 1381 CTTGACACAGCAAGATGAAGATATCACAGAAATTTGCCAATTAATTTGCTACTACAAAG 1440
    |||||||
Db 1381 CTTGACACAGCAAGATGAAGATATCACAGAAATTTGCCAATTAATTTGCTACTACAAAG 1440
QY 1441 AAACAGATGCCAAATATCTCTTCTGAAGAACAGCAACCAAGCAAGACTTAACCTACA 1500
    |||||||
Db 1441 AAACAGATGCCAAATATCTCTTCTGAAGAACAGCAACCAAGCAAGACTTAACCTACA 1500
QY 1501 TCAGAGGAAGAGTCAACAAAGGCTTGAGGCGAGTGAATAATGGCCAGCCAGAGCTGAAA 1560
    |||||||
Db 1501 TCAGAGGAAGAGTCAACAAAGGCTTGAGGCGAGTGAATAATGGCCAGCCAGAGCTGAAA 1560
QY 1561 TTTATGCTATCGAAGAAATGAAGAACACGGAAGTACTCATGTCGGAATTCGCCGAAAAC 1620
    |||||||
Db 1561 TTTATGCTATCGAAGAAATGAAGAACACGGAAGTACTCATGTCGGAATTCGCCGAAAAC 1620
QY 1621 CTGACTAATGATGCTGCTGCGCATGATGATGATGATTAATTTCTCCAAAGGAAGAGC 1680
    |||||||
Db 1621 CTGACTAATGATGCTGCTGCGCATGATGATGATGATTAATTTCTCCAAAGGAAGAGC 1680
QY 1681 AGAACACCTGAAGCCAGCAATTTCTGACACTGGAATGAAGATACACAGTGAAGAA 1740
    |||||||
Db 1681 AGAACACCTGAAGCCAGCAATTTCTGACACTGGAATGAAGATACACAGTGAAGAA 1740
QY 1741 CAAAAATATATCTGAGAGCAATTTTGTGAAGAACAGAACTGGAATTTACACAGATGAG 1800
    |||||||
Db 1741 CAAAAATATATCTGAGAGCAATTTTGTGAAGAACAGAACTGGAATTTACACAGATGAG 1800
QY 1801 ATTCTGATGATGAAGAAAGCAGATGAAGTGGTGAATAAATGAATTCGAGCTTCT 1860
    |||||||
Db 1801 ATTCTGATGATGAAGAAAGCAGATGAAGTGGTGAATAAATGAATTCGAGCTTCT 1860
QY 1861 CTTAGTTGAAGAAAGAAAGACATCTTGCATGAAATAGTACGTTGCGGGAAGAAATTT 1920
    |||||||
Db 1861 CTTAGTTGAAGAAAGAAAGACATCTTGCATGAAATAGTACGTTGCGGGAAGAAATTT 1920
QY 1921 GCCATGCTAAGACTGAGCTGAGACAAATGAACATCAGAGCCAGTAAAAAAGAAAAA 1980
    |||||||
Db 1921 GCCATGCTAAGACTGAGCTGAGACAAATGAACATCAGAGCCAGTAAAAAAGAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAA 2000
    |||||||
Db 1981 AAAAAAAAAAAAAAAAAA 2000
```

```
RESULT 27
US-09-825-301-6
: Sequence 6, Application us/09825301
: GENERAL INFORMATION:
: APPLICANT: Houghton, Raymond L.
: APPLICANT: Dillon, David C.
: APPLICANT: Molesh, David A.
: APPLICANT: Xu, Jiangchun
: APPLICANT: Zehentner, Barbara
: APPLICANT: Persing, David H.
: TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
: OF INVENTION: AND MONITORING OF BREAST CANCER
: FILE REFERENCE: 210121.513
: CURRENT APPLICATION NUMBER: US/09/825,301
: CURRENT FILING DATE: 2001-04-02
: NUMBER OF SEQ ID NOS: 77
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 6
: LENGTH: 2000
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-825-301-6

Query Match      100.0%; Score 2000; DB 31; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6, 6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTGTTGAGTTGATTCATATCCGCTGCTCTTCTGTGAAGAACCTATTGCTCTC 60
    |||||||
Db 1 ATGTTGTTGAGTTGATTCATATCCGCTGCTCTTCTGTGAAGAACCTATTGCTCTC 60
QY 61 AGAGCAAGATGGGCAAGTGGTGGCTGCTGCTTCCCTCTCAGAGAGAGCGGCAAG 120
    |||||||
Db 61 AGAGCAAGATGGGCAAGTGGTGGCTGCTGCTTCCCTCTCAGAGAGAGCGGCAAG 120
QY 121 AGCAAGCTGGGCACTTGTGAGACACAGACACTCTCTATGAAGACACTCAGAGCAAG 180
    |||||||
Db 121 AGCAAGCTGGGCACTTGTGAGACACAGACACTCTCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
    |||||||
Db 181 ATGGGCAAGTGGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 241 GGCGCTTCTGAGAGCCAGACGACTGCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
    |||||||
Db 241 GGCGCTTCTGAGAGCCAGACGACTGCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
QY 301 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
    |||||||
Db 301 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 361 GGAACATGACATGACATGCTTATGAGGCGGCAAGCAAGTGGGCAAGATCTG 420
    |||||||
Db 361 GGAACATGACATGACATGCTTATGAGGCGGCAAGCAAGTGGGCAAGATCTG 420
QY 421 GACACGCTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
    |||||||
Db 421 GACACGCTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 CTCAGGACACATGACATGACATGACATGACATGACATGACATGACATGACATGAC 540
    |||||||
Db 481 CTCAGGACACATGACATGACATGACATGACATGACATGACATGACATGACATGAC 540
QY 541 TCTGCAATGGGAATTAAGAAATGATTAATCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
    |||||||
Db 541 TCTGCAATGGGAATTAAGAAATGATTAATCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
QY 601 GTCTTGAACAACAAAAAGAGAGAGCTGCTGTAAGGCGGTACAAATCCAGGAAGTAA 660
    |||||||
Db 601 GTCTTGAACAACAAAAAGAGAGAGCTGCTGTAAGGCGGTACAAATCCAGGAAGTAA 660
QY 661 TGTGCTTAAATGTTGCTGGAACATGGCCTGATCCAAATATTCAGATGATGAAAT 720
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|||||
Db 661 TGTGGTTAATGTGTGCGAATGCGACATGCCAAATATTCAGATGATGAAAT 720
QY 721 ACCATCTGCACTAGCTATCTATATGAAGATTAATTAATGCGCAACACTGCTTAA 780
Db 721 ACCATCTGCACTAGCTATCTATATGAAGATTAATTAATGCGCAACACTGCTTAA 780
QY 781 TATGTTGCTGATATGCAATCAAAAAACAAGCATGGCCCTCACACACTGTACTGGTGA 840
Db 781 TATGTTGCTGATATGCAATCAAAAAACAAGCATGGCCCTCACACACTGTACTGGTGA 840
QY 841 CATGAGCAAAAAACAGCAAGCTGTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGA 900
Db 841 CATGAGCAAAAAACAGCAAGCTGTGAAATTTTAAATCAAGAAAAAGCGAATTTAAATGA 900
QY 901 CTTGATATGATATGAAAGGCTGCTCATACCTGCTATGTTGTTGGATCAGCAAGTATA 960
Db 901 CTTGATATGATATGAAAGGCTGCTCATACCTGCTATGTTGTTGGATCAGCAAGTATA 960
QY 961 GTGACGCTTCTACTTGAGCAAAATATGATGTATCTTCAAGATCTATCTGGACAGAG 1020
Db 961 GTGACGCTTCTACTTGAGCAAAATATGATGTATCTTCAAGATCTATCTGGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
QY 1081 AAGAGAAAAACATGCTAAATAATCTTCTGAAACAGCAATCCAGAACAAAGCTTAAAG 1140
Db 1081 AAGAGAAAAACATGCTAAATAATCTTCTGAAACAGCAATCCAGAACAAAGCTTAAAG 1140
QY 1141 CTGACATCGAGAGAGAGTCAAAAGGTTCAAAAGGAGTGAATAATGGCCAGCAGAGAA 1200
Db 1141 CTGACATCGAGAGAGAGTCAAAAGGTTCAAAAGGAGTGAATAATGGCCAGCAGAGAA 1200
QY 1201 ATGTCTCAAGAAACAGAAATTAATGAAGTGTGATAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAAACAGAAATTAATGAAGTGTGATAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
Db 1261 AAGCATGAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
QY 1321 AATGTGATATGATTAATCTCTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1321 AATGTGATATGATTAATCTCTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGAAATTAATGTTCTGACTACAAAG 1440
Db 1381 CCTGACAAAGAAAGTGAAGATATCAAGAAATTTGGAAATTAATGTTCTGACTACAAAG 1440
QY 1441 AAGAGATGCCAAATATCTCTTCTGAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db 1441 AAGAGATGCCAAATATCTCTTCTGAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGCGAGTGAATAATGGCCAGCAGAGAGAGAA 1560
Db 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGCGAGTGAATAATGGCCAGCAGAGAGAGAA 1560
QY 1561 TTTATGCTATGCAAGAAATGAAGAGCAAGAGTACTATGTCGATTCGATTTCCAGAAA 1620
Db 1561 TTTATGCTATGCAAGAAATGAAGAGCAAGAGTACTATGTCGATTCGATTTCCAGAAA 1620
QY 1621 CTGACTAATATGCTGCTGCTGCAATGATGATGATTAATTTCTCCAGAGAGAGAG 1680
Db 1621 CTGACTAATATGCTGCTGCTGCAATGATGATGATTAATTTCTCCAGAGAGAGAG 1680
QY 1681 AGAAGCAAGTGAAGAGCAAGTCTGACATGAGAAATGAAGAGATACAGGTGAGAG 1740
Db 1681 AGAAGCAAGTGAAGAGCAAGTCTGACATGAGAAATGAAGAGATACAGGTGAGAG 1740
QY 1741 CAAAATGATATCTAGAAAGATTTTGTGAAGAACAGAACTGATATTTACACAGATGAG 1800
Db 1741 CAAAATGATATCTAGAAAGATTTTGTGAAGAACAGAACTGATATTTACACAGATGAG 1800
```

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Db 1741 CAAAATGATATCTAGAAAGATTTTGTGAAGAACAGAACTGATATTTACACAGATGAG 1800
QY 1801 ATTCTGATATCAAGAAAGAGAGATAGAGTGTGAAGAAATGAATTCGTGACTTCT 1860
Db 1801 ATTCTGATATCAAGAAAGAGAGATAGAGTGTGAAGAAATGAATTCGTGACTTCT 1860
QY 1861 CTATGTTTGAAGAAAGAAAGACATCTGCAATGAATAATGATACCTTGGCGGAGAAAT 1920
Db 1861 CTATGTTTGAAGAAAGAAAGACATCTGCAATGAATAATGATACCTTGGCGGAGAAAT 1920
QY 1921 GCCATGCTAAGAGTGGAGCTAGACACATGAATGAACATCAGAGCCAGCTAAAAA 1980
Db 1921 GCCATGCTAAGAGTGGAGCTAGACACATGAATGAACATCAGAGCCAGCTAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 28
US-09-852-911-374
; Sequence 374, Application US/09852911
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedyck, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C25
; CURRENT APPLICATION NUMBER: US/09/852,911
; CURRENT FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-852-911-374

Query Match 100.0%; Score 2000; DB 32; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6.6e-226; Indels 0; Gaps 0;
Matches 2000; Conservative 0; Mismatches 0;

QY 1 ATGTGTTGAGTGTATTCATGCGGCTGCTTCTGTGAAGAGCAATTTGGCTTC 60
Db 1 ATGTGTTGAGTGTATTCATGCGGCTGCTTCTGTGAAGAGCAATTTGGCTTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGTTCCTGCTGAGAGAGAGAGAGAG 120
Db 61 AGGAGCAAGATGGGCAAGTGTGCTGCGTTCCTGCTGAGAGAGAGAGAGAG 120
QY 121 AGCAAGCTGGGCACTTCTGAGACACAGAGACTGTGCTATGAAGCACTCAGAGCAAG 180
Db 121 AGCAAGCTGGGCACTTCTGAGACACAGAGACTGTGCTATGAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGAGAGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGAGAGGAGTGGCAAGCAAGCTG 240
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Db 181 ATGGGCAAGTGTGTCGGCTGCTCCCTGCTGACAGGGGAGGCGCAAGCAACGTG 240
Oy 241 GGGCGTTGTGAGACACAGACACTGCTATGAAGACACAGGAACAAAGATGGGAG 300
Db 241 GGGCGTTGTGAGACACAGACACTGCTATGAAGACACAGGAACAAAGATGGGAG 300
Oy 301 TGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 301 TGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Oy 361 GGAAGCTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTAC 420
Db 361 GGAAGCTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTAC 420
Oy 421 GACAAGCTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 421 GACAAGCTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Oy 481 CTCAGGACACTGACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTAC 540
Db 481 CTCAGGACACTGACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTAC 540
Oy 541 TCTGCTCAATGGGAATTCAGAAAGTAAACTCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 541 TCTGCTCAATGGGAATTCAGAAAGTAAACTCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Oy 601 GTCTCTGACAAAGAAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 601 GTCTCTGACAAAGAAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Oy 661 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 661 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Oy 721 ACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 721 ACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Oy 781 TATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 781 TATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Oy 841 CATGAGCAAAAGACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATCA 900
Db 841 CATGAGCAAAAGACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATCA 900
Oy 901 CTGATGATATGGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 901 CTGATGATATGGAAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Oy 961 GTCAGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Db 961 GTCAGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Oy 1021 GCCAGAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
Db 1021 GCCAGAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
Oy 1081 AAAAGAAAAAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
Db 1081 AAAAGAAAAAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
Oy 1141 CTGACATCAGAGAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
Db 1141 CTGACATCAGAGAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
Oy 1201 ATGCTCAAGAGAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
Db 1201 ATGCTCAAGAGAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
Oy 1261 AAGATGAAGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320

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Db 1261 AAGATGAAGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
Oy 1321 AATGCTGATATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1321 AATGCTGATATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Oy 1381 CCTGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Db 1381 CCTGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
Oy 1441 AAACAGATGCCAAATFATCTTCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Db 1441 AAACAGATGCCAAATFATCTTCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
Oy 1501 TCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Db 1501 TCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
Oy 1561 TTTATGCTATCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
Db 1561 TTTATGCTATCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
Oy 1621 CTGACTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
Db 1621 CTGACTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
Oy 1681 AGAACACCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Db 1681 AGAACACCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Oy 1741 CAAATGATCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
Db 1741 CAAATGATCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800
Oy 1801 APTCTGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
Db 1801 APTCTGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
Oy 1861 CTTAGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
Db 1861 CTTAGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
Oy 1921 GCCATGCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Db 1921 GCCATGCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
Oy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 29
US-09-895-793-374
; Sequence 374, Application US/09895793
; GENERAL INFORMATION:
; APPLICANT: Xu, JIANGCHUN
; APPLICANT: Dillon, David C.
; APPLICANT: Mitchem, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retler, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: L1, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.

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APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-895-793-374

Query Match 100.0%; Score 2000; DB 33; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6,66-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGTGAGTGTGATTCATGCGGCTGCTCTGTGGAAGAGCATTTGGTCTC 60
DB 1 ATGGTGTGAGTGTGATTCATGCGGCTGCTCTGTGGAAGAGCATTTGGTCTC 60
QY 61 AGGAGCAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGCGAGGAGAGCGGCAAG 120
DB 61 AGGAGCAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGCGAGGAGAGCGGCAAG 120
QY 121 ACCAAGCTGGGCACTTCTGGAAGCAGCAGACCTGCTATGAAGACCTCAGGACAG 180
DB 121 ACCAAGCTGGGCACTTCTGGAAGCAGCAGACCTGCTATGAAGACCTCAGGACAG 180
QY 181 ATGGGCAATGTCGCGGCACTGCTTCCCTGCTGAGGGGGAGTGGCAAGACGTG 240
DB 181 ATGGGCAATGTCGCGGCACTGCTTCCCTGCTGAGGGGGAGTGGCAAGACGTG 240
QY 241 GCGCTTCTGAGACAGCAGACCTGCTATGAAGACCTCAGGACAGTGGGCAAG 300
DB 241 GCGCTTCTGAGACAGCAGACCTGCTATGAAGACCTCAGGACAGTGGGCAAG 300
QY 301 TGGTGTGCTGCTGCTTCCCTGCTGAGGGGGAGGCGGCAAGAGTGGGCGCTTG 360
DB 301 TGGTGTGCTGCTGCTTCCCTGCTGAGGGGGAGGCGGCAAGAGTGGGCGCTTG 360
QY 361 GGAAGCTAGATGACAGTCTTCATGAGCCAGGTACCACTCCGTGGAGAAATCTG 420
DB 361 GGAAGCTAGATGACAGTCTTCATGAGCCAGGTACCACTCCGTGGAGAAATCTG 420
QY 421 GACAAGCTCAGAGAGCTGCTGAGGGTAAAGTCCCGAAGAGATGCTCATGCTCATG 480
DB 421 GACAAGCTCAGAGAGCTGCTGAGGGTAAAGTCCCGAAGAGATGCTCATGCTCATG 480
QY 481 CTCAGGAGACCTGAGTGAACAAGAGCAAGCAAGAGAGAGCTCTCATCTGCGCC 540
DB 481 CTCAGGAGACCTGAGTGAACAAGAGCAAGCAAGAGAGAGCTCTCATCTGCGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGAGCAGAGAGTCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGAGCAGAGAGTCAACTTAAT 600
QY 601 GTCTCTGACAAAGAGAGAGCTGATTAAGGCGGTACATGCGCAGAAATGAA 660
DB 601 GTCTCTGACAAAGAGAGAGCTGATTAAGGCGGTACATGCGCAGAAATGAA 660
QY 661 TGTGCGTAAATGTGCTGAGACAGTGTATCAAAATATTCAGATGATGGAAT 720
DB 661 TGTGCGTAAATGTGCTGAGACAGTGTATCAAAATATTCAGATGATGGAAT 720
QY 721 ACCAGCTGACAGCTATCTATATGAAGATTAATTAATGCGCAAGACGCTCTTA 780
DB 721 ACCAGCTGACAGCTATCTATATGAAGATTAATTAATGCGCAAGACGCTCTTA 780

QY 781 TATGTGCTGATATCGAATCAAAAAACAGCATGCGCTCACACCACTGTTAGTGTGA 840
DB 781 TATGTGCTGATATCGAATCAAAAAACAGCATGCGCTCACACCACTGTTAGTGTGA 840
QY 841 CATGACAAAAACAGCAAGTCTGAAATTTTATATCAAGAAAAACGAATTTAAATGCA 900
DB 841 CATGACAAAAACAGCAAGTCTGAAATTTTATATCAAGAAAAACGAATTTAAATGCA 900
QY 901 CTGATAGATATGGAAGAGAGTCTCATCTGCTGATGCTGATGCTGAGTACAGCAATTA 960
DB 901 CTGATAGATATGGAAGAGAGTCTCATCTGCTGATGCTGATGCTGAGTACAGCAATTA 960
QY 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATATCTTCTCAAGATCATCTGAGACAG 1020
DB 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATATCTTCTCAAGATCATCTGAGACAG 1020
QY 1021 GCCAGAGATATGCTGTTCTGATCATCATATGTAATTTGCCAGTTACTTTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTCTGATCATCATATGTAATTTGCCAGTTACTTTGACTAC 1080
QY 1081 AAGAAAAACAGATGCTAAAAATCTCTGGAAGACAGCAATCCAGAACAGCTTAAAG 1140
DB 1081 AAGAAAAACAGATGCTAAAAATCTCTGGAAGACAGCAATCCAGAACAGCTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCAACAAGGTTCAAAAGCAGTGAATAATGAGCCAGAGAAA 1200
DB 1141 CTGACATCAGAGAGAGAGTCAACAAGGTTCAAAAGCAGTGAATAATGAGCCAGAGAAA 1200
QY 1201 ATGTCTCAAGACCAAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAAATGAA 1260
DB 1201 ATGTCTCAAGACCAAGAAATTAATTAAGATGATGATGAGAGGTTGAAGAAATGAA 1260
QY 1261 AAGCATGAAGATATATGAGGATATCTGAAAGCACTGATATGATGCTGCTGCTG 1320
DB 1261 AAGCATGAAGATATATGAGGATATCTGAAAGCACTGATATGATGCTGCTGCTGCTG 1320
QY 1321 AATGCTGATATGATTAATCTCTCAAGAGAGAGAGCAACACCTGAAATAGCAATTT 1380
DB 1321 AATGCTGATATGATTAATCTCTCAAGAGAGAGAGCAACACCTGAAATAGCAATTT 1380
QY 1381 CCGTGAACAGAAAGTGAAGATATCAACAGATTTGCGAATTAAGTTCTGACTCAAAAGAA 1440
DB 1381 CCGTGAACAGAAAGTGAAGATATCAACAGATTTGCGAATTAAGTTCTGACTCAAAAGAA 1440
QY 1441 AAACAGATGCCAAATATCTTCTGAAAGCAGAACCCAGAACAAAGCTTAAAGCTGACA 1500
DB 1441 AAACAGATGCCAAATATCTTCTGAAAGCAGAACCCAGAACAAAGCTTAAAGCTGACA 1500
QY 1501 TCAGAGGAGAGTCAACAAGGCTTGAAGGCGAGTGAATAATGGCCAGAGCTAGAAAAT 1560
DB 1501 TCAGAGGAGAGTCAACAAGGCTTGAAGGCGAGTGAATAATGGCCAGAGCTAGAAAAT 1560
QY 1561 TTTATGGCTATCGAAGAAATGAAGAGCAAGCAAGTACTATGCGAATTCACAGAAAC 1620
DB 1561 TTTATGGCTATCGAAGAAATGAAGAGCAAGCAAGTACTATGCGAATTCACAGAAAC 1620
QY 1621 CTGACTAATGCTGCCACTGCTGCAATGCTGATGATGATTAATTTCTCCAAAGAAAGC 1680
DB 1621 CTGACTAATGCTGCCACTGCTGCAATGCTGATGATGATTAATTTCTCCAAAGAAAGC 1680
QY 1681 AGAACACTGTAAGAGCAGCAATTTCTGACACTGAGAAATGAAGATATCAATGACGAA 1740
DB 1681 AGAACACTGTAAGAGCAGCAATTTCTGACACTGAGAAATGAAGATATCAATGACGAA 1740
QY 1741 CAAATGATATCTGAGAAATTTTGAAGAACAGACACTGGAATATATACAGATGAG 1800
DB 1741 CAAATGATATCTGAGAAATTTTGAAGAACAGACACTGGAATATATACAGATGAG 1800
QY 1801 ATTCTGATTCATGAAGAAAGAGATAGAGTGGTGAAGAAATGAATTTGAGCTTTCT 1860
DB 1801 ATTCTGATTCATGAAGAAAGAGATAGAGTGGTGAAGAAATGAATTTGAGCTTTCT 1860
QY 1861 CTATGTTGTAAAGAAAAAAGACATCTTGCAATGAATAATAGTATGCTGGGAAAGAAAT 1920

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|||||
Db 1861 CTTAGTTGTAAGAAAGAAAAAGACATCTTCATGATAAATAAGTTCGGGGAAGAAAT 1920
QY 1921 GCCATGCTAGACGTGAGCTGACACAATGAATCATGAGACCCAGCTTAAATAAAAA 1980
Db 1921 GCCATGCTAGACGTGAGCTGACACAATGAATCATGAGACCCAGCTTAAATAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 30
US-09-895-814-374
; Sequence 374, Application US/09895814
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-895-814-374

Query Match 100.0%; Score 2000; DB 33; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6.6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 241 GCGCTTCTGAGACACAGAGACTGCTATGAAGACACTCAGGAACAGATGGCAAG 300
QY 301 TGTGCTGCCACTGCTTCCCTGGTGCAGGGGGAGCGGCAAGAGAGTGGCGCTTGG 360
Db 301 TGTGCTGCCACTGCTTCCCTGGTGCAGGGGGAGCGGCAAGAGAGTGGCGCTTGG 360
QY 361 GGAGACTACGATGACAGAGTGCCTTTCATGAGGCCAGGTACCAAGTCCGTGGAGAAATCTG 420
Db 361 GGAGACTACGATGACAGAGTGCCTTTCATGAGGCCAGGTACCAAGTCCGTGGAGAAATCTG 420
QY 421 GACAAAGCTCCACAGAGCTGCTGGTGGGGTAAATGCCACAAAGAGATCTATGTCATG 480
Db 421 GACAAAGCTCCACAGAGCTGCTGGTGGGGTAAATGCCACAAAGAGATCTATGTCATG 480
QY 481 CTCAGGGACACTGACGTGTAACAGAGAGCAAGCAAAAGAGAGCTCTCATCTGGCC 540
Db 481 CTCAGGGACACTGACGTGTAACAGAGAGCAAGCAAAAGAGAGCTCTCATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGACAGACAGATGCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGACAGACAGATGCAACTTAAT 600
QY 601 GTCTTGACAAACAAAAGAGACAGCTGTGATAAGCCGTCACAAATGCCAGGAAGATGAA 660
Db 601 GTCTTGACAAACAAAAGAGACAGCTGTGATAAGCCGTCACAAATGCCAGGAAGATGAA 660
QY 661 TGTGCGTTAATGTTGCTGTAACATGGCACTGATCCAAATATTCAGATGATGAAAT 720
Db 661 TGTGCGTTAATGTTGCTGTAACATGGCACTGATCCAAATATTCAGATGATGAAAT 720
QY 721 ACCACTGTGACACTACGCTATCTATATGAAGATAAATTAATGGCCAAAGCACTGCTTA 780
Db 721 ACCACTGTGACACTACGCTATCTATATGAAGATAAATTAATGGCCAAAGCACTGCTTA 780
QY 781 TATGCTGTGATATGCAATCAAAAAACAGCATGGCCACACCACTGTCCTGGTGA 840
Db 781 TATGCTGTGATATGCAATCAAAAAACAGCATGGCCACACCACTGTCCTGGTGA 840
QY 841 CATGAGCAAAAACAGCAAGCTGTAATTTTAATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGCTGTAATTTTAATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATAGATATGGAAGAGCTGCTCATACCTGCTGATGATGATGATGATGATGATGAT 960
Db 901 CTGATAGATATGGAAGAGCTGCTCATACCTGCTGATGATGATGATGATGATGATGAT 960
QY 961 GTCAAGCTTCTACTTGAAGCAAAATATGATGATGATGATGATGATGATGATGATGATGAT 1020
Db 961 GTCAAGCTTCTACTTGAAGCAAAATATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTCCAGTTCCTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTCCAGTTCCTTCTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGA AAAACAGCAATCCAGAAACAAGACTTAAAG 1140
Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGA AAAACAGCAATCCAGAAACAAGACTTAAAG 1140
QY 1141 CTGACATTCAGAGAAAGTTCACAAAGTTCAAAGGCAAGTGAATATAGCACCCAGAGAAA 1200
Db 1141 CTGACATTCAGAGAAAGTTCACAAAGTTCAAAGGCAAGTGAATATAGCACCCAGAGAAA 1200
QY 1201 ATGCTCAAGAACAGAAATTAATTAAGATGCTATAGAGAGTGTGAAGAAATGAAG 1260
Db 1201 ATGCTCAAGAACAGAAATTAATTAAGATGCTATAGAGAGTGTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGTAATTAATGTTGGATTTACTAGAAAACCTGACTAATGTTGCTACTGCTGGC 1320
Db 1261 AAGCATGAAGTAATTAATGTTGGATTTACTAGAAAACCTGACTAATGTTGCTACTGCTGGC 1320
QY 1321 AATGCTGAATTAATGATTAATCTCTCAAGAGAGCAAGACACTGAAATACAGCAATTT 1380
Db 1321 AATGCTGAATTAATGATTAATCTCTCAAGAGAGCAAGACACTGAAATACAGCAATTT 1380
```

Qy	1381	CTGACACAGCAAGTGAAGATATCAACAATTTCCGATATTGTTTCGTACTACAAAGA	1440
Dp	1381	CTGTACACAGAAAGTGAAGATATCAACAATTTGGGAATTAGTTTCGTACTACAAAGA	1440
Qy	1441	AAACAGATGCCAAAATATCTTCTCGAAAAACAGCAACCAGAACAGACTTTAAAGCTGACA	1500
Dp	1441	AAACAGATGCCAAAATATCTTCTCGAAAAACAGCAACCAGAACAGACTTTAAAGCTGACA	1500
Qy	1501	TCAGAGGAGAGATGCACAAAGGCTTGAGGCGAGTGAAAATGGCCAGCCAGAGCTAGAAAAT	1560
Dp	1501	TCAGAGGAGAAAGTCACAAAGGCTTGAGGCGAGTGAAAATGGCCAGCCAGAGCTAGAAAAT	1560
Qy	1561	TTTATGGCTTTCGAAAGAAATGAAAGACACGGAGTACTCATGTGCGAATTTCCCGAANAAC	1620
Dp	1561	TTTATGGCTTTCGAAAGAAATGAAAGACACGGAGTACTCATGTGCGAATTTCCCGAANAAC	1620
Qy	1621	CTGACTAATGATGCCACTGCTGGCAATGGTGTGATGTGATTAATTCCTCCAAAGAGAGAC	1680
Dp	1621	CTGACTAATGATGGTGCACACTGCTGGCAATGGTGTGATGTGATTAATTCCTCCAAAGAGAGAC	1680
Qy	1681	AGAACACCTGAAAGCCAGCAATTTCTGTGACACTGAGAAATGAAGATATCACAGTGACGAA	1740
Dp	1681	AGAACACCTTAAAGCCAGCAATTTCTGTGACACTGAGAAATGAAGATATCACAGTGACGAA	1740
Qy	1741	CAAAATATCTCTAGAAAGCAATTTGTGAAAGAACAGACATGGAATTTTACACAGATAG	1800
Dp	1741	CAAAATATATCTAGAAAGCAATTTGTGAAAGAACAGACATGGAATTTTACACAGATAG	1800
Qy	1801	ATTCTGATTCATGAGCAAAAGCAGATAGAGAGTGTTGAAAAAATGAATTCGTGAGCTTCT	1860
Dp	1801	ATTCTGATTCATGAGCAAAAGCAGATAGAGAGTGTTGAAAAAATGAATTCGTGAGCTTCT	1860
Qy	1861	CTTAGTGTGAAGAAAAAGACATCTTGCAATGAATAATGATCTGCGGGAGCAATTT	1920
Dp	1861	CTTAGTGTGAAGAAAAAGACATCTTGCAATGAATAATGATCTGCGGGAGCAATTT	1920
Qy	1921	GCCATGCTAGAGCTGAGCTAGACACAAATGAAGAAATCAGAGCCACTTAAAAAATTTT	1980
Dp	1921	GCCATGCTAGAGCTGAGCTAGACACAAATGAAGAAATCAGAGCCACTTAAAAAATTTT	1980
Qy	1981	AAAAAAAAAAAAAAAAAAAA 2000	
Dp	1981	AAAAAAAAAAAAAAAAAAAA 2000	

```

RESULT 31
US-09-924-400-302
? Sequence 302, Application US/09924400
? GENERAL INFORMATION:
? APPLICANT: Frudakis, Tony N.
? APPLICANT: Reed, Steven G.
? APPLICANT: Smith, John M.
? APPLICANT: Mishner, Lynda E.
? APPLICANT: Dillon, Davin C.
? APPLICANT: Retter, Marc W.
? APPLICANT: Wang, Aljun
? APPLICANT: Skeiky, Yasir A. W.
? APPLICANT: Harlocker, Susan L.
? APPLICANT: Day, Craig H.
? APPLICANT: Li, Samuel X.
? APPLICANT: Deng, Ta
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
? TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
? FILE REFERENCE: 210121.419C12
? CURRENT APPLICATION NUMBER: US/09/924,400
? NUMBER OF SEQ ID NOS: 340
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 302
? LENGTH: 2000
? TYPE: DNA
? ORGANISM: Homo sapiens

```

US-09-924-400-302

Query Match	100.0%;	Score 2000;	DB 34;	Length 2000;
Best Local Similarity	100.0%;	Pred. No. 6.6e-226;		
Matches 2000; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

OY	1	ATATGGTTAGAGGTTGATTTCCATGTCGCCGGCCCTCTTCTGTAAAGACATTGGTCTC	60
OY	1	ATATGGTTAGAGGTTGATTTCCATGTCGCCGGCCCTCTTCTGTGTAAAGACATTGGTCTC	60
DB	1	ATATGGTTAGAGGTTGATTTCCATGTCGCCGGCCCTCTTCTGTGTAAAGACATTGGTCTC	60
OY	61	AGGAGCAAGATGGGCAAGTGGTGGCTGCGCTTGGCTTCCCTGGTGCAGGAGAGCGGCAAG	120
OY	61	AGGAGCAAGATGGGCAAGTGGTGGCTGCGCTTGGCTTCCCTGGTGCAGGAGAGCGGCAAG	120
DB	61	AGGAGCAAGATGGGCAAGTGGTGGCTGCGCTTGGCTTCCCTGGTGCAGGAGAGCGGCAAG	120
OY	121	AGCAACGTGGGCACTTCTTGGAGACACAGACGATCTTGTCTATGAAGACACTCAGGAGCAAG	180
DB	121	AGCAACGTGGGCACTTCTTGGAGACACACAGACGATCTTGTCTATGAAGACACTCAGGAGCAAG	180
OY	181	ATGGGCAAGTGGTCCGCCCACTGCTTCCCTGCTGCAGGGGAGTGGCAAGGACAACGTG	240
DB	181	ATGGGCAAGTGGTCCGCCCACTGCTTCCCTGCTGCAGGGGAGTGGCAAGGACAACGTG	240
OY	241	GGCCGCTTCTGGAGACACACAGACACTGCTATGAACACTCAGGAACAAGTGGGCAAG	300
DB	241	GGCCGCTTCTGGAGACACACAGACACTGCTATGAACACTCAGGAACAAGTGGGCAAG	300
OY	301	TGGTGTCCGCACTCTTCCCTGCTGCAGGGGAGGGAGCAAGCAAGTGGGCGCTTGG	360
DB	301	TGGTGTCCGCACTCTTCCCTGCTGCAGGGGAGGGAGCAAGCAAGTGGGCGCTTGG	360
OY	361	GGAGACTACGATGACAGTGGCTTCTATGAGAGCCAGGTACCAAGTCCGTGGAGAGACTG	420
DB	361	GGAGACTACGATGACAGTGGCTTCTATGAGAGCCAGGTACCAAGTCCGTGGAGAGACTG	420
OY	421	GACAAGCTCCACAAGGTGGCTGGTGGGGTAAAGTCCCAAGAAAGATCTCATCTCATG	480
DB	421	GACAAGCTCCACAAGGTGGCTGGTGGGGTAAAGTCCCAAGAAAGATCTCATCTCATG	480
OY	481	CTCAGGGACACTGACGTGAAACAAGAGGACAGCAAAAAGACACTGCTTACATCTGGCC	540
DB	481	CTCAGGGACACTGACGTGAAACAAGAGGACAGCAAAAAGACACTGCTTACATCTGGCC	540
OY	541	TCTGCAATGGGAAATTCAGAAAGTAGTAAACCTCTGCTGCAGACAGATGTCAACTTAAT	600
DB	541	TCTGCAATGGGAAATTCAGAAAGTAGTAAACCTCTGCTGCAGACAGATGTCAACTTAAT	600
OY	601	GTCCTTGACAACAAAAAGAGACAGCTCTGATTAAGGGCGTACATGCCAGAGATGAA	660
DB	601	GTCCTTGACAACAAAAAGAGAGACAGCTCTGATTAAGGGCGTACAAATGCCAGAGATGAA	660
OY	661	TGTGGGTAAATGTTGCTGAGAAACATGGGACTGATCCAAATATTCACAGATCAGTATGGAAT	720
DB	661	TGTGGGTAAATGTTGCTGAGAAACATGGGACTGATCCAAATATTCACAGATCAGTATGGAAT	720
OY	721	ACCACTGTGCACTACGCTATCTATATGAAGATAAATTAATGGCCAAAGCACTGCTTGA	780
DB	721	ACCACTGTGCACTACGCTATCTATATGAAGATAAATTAATGGCCAAAGCACTGCTTGA	780
OY	781	TATGGTGTGATATTCGAATCAAAAACACAGATGGGCTCACACACCTGTACTTGGTGA	840
DB	781	TATGGTGTGATATTCGAATCAAAAACACAGATGGGCTCACACACCTGTACTTGGTGA	840
OY	841	CATGAGCAAAAACAGCAAGTCTGGAATTTTTTAATCAAGAAAAAAGCGAATTTAAATGCA	900
DB	841	CATGAGCAAAAACAGCAAGTCTGGAATTTTTTAATCAAGAAAAAAGCGAATTTAAATGCA	900
OY	901	CTGATATGATATGGAAGAGACTGCTCTCATCTTGTCTGTATGTTGTGATCCAAAGTATA	960
DB	901	CTGATATGATATGGAAGAGACTGCTCTCATCTTGTCTGTATGTTGTGATCCAAAGTATA	960
OY	961	GTCAGCCTTCTACTTGTAGCAAAATATTGATGTATCTTCTCAAGATCTATCTGGACAGAG	1020
DB	961	GTCAGCCTTCTACTTGTAGCAAAATATTGATGTATCTTCTCAAGATCTATCTGGACAGAG	1020


```

QY 1021 GCCAGAGATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
    |||||||
Db 1021 GCCAGAGATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
QY 1081 AAAAGAAAAAGATGCTAAAAATCTCTCTGAAAAACAGCATCCAGAAACAGACTTAAAG 1140
    |||||||
Db 1081 AAAAGAAAAAGATGCTAAAAATCTCTCTGAAAAACAGCATCCAGAAACAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAAAGCTCAAAAGGTTCAAGAGCAGTGAATAATGACGACAGAGAAA 1200
    |||||||
Db 1141 CTGACATCAGAGAAAGCTCAAAAGGTTCAAAAGCAGTGAATAATGACGACAGAGAAA 1200
QY 1201 ATGTCCTCAAGAACAGAAATTAATTAAGAGTGTGATAGAGAGTTGAAGAAATGAAG 1260
    |||||||
Db 1201 ATGTCCTCAAGAACAGAAATTAATTAAGAGTGTGATAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAATTAATTAATGTTGGGATTAATAGAAAAACCTGACTAATGTTGCTGCTGGC 1320
    |||||||
Db 1261 AAGCATGAAATTAATTAATGTTGGGATTAATAGAAAAACCTGACTAATGTTGCTGCTGGC 1320
QY 1321 AATGGTGAATAGATTAATTAATCTCAAGAAAGAGACAGAACACCTGAATAATCAGCAATTT 1380
    |||||||
Db 1321 AATGGTGAATAGATTAATTAATCTCAAGAAAGAGACAGAACACCTGAATAATCAGCAATTT 1380
QY 1381 CCTGACAAACGAAGTGAAGAGTATCAGAAATTTGCGAATTAATGTTTCTGACTACAAAGAA 1440
    |||||||
Db 1381 CCTGACAAACGAAGTGAAGAGTATCAGAAATTTGCGAATTAATGTTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAATTAATCTCTGGAANAACAGCAACCCAGAACAAAGATTAAGAGTGA 1500
    |||||||
Db 1441 AAACAGATGCCAAATTAATCTCTGGAANAACAGCAACCCAGAACAAAGATTAAGAGTGA 1500
QY 1501 TCAGAGGAAAGAGTACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGACTAGAAAT 1560
    |||||||
Db 1501 TCAGAGGAAAGAGTACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGACTAGAAAT 1560
QY 1561 TTTATGGCTATCGAAGAAATGAAGAGCAGGAAAGTACTCATGTCGGATGCCAGAAAAAC 1620
    |||||||
Db 1561 TTTATGGCTATCGAAGAAATGAAGAGCAGGAAAGTACTCATGTCGGATGCCAGAAAAAC 1620
QY 1621 CTGACTAATGTCGCACTGCTGCGCAATGCTGATGATGATTAATTTCCCTCCAGAGAAAGC 1680
    |||||||
Db 1621 CTGACTAATGTCGCACTGCTGCGCAATGCTGATGATGATTAATTTCCCTCCAGAGAAAGC 1680
QY 1681 AGAACACCTGAAGCCAGCAATTTCTGACACTGAGATGAAGATATCAGAGTGAAGCA 1740
    |||||||
Db 1681 AGAACACCTGAAGCCAGCAATTTCTGACACTGAGATGAAGATATCAGAGTGAAGCA 1740
QY 1741 CAAATATGATCTCAGAAAGCAATTTTGTGAAGAGCAAGCACTGGAAATATACAGATAG 1800
    |||||||
Db 1741 CAAATATGATCTCAGAAAGCAATTTTGTGAAGAGCAAGCACTGGAAATATACAGATAG 1800
QY 1801 ATTCTGATCTCAGAAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
    |||||||
Db 1801 ATTCTGATCTCAGAAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1860
QY 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGCATGAAAAATAGTACGTTGCGGGAAGAAAT 1920
    |||||||
Db 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGCATGAAAAATAGTACGTTGCGGGAAGAAAT 1920
QY 1921 GCCATGCTAGAGCTGAGAGCTAGACAAATGAACATCAGAGCCAGCTAAAAAAGAAAAA 1980
    |||||||
Db 1921 GCCATGCTAGAGCTGAGAGCTAGACAAATGAACATCAGAGCCAGCTAAAAAAGAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
    |||||||
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

```

RESULT 32
US-10-006-920-374
; Sequence 374, Application US/10006920

```

: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Devin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yugu
: APPLICANT: Kalos, Michael D.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedrick, Thomas S.
: APPLICANT: Carter, Derrick
: APPLICANT: Li, Samuel X.
: APPLICANT: Wang, Aljun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William T.
: APPLICANT: Henderson, Robert A.
: APPLICANT: Hural, John
: APPLICANT: McNeill, Patricia D.
: APPLICANT: Houghcon, Raymond L.
: APPLICANT: Vinals de Bassols, Carlota
: APPLICANT: Foy, Teresa
: APPLICANT: Fanger, Gary R.
: APPLICANT: Mantanabe, Yoshinori
: APPLICANT: Meagher, Madeleine Joy
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: FILE REFERENCE: 210121.427C27
: CURRENT APPLICATION NUMBER: US/10/006,920
: NUMBER OF SEQ ID NOS: 1011
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 374
: LENGTH: 2000
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-006-920-374

```

```

Query Match 100.0%; Score 2000; DB 38; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6,6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTGTTGAGGTGATTCATGCGCGCTGCTCTTCTGTAAGAACCATTTGCTGTC 60
    |||||||
Db 1 ATGCTGTTGAGGTGATTCATGCGCGCTGCTCTTCTGTAAGAACCATTTGCTGTC 60
QY 61 AGAGCAAGATGGGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
    |||||||
Db 61 AGAGCAAGATGGGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 121 AGCAACGTGGGCACTTCTGAGACACAGCACTCTGCTATGAAGACACTCAGAGCAAG 180
    |||||||
Db 121 AGCAACGTGGGCACTTCTGAGACACAGCACTCTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
    |||||||
Db 181 ATGGGCAAGTGTGCGCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
QY 241 GGGCGTTCTGGAGACACAGAGCACTGCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
    |||||||
Db 241 GGGCGTTCTGGAGACACAGAGCACTGCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
QY 301 TGTGCTGCCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGCTGGCGCTTGG 360
    |||||||
Db 301 TGTGCTGCCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGCTGGCGCTTGG 360
QY 361 GGAGACTACGATGACAGTGCCTTCATGAGGCCAGGTACCAAGCTGCGTGAGAGATCTG 420
    |||||||
Db 361 GGAGACTACGATGACAGTGCCTTCATGAGGCCAGGTACCAAGCTGCGTGAGAGATCTG 420
QY 421 GACAAAGCTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
    |||||||
Db 421 GACAAAGCTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480

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Oy 481 CTCAGGACACTGACGTGAACAAGAGCAAGCAAAAGAGGACTGCTACATCGGCC 540
    |||||||
Db 481 CTCAGGACACTGACGTGAACAAGAGCAAGCAAAAGAGGACTGCTACATCGGCC 540
Oy 541 TCTGCCAATGGGAATTCAGAAAGTAGTAAAACTCTGCTGGACAGAGATGCAACTTAAT 600
    |||||||
Db 541 TCTGCCAATGGGAATTCAGAAAGTAGTAAAACTCTGCTGGACAGAGATGCAACTTAAT 600
Oy 601 GTCTCTTGACACAAAAGAGGACAGCTGATTAAGGCCGTGCAATGCCAGAGATGAA 660
    |||||||
Db 601 GTCTCTTGACACAAAAGAGGACAGCTGATTAAGGCCGTGCAATGCCAGAGATGAA 660
Oy 661 TGTGGCTTAATGTGTGGAAATGGAATGCAATATTCAGATAGATGGAAT 720
    |||||||
Db 661 TGTGGCTTAATGTGTGGAAATGGAATGCAATATTCAGATAGATGGAAT 720
Oy 721 ACCACTCTGCACTAGCTATCTATATGAAGATTAATTAATGCGCAAGCACTGCTCTTA 780
    |||||||
Db 721 ACCACTCTGCACTAGCTATCTATATGAAGATTAATTAATGCGCAAGCACTGCTCTTA 780
Oy 781 TATGTGCTGATATGCAATCAAAAACAGCATGGCCTCACACCACCTGTTACTTGGTGA 840
    |||||||
Db 781 TATGTGCTGATATGCAATCAAAAACAGCATGGCCTCACACCACCTGTTACTTGGTGA 840
Oy 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
    |||||||
Db 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
Oy 901 CTGATAGATATGAAGAGCACTGCTCATATCTGCTATGTTGTTGATCAGCAAGTATA 960
    |||||||
Db 901 CTGATAGATATGAAGAGCACTGCTCATATCTGCTATGTTGTTGATCAGCAAGTATA 960
Oy 961 GTACACCTCTCTCTGAGCAAAATATGATGATCTCTTCAAGATCTATCTGACAGAG 1020
    |||||||
Db 961 GTACACCTCTCTCTGAGCAAAATATGATGATCTCTTCAAGATCTATCTGACAGAG 1020
Oy 1021 GCCAGAGATATGCTGTTCTATGATCATCATGATTAATTTGCGAGTTACTTCTGCTAC 1080
    |||||||
Db 1021 GCCAGAGATATGCTGTTCTATGATCATCATGATTAATTTGCGAGTTACTTCTGCTAC 1080
Oy 1081 AAAGAAAAACAGATCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
    |||||||
Db 1081 AAAGAAAAACAGATCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
Oy 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAAAGCAGTGAATAATGAGCCAGAGAAA 1200
    |||||||
Db 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAAAGCAGTGAATAATGAGCCAGAGAAA 1200
Oy 1201 ATGTCTCAAGAACCAAAATTAATAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
    |||||||
Db 1201 ATGTCTCAAGAACCAAAATTAATAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
Oy 1261 AAGCATGAAGATTAATATGATGAGATTAAGAAACCTGACTAATGTTCACTGCTGCG 1320
    |||||||
Db 1261 AAGCATGAAGATTAATATGATGAGATTAAGAAACCTGACTAATGTTCACTGCTGCG 1320
Oy 1321 AATGTGATATGATTAATTTCTCAAGGAAGAGCAGAACCTGAAAATCAGCAATTT 1380
    |||||||
Db 1321 AATGTGATATGATTAATTTCTCAAGGAAGAGCAGAACCTGAAAATCAGCAATTT 1380
Oy 1381 CCTGACACGAAGAGAGATATCAGAAATTTGGATTTGTTCTGACATCAAGAA 1440
    |||||||
Db 1381 CCTGACACGAAGAGAGATATCAGAAATTTGGATTTGTTCTGACATCAAGAA 1440
Oy 1441 AAACAGATGCCAAATACTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAGCTGACA 1500
    |||||||
Db 1441 AAACAGATGCCAAATACTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAGCTGACA 1500
Oy 1501 TTAGAGAGAGATCACAAGAGCTTGAGGCACTGAAATGGCCAGCAGAGCTAGAAAAT 1560
    |||||||
Db 1501 TTAGAGAGAGATCACAAGAGCTTGAGGCACTGAAATGGCCAGCAGAGCTAGAAAAT 1560

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Oy 1561 TTTATGCTATGAGAAATGAAGAAGCACGGAAGTACTGATGCTGATTTCCAGAAAA 1620
    |||||||
Db 1561 TTTATGCTATGAGAAATGAAGAAGCACGGAAGTACTGATGCTGATTTCCAGAAAA 1620
Oy 1621 CTGACTAATGTTGCCACTGCTGGCAATGGTATGATGATTAATTCCTCAAGAAAGAC 1680
    |||||||
Db 1621 CTGACTAATGTTGCCACTGCTGGCAATGGTATGATGATTAATTCCTCAAGAAAGAC 1680
Oy 1681 AGAACACCTGAAAGCAGCAATTTCTGCTGACATGAGAAATGAAGATATACAGTACGA 1740
    |||||||
Db 1681 AGAACACCTGAAAGCAGCAATTTCTGCTGACATGAGAAATGAAGATATACAGTACGA 1740
Oy 1741 CAAATGATATCTCAGAGCAATTTTGTGAAGAACAGAACTGAAATATTACAGTGA 1800
    |||||||
Db 1741 CAAATGATATCTCAGAGCAATTTTGTGAAGAACAGAACTGAAATATTACAGTGA 1800
Oy 1801 ATTCTGATTCATGAAGAAAGCAGATGAAGTGTGTAAGAAAAATGAATTCAGCTTTCT 1860
    |||||||
Db 1801 ATTCTGATTCATGAAGAAAGCAGATGAAGTGTGTAAGAAAAATGAATTCAGCTTTCT 1860
Oy 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGATGAATAATGATGCTGCGGGAAGAAAT 1920
    |||||||
Db 1861 CTTAGTTGTAAGAAAGAAAGACATCTTGATGAATAATGATGCTGCGGGAAGAAAT 1920
Oy 1921 GCCATGCTAAGACTGAGCTAGACACAAATGAACATCAGAGCAGCTAAAAA 1980
    |||||||
Db 1921 GCCATGCTAAGACTGAGCTAGACACAAATGAACATCAGAGCAGCTAAAAA 1980
Oy 1981 AAAAAAAAAAAAAAAAAA 2000
    |||||||
Db 1981 AAAAAAAAAAAAAAAAAA 2000

```

```

RESULT 33
US-10-010-940-374
; Sequence 374, Application US/10010940
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuyun
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Solk, John
; APPLICANT: Retler, Mark
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427D3
; CURRENT APPLICATION NUMBER: US/10/010.940
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-010-940-374

```

```

Query Match      100.0%   Score 2000:   DB 38:   Length 2000:
Best Local Similarity 100.0%:   Pred. No. 6.6e-226:
Matches 2000:   Conservative   0:   Mismatches   0:   Indels   0:   Gaps   0:

Oy 1 ATGGTGGTTGAGGTGATTCATAGCCGCTGCTCTTCTGTAAGAAAGCCATTTGGTCTC 60
    |||||||
Db 1 ATGGTGGTTGAGGTGATTCATAGCCGCTGCTCTTCTGTAAGAAAGCCATTTGGTCTC 60
Oy 61 AGAGCAGATGGGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
    |||||||
Db 61 AGAGCAGATGGGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

```


APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Basols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Mantanabe, Yoshinro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-896-374

Query Match 100.0%; Score 2000; DB 38; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6,6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGGTGATTCATGCGCGCTCTTCTGTGAAGAAGCATTTGGTCTC 60
DB 1 ATGGTGGTTGAGGTGATTCATGCGCGCTCTTCTGTGAAGAAGCATTTGGTCTC 60
QY 61 AGGACAGATGGGGAAGGTGTCGCTGCTTCCCTGCTGCGAGGAGCGGCAAG 120
DB 61 AGGACAGATGGGGAAGGTGTCGCTGCTTCCCTGCTGCGAGGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACACGACGACTGCTATGAAGCACTCAGAGCAAG 180
DB 121 AGCAAGTGGGCACTTCTGAGACACGACGACTGCTATGAAGCACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTCCCGCCACTGCTTCCCTGCTGCGAGGAGGTGGCAAGCAAGT 240
DB 181 ATGGGCAAGTGGTCCCGCCACTGCTTCCCTGCTGCGAGGAGGTGGCAAGCAAGT 240
QY 241 GCGGCTTGGAGACGACGACGACTGCTATGAAGCACTCAGAGCAAGATGGGCAAG 300
DB 241 GCGGCTTGGAGACGACGACGACTGCTATGAAGCACTCAGAGCAAGATGGGCAAG 300
QY 301 TGGTCTGCACTGCTTCCCTGCTGTCAGGAGGAGCGCAAGAGTGGGCGCTTG 360
DB 301 TGGTCTGCACTGCTTCCCTGCTGTCAGGAGGAGCGCAAGAGTGGGCGCTTG 360
QY 361 GGAGACTACGATGACAGTCTTCAATGAGCCAGGTACCAAGTCCGTGGAGAAGTCTG 420
DB 361 GGAGACTACGATGACAGTCTTCAATGAGCCAGGTACCAAGTCCGTGGAGAAGTCTG 420
QY 421 GACAAGCTCCAGAGAGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATCTGAG 480
DB 421 GACAAGCTCCAGAGAGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATCTGAG 480
QY 481 CTCAGGACACTGACGTGAACAAGAGCAAGCAAAAGAGACTCTTACATCTGGCC 540
DB 481 CTCAGGACACTGACGTGAACAAGAGCAAGCAAAAGAGACTCTTACATCTGGCC 540
QY 541 TGTGCCAATGGGAATTCAGAACTAGTAAATCTCTGCTGACAGAGATGTCAACTTAAT 600
DB 541 TGTGCCAATGGGAATTCAGAACTAGTAAATCTCTGCTGACAGAGATGTCAACTTAAT 600
QY 601 GTCCCTTGAACAACAAAAAGAGACAGCTCTGATTAAGGCGGTACAAAGCCAGGAAGTGA 660
DB 601 GTCCCTTGAACAACAAAAAGAGACAGCTCTGATTAAGGCGGTACAAAGCCAGGAAGTGA 660
QY 661 TGTGCTTAATGTGCTGGAACATGGCACTGATCCAAATATTCCAGATGATGAAT 720

|||||
DB 661 TGTGCTTAATGTGCTGGAACATGGCACTGATCCAAATATTCCAGATGATGAAT 720
QY 721 ACCACTCTGCACTACGCTATCTATTAATGAAGTAATTAATGCGCAAGCACTGCTTA 780
DB 721 ACCACTCTGCACTACGCTATCTATTAATGAAGTAATTAATGCGCAAGCACTGCTTA 780
QY 781 TATGGCTGATATGAATCAAAAAAAGCAATGGCGTACACACTGTACTTGGTGA 840
DB 781 TATGGCTGATATGAATCAAAAAAAGCAATGGCGTACACACTGTACTTGGTGA 840
QY 841 CATGAGCAAAAACAGCAAGTCTGAAATTTTAAATCAAAAAAAGCGAATTTAAATGA 900
DB 841 CATGAGCAAAAACAGCAAGTCTGAAATTTTAAATCAAAAAAAGCGAATTTAAATGA 900
QY 901 CTGATATGATATGAAGAGCTGCTCATCTGCTGATATGTTGGATCAGCAAGTATA 960
DB 901 CTGATATGATATGAAGAGCTGCTCATCTGCTGATATGTTGGATCAGCAAGTATA 960
QY 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGACAGAG 1020
DB 961 GTGAGCTTCTACTGAGCAAAATATGATGATCTTCAAGATCTATCTGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGAAGACAGCAATCCAGACAGACTTAAG 1140
DB 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGAAGACAGCAATCCAGACAGACTTAAG 1140
QY 1141 CTGACATCAGAGGAAGAGTCACAAAAGGTTCAAAAGGAGTGAATTTGCCAGAGAA 1200
DB 1141 CTGACATCAGAGGAAGAGTCACAAAAGGTTCAAAAGGAGTGAATTTGCCAGAGAA 1200
QY 1201 ATGTCTCAAGAACCAAAATTAATTAAGATGATGATAGAGAGTTGAAAGAAATGAAG 1260
DB 1201 ATGTCTCAAGAACCAAAATTAATTAAGATGATGATAGAGAGTTGAAAGAAATGAAG 1260
QY 1261 AAGCATGAAGATTAATTAATGAGATTAATTAAGAAACCTACTAATGCTGCTGTC 1320
DB 1261 AAGCATGAAGATTAATTAATGAGATTAATTAAGAAACCTACTAATGCTGCTGTC 1320
QY 1321 AATGATTAATGATTAATTTCTTCAAGAGAGAGAGACACTGAAATACGCAATTT 1380
DB 1321 AATGATTAATGATTAATTTCTTCAAGAGAGAGAGACACTGAAATACGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTGAAGATATCAGAAATTTGCAATTTAGTTCTGACTACAAAGAA 1440
DB 1381 CCTGACAAAGAAAGTGAAGATATCAGAAATTTGCAATTTAGTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATCCCAAAATACCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
DB 1441 AAACAGATCCCAAAATACCTTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGGAAGAGTCAAAAGGCTTGAGGCAAGTGAAGAAAGGCGCAGAGCTAGAAAT 1560
DB 1501 TCAGAGGAAGAGTCAAAAGGCTTGAGGCAAGTGAAGAAAGGCGCAGAGCTAGAAAT 1560
QY 1561 TTTATGGCTATGCAAGAAATGAAGAGCAAGAGTACTCATGTCGATTTCCAGAAAA 1620
DB 1561 TTTATGGCTATGCAAGAAATGAAGAGCAAGAGTACTCATGTCGATTTCCAGAAAA 1620
QY 1621 CTGACTAATGTTGCCACTGCTGGCAATGCTGATGATTAATTTCTTCCAAAGAAAGAC 1680
DB 1621 CTGACTAATGTTGCCACTGCTGGCAATGCTGATGATTAATTTCTTCCAAAGAAAGAC 1680
QY 1681 AGAACCTGGAAGCCAGCAATTTCTGACACTGGAAGAAAGAGATACAGTGCAGAA 1740
DB 1681 AGAACCTGGAAGCCAGCAATTTCTGACACTGGAAGAAAGAGATACAGTGCAGAA 1740
QY 1741 CAAAATGATCTCAGAAAGCAATTTTGTGAAGAAAGAACACTGATATTACAGATGAG 1800

Db 1741 CAAATATATCTCAGAACATTTTGTGAAGACAGAACTGGAAATATTACAGATGAG 1800
Qy 1801 ATCTGATTCATGAAGAAAAAGACAGATAGAACTGGTGTGAAAAAATGAAATTCGACTTTC 1860
Db 1801 ATTCTGATTCATGAAGAAAAAGACAGATAGAACTGGTGTGAAAAAATGAAATTCGACTTTC 1860
Qy 1861 CTATGATTGAAGAAAAAGACATCTTTCATGAAAAATAGTACCTGCGGGAAGAAAT 1920
Db 1861 CTATGATTGAAGAAAAAGACATCTTTCATGAAAAATAGTACCTGCGGGAAGAAAT 1920
Qy 1921 GCCATGCTAGACGTGAGCTGACACATGAAATGAAATGAAAGCCGCTRAAAAAA 1980
Db 1921 GCCATGCTAGACGTGAGCTGACACATGAAATGAAATGAAAGCCGCTRAAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 35
US-10-079-137B-302
; Sequence 302, Application us/10079137B
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misner, Lynda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A. W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; APPLICANT: Li, Samuel X.
; APPLICANT: Deng, Ta
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C13
; CURRENT APPLICATION NUMBER: US/10/079.137B
; CURRENT FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-079-137B-302

Query Match 100.0%; Score 2000; DB 39; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6.6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGTTGAGTTGATTCATCCGCGTCCCTCTCTGTGAAGAACATTTGGTCTC 60
Db 1 ATGCTGTTGAGTTGATTCATCCGCGTCCCTCTCTGTGAAGAACATTTGGTCTC 60
Qy 61 AGGAGCAAGATGGGCAAGTGGTGGTCCGTTCCCTCCCTGCTCAGAGGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGGTGGTCCGTTCCCTCCCTGCTCAGAGGAGCGGCAAG 120
Qy 121 AGCAACTGGGCACTTTGTGAGACACAGAGACCTCTGTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAACTGGGCACTTTGTGAGACACAGAGACCTCTGTATGAAGACACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGGTGGTCCGCACTGCTCCCTGCTGCAAGGGGAGTGGCAAGAGCAAGT 240
Db 181 ATGGGCAAGTGGTGGTCCGCACTGCTCCCTGCTGCAAGGGGAGTGGCAAGAGCAAGT 240
Qy 241 GGGCTTTCTGGAGACACGAGACTCTGTATGAAGACACTCAGAGCAAGAGATGGCAAG 300
Db 241 GGGCTTTCTGGAGACACGAGACTCTGTATGAAGACACTCAGAGCAAGAGATGGCAAG 300
Qy 301 TGGTGTGCTCCACTGCTCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGGTGGCGCTTGG 360

Db 301 TGGTGTGCTCCACTGCTCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGGTGGCGCTTGG 360
Qy 361 GGAGACTACGATGACAGTCCCTTCATGAGGCCAGGATACACAGTCCGCTGGAGAGATCTG 420
Db 361 GGAGACTACGATGACAGTCCCTTCATGAGGCCAGGATACACAGTCCGCTGGAGAGATCTG 420
Qy 421 GACAACTCCACAGAGTCCCTGCTGGGATTAAGTCCCGAGAAAGATCTCATGCTATG 480
Db 421 GACAACTCCACAGAGTCCCTGCTGGGATTAAGTCCCGAGAAAGATCTCATGCTATG 480
Qy 481 CTCAGGACACTGACGTGACACAGACACAGCAAGAAAGAGACTGCTTCATCTGCGC 540
Db 481 CTCAGGACACTGACGTGACACAGACACAGCAAGAAAGAGACTGCTTCATCTGCGC 540
Qy 541 TCTGCCAATGGGAATTCAGAAATGATTAACCTCCGCTGGGACAGAGATGCACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATGATTAACCTCCGCTGGGACAGAGATGCACTTAAT 600
Qy 601 GTCCCTGACAAACAAAAGAGACAGCTCTGATAAAGCCGCTACAAATGCCAGGAAGATGAA 660
Db 601 GTCCCTGACAAACAAAAGAGACAGCTCTGATAAAGCCGCTACAAATGCCAGGAAGATGAA 660
Qy 661 TGTGCTTAAATGTTGCTGGAACATGCGACATGCAAAATATTCAGATGAGTATGAAAT 720
Db 661 TGTGCTTAAATGTTGCTGGAACATGCGACATGCAAAATATTCAGATGAGTATGAAAT 720
Qy 721 ACCACTGACACTGAGTATCTATATGAAGATTAATTAATGAGCAAGCAAGCTCTCTTA 780
Db 721 ACCACTGACACTGAGTATCTATATGAAGATTAATTAATGAGCAAGCAAGCTCTCTTA 780
Qy 781 TATGTCCTGATATGATGATCAACAAAAGACAGCCCTCACACCACTGTTACTGTGATA 840
Db 781 TATGTCCTGATATGATGATCAACAAAAGACAGCCCTCACACCACTGTTACTGTGATA 840
Qy 841 CATAGCAAAAACAGCAAGTCTGTAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATAGCAAAAACAGCAAGTCTGTAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
Qy 901 CTGATATGATATGGAAGAGACTGCTCTCATCTGCTATGTTGTTGATCAGCAAGATATA 960
Db 901 CTGATATGATATGGAAGAGACTGCTCTCATCTGCTATGTTGTTGATCAGCAAGATATA 960
Qy 961 GTACGCTTCTACTTGAGCAAAATATTTGATGATCTTCTCAAGATATCTGACAGACAG 1020
Db 961 GTACGCTTCTACTTGAGCAAAATATTTGATGATCTTCTCAAGATATCTGACAGACAG 1020
Qy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGATTAATTTGCCAGTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGATTAATTTGCCAGTACTTCTGACTAC 1080
Qy 1081 AAAGAAAAACAGATGTAAAAAATCTCTTGAAAGACAGCAATCCAGAAAGACTTAAAG 1140
Db 1081 AAAGAAAAACAGATGTAAAAAATCTCTTGAAAGACAGCAATCCAGAAAGACTTAAAG 1140
Qy 1141 CTGACATCAGAGAGAGTCACAAAAGTTCAGAAAGAGTGAAGTATACCGCCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGTCACAAAAGTTCAGAAAGAGTGAAGTATACCGCCAGAGAAA 1200
Qy 1201 ATGTCACAAAGACCAAGAAATTAAGATGCTATGACAGGTTGAAGAAAGAAATGAAG 1260
Db 1201 ATGTCACAAAGACCAAGAAATTAAGATGCTATGACAGGTTGAAGAAAGAAATGAAG 1260
Qy 1261 AAGCATGAAAGTATATGTTGGGATTTCTGAAAGAACTGACTAATGCTGCTGCTGCGC 1320
Db 1261 AAGCATGAAAGTATATGTTGGGATTTCTGAAAGAACTGACTAATGCTGCTGCTGCGC 1320
Qy 1321 AATGATATATGATTAATTTCTCAAGAGAGACGAAACACCTGAAATTCAGCAATTT 1380
Db 1321 AATGATATATGATTAATTTCTCAAGAGAGACGAAACACCTGAAATTCAGCAATTT 1380
Qy 1381 CTTGACAAAGAAATGAAAGATATCAGAAATTTGGCAATTAATGTTGCTGACTACAAAGAA 1440
Db 1381 CTTGACAAAGAAATGAAAGATATCAGAAATTTGGCAATTAATGTTGCTGACTACAAAGAA 1440

Db	1381	CGTGACACAGAAAGTGAAGAGTATCACAGAAATTTGGGAATTTAGTTCTGACTACAAAAGAA	1440
Qy	1441	AAACAGATGCCAAAATATCTTCTTGAAAACACAGAACCCAGAACAAAGACTTAAAGTGCACA	1500
Db	1441	AAACAGATGCCAAAATATCTTCTTGAAAACACAGAACCCAGAACAAAGACTTAAAGTGCACA	1500
Qy	1501	TCAGAGAAAGATGCATAAAGGCTTGAGGGCAGTGAATAATGGCCAGCAGAGCTAGAAAAT	1560
Db	1501	TCAGAGAAAGATGCATAAAGGCTTGAGGGCAGTGAATAATGGCCAGCAGAGCTAGAAAAT	1560
Qy	1561	TTTATGGCTATTCGAGAATAATGAAAGACACGGAAAGTACTCATGTGCGATTTCCACGAAAAC	1620
Db	1561	TTTATGGCTATTCGAGAATAATGAAAGACACGGAAAGTACTCATGTGCGATTTCCACGAAAAC	1620
Qy	1621	CTGACTATATGTGTCGCACACTGCTGGCAATGCTGATGATGATTATTTCTTCACGAAGAGC	1680
Db	1621	CTGACTATATGTGTCGCACACTGCTGGCAATGCTGATGATGATTATTTCTTCACGAAGAGC	1680
Qy	1681	AGAACACCTGAAGACCCAGCAATTTCTGTGACCTGAGAAATGAAGAGTATCACAGTGACGAA	1740
Db	1681	AGAACACCTGAAGACCCAGCAATTTCTGTGACCTGAGAAATGAAGAGTATCACAGTGACGAA	1740
Qy	1741	CAAAATGATACTCAGAAAGCAATTTTGTGAAGAACAGAACACTGGAATTTACACAGATGAG	1800
Db	1741	CAAAATGATACTCAGAAAGCAATTTTGTGAAGAACAGAACACTGGAATTTACACAGATGAG	1800
Qy	1801	ATTCTGATTCATGAGAAGAAAGCAGATAGAAAGTGTTGAAAAAATGAATTCGAGCTTCT	1860
Db	1801	ATTCTGATTCATGAGAAGAAAGCAGATAGAAAGTGTTGAAAAAATGAATTCGAGCTTCT	1860
Qy	1861	CTTAGTGTGAAGAAAGAAAGCACTTGTGCATGAAAATATGATCTTCCGGGAGAAATTT	1920
Db	1861	CTTAGTGTGAAGAAAGAAAGCACTTGTGCATGAAAATATGATCTTCCGGGAGAAATTT	1920
Qy	1921	GCCATGCTAGATGAGAGCTAGACACAAATGAAGAAACATCAGAGCCACTAAAAA	1980
Db	1921	GCCATGCTAGATGAGAGCTAGACACAAATGAAGAAACATCAGAGCCACTAAAAA	1980
Qy	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
RESULT 36			
US-10-144-678A-374			
: Sequence 374, Application US/10144678A			
: GENERAL INFORMATION:			
: APPLICANT: Xu, Jiangchun			
: APPLICANT: Dillon, Devin C.			
: APPLICANT: Mitcham, Jennifer L.			
: APPLICANT: Harlocker, Susan L.			
: APPLICANT: Jiang, Yugu			
: APPLICANT: Henderson, Robert A.			
: APPLICANT: Kalos, Michael D.			
: APPLICANT: Ranger, Gary R.			
: APPLICANT: Reiter, Marc W.			
: APPLICANT: Stolk, John A.			
: APPLICANT: Day, Craig H.			
: APPLICANT: Vedvick, Thomas S.			
: APPLICANT: Carter, Darrick			
: APPLICANT: Li, Samuel X.			
: APPLICANT: Wang, Aijun			
: APPLICANT: Skeiky, Yasir A. W.			
: APPLICANT: Hepler, William T.			
: APPLICANT: Hurst, John			
: APPLICANT: McNeill, Patricia D.			
: APPLICANT: Houghton, Raymond L.			
: APPLICANT: Vinals y de Bassols, Carlota			
: APPLICANT: Foy, Teresa M.			
: APPLICANT: Watanabe, Yoshihiro			
: APPLICANT: Deng, Ta			
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER			

Query Match	100.0%	Score 2000;	DB 40;	Length 2000;
Best Local Similarity	100.0%	Prod. No. 6,6e-226;		
Matches 2000;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
<p>FILE REFERENCE: 210121.427C28 CURRENT APPLICATION NUMBER: US/10/144,678A CURRENT FILING DATE: 2002-08-12 NUMBER OF SEQ ID NOS: 1033 SOFTWARE: FastSeq for Windows Version 3.0 SEQ ID NO 374 LENGTH: 2000 TYPE: DNA ORGANISM: Homo sapiens US-10-144-678A-374</p>				
QY	1	ATGTGGTTGAGTGTGATTCATGCCGGCGCTCTTCTGTGAAGAAGCATTTGTC	60	
Db	1	ATGTGGTTGAGTGTGATTCATGCCGGCGCTCTTCTGTGAAGAAGCATTTGTC	60	
QY	61	AGGACCAAGATGGGCAATGTGTGTCGGCTTCCCTGCTGCAAGGAGCGGCAAG	120	
Db	61	AGGACCAAGATGGGCAATGTGTGTCGGCTTCCCTGCTGCAAGGAGCGGCAAG	120	
QY	121	AGCAACGGGGGACCTTCGAGACCAACGACGCTGCTATGACACACTGAGGACAG	180	
Db	121	AGCAACGGGGGACCTTCGAGACCAACGACGCTGCTATGACACACTGAGGACAG	180	
QY	181	ATGGCAAGTGTGTCGGGACACTCTTCCCTCTCAGAGGGGAGTGGCAAGCAACTG	240	
Db	181	ATGGCAAGTGTGTCGGGACACTCTTCCCTCTCAGAGGGGAGTGGCAAGCAACTG	240	
QY	241	GCGCGTTCTGGAGACACGACGACTCTGCTATGAAGACACTCAGGAACAAGATGGCAAG	300	
Db	241	GCGCGTTCTGGAGACACGACGACTCTGCTATGAAGACACTCAGGAACAAGATGGCAAG	300	
QY	301	TGTGCTCCGCACTGCTTCCCTGTCGAGAGGGGAGCGGCAAGCAAGATGGCGCTGG	360	
Db	301	TGTGCTCCGCACTGCTTCCCTGTCGAGAGGGGAGCGGCAAGCAAGATGGCGCTGG	360	
QY	361	GGAGACTACGATGACAGTGCCTTCATGTGAGCCGACGATACAGCTCGTGGAAAGATCTG	420	
Db	361	GGAGACTACGATGACAGTGCCTTCATGTGAGCCGACGATACAGCTCGTGGAAAGATCTG	420	
QY	421	GACAAAGCTCCAGAGCTGCTGTTGGGTTAAAGTCCCCAGAAAGATCTATCGTCATG	480	
Db	421	GACAAAGCTCCAGAGCTGCTGTTGGGTTAAAGTCCCCAGAAAGATCTATCGTCATG	480	
QY	481	CTCAGGGACACTGACGTGACCAAGAAAGCAAGCAAAAGAGACATGCTTACATCTGGCC	540	
Db	481	CTCAGGGACACTGACGTGACCAAGAAAGCAAGCAAAAGAGACATGCTTACATCTGGCC	540	
QY	541	TCTGCAATGGGAATTCAGAAAGTACTTAAACCTCGCTGAGACAGACGATGCAACTTAT	600	
Db	541	TCTGCAATGGGAATTCAGAAAGTACTTAAACCTCGCTGAGACAGACGATGCAACTTAT	600	
QY	601	GTCCTTGAACAACAAAGAGGACAGCTCTGATTAAGGCGCTCAATGCGCAGGAAGATGA	660	
Db	601	GTCCTTGAACAACAAAGAGGACAGCTCTGATTAAGGCGCTCAATGCGCAGGAAGATGA	660	
QY	661	TGTGCGTTAATGTCTGTGGAACATGGCACTGATTCCAAATATTCGAGTATGGAAT	720	
Db	661	TGTGCGTTAATGTCTGTGGAACATGGCACTGATTCCAAATATTCGAGTATGGAAT	720	
QY	721	ACCACCTGACACTAGCTATCTATATATGAATTAATTAATGCGCAAGACATGGCTTAT	780	
Db	721	ACCACCTGACACTAGCTATCTATATGAATTAATTAATGCGCAAGACATGGCTTAT	780	
QY	781	TATGCTGCTGATATGCAATCAAAAAAAGACATGGCGCTCACACCACTGTACTTGGTGA	840	
Db	781	TATGCTGCTGATATGCAATCAAAAAAAGACATGGCGCTCACACCACTGTACTTGGTGA	840	
QY	841	CATGACAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA	900	

Db 841 CATGACAAAAACAGCAAGCTGTGAATTTTAAATCAAGAAAAAGCGAAATTTAAATGCA 900
QY CTGATAGATATGAGAGAGACTGCTCATACTGCTGATGTGTGATCAGCAAGTATA 960
|||
Db 901 CTGATAGATATGAGAGAGAGACTGCTCATACTGCTGATGTGTGATCAGCAAGTATA 960
QY 961 GTGAGCCTTCTACTTGAGCAAAATATTGANGTATCTCTCAGATCTATCTGACAGAG 1020
|||
Db 961 GTGAGCCTTCTACTTGAGCAAAATATTGANGTATCTCTCAGATCTATCTGACAGAG 1020
961 GTGAGCCTTCTACTTGAGCAAAATATTGANGTATCTCTCAGATCTATCTGACAGAG 1020
QY 1021 GCCAGAGAGTATGCTGTTCTTACATCANCATGTAAATTTCCCGTAACTTCTGACAG 1080
|||
Db 1021 GCCAGAGAGTATGCTGTTCTTACATCANCATGTAAATTTCCCGTAACTTCTGACAG 1080
QY 1081 AAGAAAAACAGATGCTTAAAAATCTCTCTGAAAAACAGCAATCCAGAAACAGACTTAAAG 1140
|||
Db 1081 AAGAAAAACAGATGCTTAAAAATCTCTCTGAAAAACAGCAATCCAGAAACAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCAAAAAGTTCAAAGGAGAGTGAATATAGCCAGCAGAGAAA 1200
|||
Db 1141 CTGACATCAGAGAGAGAGTCAAAAAGTTCAAAGGAGAGTGAATATAGCCAGCAGAGAAA 1200
QY 1201 ATGCTCAGAGAGAGAGAGTCAAAAATTAAGAGTGTATAGAGAGTGAAGAGAAATGAG 1260
|||
Db 1201 ATGCTCAGAGAGAGAGAGTCAAAAATTAAGAGTGTATAGAGAGTGAAGAGAAATGAG 1260
QY 1261 AAGCATGAAAGTAAATATGTTGGATTAAGTAAACCTGACTAATGCTGCTGCTGCG 1320
|||
Db 1261 AAGCATGAAAGTAAATATGTTGGATTAAGTAAACCTGACTAATGCTGCTGCTGCG 1320
QY 1321 AATGGTATATGATTAATTTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
|||
Db 1321 AATGGTATATGATTAATTTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 CCTGACAGAGAGAGAGAGAGAGATCAGAGAGTGTGCGAATTAAGTTTCTGATACAGAGAA 1440
|||
Db 1381 CCTGACAGAGAGAGAGAGAGATCAGAGAGTGTGCGAATTAAGTTTCTGATACAGAGAA 1440
QY 1441 AAACAGATGCCAAATATCTCTTGTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
|||
Db 1441 AAACAGATGCCAAATATCTCTTGTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
QY 1501 TCAG 1560
|||
Db 1501 TCAG 1560
QY 1561 TTTATGCTATCGAAG 1620
|||
Db 1561 TTTATGCTATCGAAG 1620
QY 1621 CTGACTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
|||
Db 1621 CTGACTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
QY 1681 AGAAGACCTGAG 1740
|||
Db 1681 AGAAGACCTGAG 1740
QY 1741 CAAAATATCTGAG 1800
|||
Db 1741 CAAAATATCTGAG 1800
QY 1801 ATTCTGATTCATGAG 1860
|||
Db 1801 ATTCTGATTCATGAG 1860
QY 1861 CTTAGTTGTAG 1920
|||
Db 1861 CTTAGTTGTAG 1920
QY 1921 GCCATGCTAG 1980
|||
Db 1921 GCCATGCTAG 1980

QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
|||
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
RESULT 37
US-10-212-679-302
; Sequence 302, Application US/10212679
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, Davin
; APPLICANT: Foy, Teresa
; APPLICANT: Houghton, Ray
; APPLICANT: Persing, David
; APPLICANT: Kalos, Michael
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.419C14
; CURRENT APPLICATION NUMBER: US/10/212,679
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ. ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-212-679-302
Query Match 100.0%; Score 2000; DB 42; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6,6e-226;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGGTGGAGTGGATTCATCCGCGGCGCTTCTGTGAAGAGCAATTTGGTCTC 60
Db 1 ATGTGGTGGAGTGGATTCATCCGCGGCGCTTCTGTGAAGAGCAATTTGGTCTC 60
QY 61 AGAGCAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
|||
Db 61 AGAGCAAGATGGGCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 120
QY 121 AGCAAGTGGGCACTTGTGAGACACAGACAGACTGCTATGAAGACACTCAGAGCAAG 180
|||
Db 121 AGCAAGTGGGCACTTGTGAGACACAGACAGACTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGGCGGCACTGCTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
|||
Db 181 ATGGGCAAGTGGTGGGCGGCACTGCTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
QY 241 GGGCTTCTGAGAGACACAGAGACTGCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
|||
Db 241 GGGCTTCTGAGAGACACAGAGACTGCTATGAAGACACTCAGAGCAAGATGGGCAAG 300
QY 301 TGGTGGTGGCACTGCTTCCCTGCTGCAAGGGGAGGCGGCAAGAGTGGGCGCTTGG 360
|||
Db 301 TGGTGGTGGCACTGCTTCCCTGCTGCAAGGGGAGGCGGCAAGAGTGGGCGCTTGG 360
QY 361 GGAAGACTACATGACATGCTGCTTATGAGAGCCAGAGTACACAGTCCCTGGAAGAGACTG 420
|||
Db 361 GGAAGACTACATGACATGCTGCTTATGAGAGCCAGAGTACACAGTCCCTGGAAGAGACTG 420
QY 421 GACAAAGTCCACAGAGTGGCTGGTGGGATTAAGTCCCGAAGAAAGATCTCATGCTCATG 480
|||
Db 421 GACAAAGTCCACAGAGTGGCTGGTGGGATTAAGTCCCGAAGAAAGATCTCATGCTCATG 480
QY 481 CTCAGGAGACATGACGTGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
|||
Db 481 CTCAGGAGACATGACGTGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 TCTGCAATGGGAATTCAGAGATGATTAAGTCTGCTGAGAGAGAGATCAACTTAAT 600
|||
Db 541 TCTGCAATGGGAATTCAGAGATGATTAAGTCTGCTGAGAGAGAGATCAACTTAAT 600

Oy	301	TGGTGGCCACACCTGCTCCCTCTCTCAGGGGAGGGGAGCAAGCAAGTGGCGCTTGG	360
Oy	301	TGGTGGCCACACCTGCTCCCTCTCTCAGGGGAGGGGAGCAAGCAAGTGGCGCTTGG	360
Oy	361	GGAGACTACGATGTACGTGCTTCATGAGAGCCAGGTACACGTCCTCGGAGAAAGATCG	420
Db	361	GGAGACTACGATGTACGTGCTTCATGAGAGCCAGGTACACGTCCTCGGAGAAAGATCG	420
Oy	421	GACAAAGTCCACAGAGCTGCTGGTGGGGTAAAGTCCCGAAGAAAGATCTCATGCTATG	480
Db	421	GACAAAGTCCACAGAGCTGCTGGTGGGGTAAAGTCCCGAAGAAAGATCTCATGCTATG	480
Oy	481	CTCAGGGACACTGCAGTGAACAAGAGCAACAAAGAGACTGCTACATGTGCC	540
Db	481	CTCAGGGACACTGCAGTGAACAAGAGCAACAAAGAGACTGCTACATGTGCC	540
Oy	541	TCCTGCCAATGGGAATTCAGAGTAGTAAACCTCTGCTGAGACAGATGTCACTTAAT	600
Db	541	TCCTGCCAATGGGAATTCAGAGTAGTAAACCTCTGCTGAGACAGATGTCACTTAAT	600
Oy	601	GTCCCTGCAACAAAGAGAGACAGCTCGATTAAGAGCCGTCAATGCGAGGAACATGA	660
Db	601	GTCCCTGCAACAAAGAGAGACAGCTCGATTAAGAGCCGTCAATGCGAGGAACATGA	660
Oy	661	TGTGCGTTAATGTTGCTGGAACATGGCAGCTGATCCAAATATTCAGATGAGTGAAT	720
Db	661	TGTGCGTTAATGTTGCTGGAACATGGCAGCTGATCCAAATATTCAGATGAGTGAAT	720
Oy	721	ACCACTGCACTACGCTATCTATTAATGAAGATTAATTAAGCCAAAGCACTGCTCTTA	780
Db	721	ACCACTGCACTACGCTATCTATTAATGAAGATTAATTAAGCCAAAGCACTGCTCTTA	780
Oy	781	TATGGTGTGATATCGAATCAAAAACAAAGCATGGCCTCACACACTGTTACTTGGTGA	840
Db	781	TATGGTGTGATATCGAATCAAAAACAAAGCATGGCCTCACACACTGTTACTTGGTGA	840
Oy	841	CATGAGCAAAAACAGCAAGTCGTAATTTTATACAAAAAAGCGAATTTAAATGCA	900
Db	841	CATGAGCAAAAACAGCAAGTCGTAATTTTATACAAAAAAGCGAATTTAAATGCA	900
Oy	901	CTGATGATATGGAAGAGCTGCGTCATCTGCTGATGTTGTTGGAGATCACACATGTA	960
Db	901	CTGATGATATGGAAGAGCTGCGTCATCTGCTGATGTTGTTGGAGATCACACATGTA	960
Oy	961	GTCAGCCTTACTTGAGCAAAATATTGATGATCTTCTCAAGATCTATCTGGACAGAG	1020
Db	961	GTCAGCCTTACTTGAGCAAAATATTGATGATCTTCTCAAGATCTATCTGGACAGAG	1020
Oy	1021	GCCAGAGATGCTGTTCTTACTGATCATCATGTAATTTGGCACTTACTTCTGACATAC	1080
Db	1021	GCCAGAGATGCTGTTCTTACTGATCATCATGTAATTTGGCACTTACTTCTGACATAC	1080
Oy	1081	AAAGAAAAACAGATGCTTAAAAATCTCTTGAAAGACAGCATCCAGAACAGACTTAAAG	1140
Db	1081	AAAGAAAAACAGATGCTTAAAAATCTCTTGAAAGACAGCATCCAGAACAGACTTAAAG	1140
Oy	1141	CTGACATCAGAGAGAGAGTCAACAAGGCTTCAAGAGCTGAATAATGCCAGCAGAGAA	1200
Db	1141	CTGACATCAGAGAGAGAGTCAACAAGGCTTCAAGAGCTGAATAATGCCAGCAGAGAA	1200
Oy	1201	ATGCTCTCAAGAACCAAGAAATTAATTAAGAGATGGTGAATAGAGAGTTGAAAGAAATGAG	1260
Db	1201	ATGCTCTCAAGAACCAAGAAATTAATTAAGAGATGGTGAATAGAGAGTTGAAAGAAATGAG	1260
Oy	1261	AAGCATGAAAGTAAATATGTTGGGATTACTAGAAAACCTGACTAATGTTGCTCACTGCTGC	1320
Db	1261	AAGCATGAAAGTAAATATGTTGGGATTACTAGAAAACCTGACTAATGTTGCTCACTGCTGC	1320
Oy	1321	AATGGTATATATGATTAATTTCTCAAGAGAGAGAGACAACCTCGAAATATAGCAATTT	1380
Db	1321	AATGGTATATATGATTAATTTCTCAAGAGAGAGAGACAACCTCGAAATATAGCAATTT	1380

QY	1381	CGTACCAAGAAAGTGAAGAGTTCACAGCAATTCGGATTGTTCGACTACCAACAA	1440
Db	1381	CCTGACACAGCAAGGTGAAGAGTTCACAGCAATTCGGATTGTTCGACTACCAACAA	1440
QY	1441	AAAGAGATGCCAAAATCTCTTCGAAAACAGCAACCCAGAACACTTAAAGCTGACA	1500
Db	1441	AAAGAGATGCCAAAATCTCTTCGAAAACAGCAACCCAGAACAAAGACTTAAAGCTGACA	1500
QY	1501	TCAGAGAAAGAGTTCACAAAGGCTTTGAGGGCAGTGAATAATGGCCAGCCACAG	1551
Db	1501	TCAGAGAGAGAGTTCACAAAGGCTTTGAGGGCAGTGAATAATGGCCAGCCAGAG	1551

	RESULT	39	
	US-09-288-946-375		
	; Sequence	375; Application	us/09288946
	; GENERAL INFORMATION:		
	; APPLICANT:	Xu, Jlangchun	
	; APPLICANT:	Dillon, Davin C.	
	; APPLICANT:	Mitcham, Jennifer Lynn	
	; TITLE OF INVENTION:	COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS	
	; FILE REFERENCE:	210121.427C7	
	; CURRENT APPLICATION NUMBER:	US/09/288.946	
	; CURRENT FILING DATE:	1999-04-09	
	; NUMBER OF SEQ ID NOS:	381	
	; SOFTWARE:	FastsEQ for Windows Version 3.0	
	; SEQ ID NO	375	
	; LENGTH:	2040	
	; TYPE:	DNA	
	; ORGANISM:	Homo sapien	
	US-09-288-946-375		
	Query Match	77.5%; Score 1551;	DB 16; Length 2040;
	Best Local Similarity	100.0%; Pred. No. 1.9e-173;	
	Matches 1551;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
OY	1	ATGTGCTTTGAAGTTCATTCCATGCCGGCTGCCTCTTCTGTAAAGAAGCATTTGGTCTC	60
Db	1	ATGTGGTTTGAGTTGATTCATATGCCGGCTGCCTCTTCTGTAAAGAAGCATTTGGTCTC	60
OY	61	AGGACCAAGATGGCGAAGTGGTGTGCGCTTCCCCTGCTGCAAGAGAGAGCGCAAG	120
Db	61	AGGACCAAGATGGCGAAGTGGTGTGCGCTTCCCCTGCTGCAAGAGAGAGCGCGAAG	120
OY	121	AGCAAAGTGGGCACTTCTGGAGACCAGCAGACTCTGCTATGAAGACACTCAGAGCAAG	180
Db	121	AGCAACGTTGGGCACTTCTGGAGACCAGCAGCACTCTGCTATGAACAACACTCAGAGCAAG	180
OY	181	ATGGCAGATGGTGGCGGCACACTGCTTCCCCTGCTGCAAGGGGAGTGGCAAGAGCAACGG	240
Db	181	ATGGCAGATGGTGGCGGCACACTGCTTCCCCTGCTGCAAGGGGAGTGGCAAGAGCAACGG	240
OY	241	GCGCGTTTGGAGACAGACGACACTCTGCTATGAAGACACTTAGSAAACAAGATGGGCAAG	300
Db	241	GCGCGTTTGGAGAGCACAGAGACACTCTGCTATGAAGACACTTAGSAAACAAGATGGGCAAG	300
OY	301	TGTGTCTGCCACTGCTTCCCCTGCTGTGCAAGGGGAGCGGCAAGAGCAAGTGGGCGCTTGG	360
Db	301	TGTGTCTGCCACTGCTTCCCCTGCTGTGCAAGGGGAGCGGCAAGAGCAAGTGGGCGCTTGG	360
OY	361	GGAGACTAGAGTGAAGTGGCTTCAATGAGAGCCAGAGTACACAGCTCCGTGTGAAGATCTG	420
Db	361	GGAGACTAGAGTGAAGTGGCTTCAATGAGAGCCAGAGTACACAGCTCCGTGTGAAGATCTG	420
OY	421	GACAAGCTTCCAAGAGCTGCTGTGGGGTAAGTCCCCAGAAAGATCTCATTCGTATG	480
Db	421	GACAAGCTTCCAAGAGCTGCTGTGGGGTAAGTCCCCAGAAAGATCTCATTCGTATG	480
OY	481	CTCAGAGCACTGAGAGTGAACAAGAGCAACAAGAGAGCACTGCTACATCTGGCC	540
Db	481	CTCAGAGCACTGAGAGTGAACAAGAGCAACAAGAGAGAGCACTGCTACATCTGGCC	540

541 TCTGCCAATGGGAATTCAGAAAGTAGTAAACCTCTGCTGAGACAGATGTCACCTTAAT 600
541 TCTGCCAATGGGAATTCAGAAAGTAGTAAACCTCTGCTGAGACAGATGTCACCTTAAT 600
601 GTCCCTTGACACAAAAAGGACAGCTCTGATTAAGGCGCTACATGCCAGAGATGAA 660
601 GTCCCTTGACACAAAAAGGACAGCTCTGATTAAGGCGCTACATGCCAGAGATGAA 660
661 TGTGGCTTAATGTTGTGGAAACATGGCACTGATCCAAATATTCACATAGTATGGAAT 720
661 TGTGGCTTAATGTTGTGGAAACATGGCACTGATCCAAATATTCACATAGTATGGAAT 720
721 ACCACTCTGCTAGCTATCTATTAATGAAGATTAATTAATGAGCAACACTGCTCTTA 780
721 ACCACTCTGCTAGCTATCTATTAATGAAGATTAATTAATGAGCAACACTGCTCTTA 780
781 TATGGTCTGATATGCAATCAAAAAACAAGCATGGCTCACACACTGTTACTTGTGTA 840
781 TATGGTCTGATATGCAATCAAAAAACAAGCATGGCTCACACACTGTTACTTGTGTA 840
841 CATGAGCAAAAAACAGCAAGTCGTAATTTTAAATCAAGAAAAACGAAATTAATGA 900
841 CATGAGCAAAAAACAGCAAGTCGTAATTTTAAATCAAGAAAAACGAAATTAATGA 900
901 CTGATATGATATGAAGAGACTGCTCATATCTGCTATGTTGTTGATCAGCAAGTATA 960
901 CTGATATGATATGAAGAGACTGCTCATATCTGCTATGTTGTTGATCAGCAAGTATA 960
961 GTACAGCTTCTACTTGAGCAAAAAATATGATGATCTTCAAGATCTATCTGACAGAG 1020
961 GTACAGCTTCTACTTGAGCAAAAAATATGATGATCTTCAAGATCTATCTGACAGAG 1020
1021 GCCAGAGATATGCTGTTCTATGTCATCATATGTAATTTGCGAGTACTTCTGCTAC 1080
1021 GCCAGAGATATGCTGTTCTATGTCATCATATGTAATTTGCGAGTACTTCTGCTAC 1080
1081 AAAGAAAAACAGATGCTAAATAATCTCTTCTGAAGACAGATCCAGAACAGACTTAAG 1140
1081 AAAGAAAAACAGATGCTAAATAATCTCTTCTGAAGACAGATCCAGAACAGACTTAAG 1140
1141 CTGACATCAGAGAGAGATGTCACAAAGGTCAAAGGTCGAAATATGCCAGCCAGAGAA 1200
1141 CTGACATCAGAGAGAGATGTCACAAAGGTCGAAATATGCCAGCCAGAGAA 1200
1201 ATGTCTCAAGAACCAAGAAATTAATGAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
1201 ATGTCTCAAGAACCAAGAAATTAATGAAGATGATGATGAGAGGTTGAAGAAATGAAG 1260
1261 AAGCATGAAAGTAAATATGTTGGGATTAATGAAGAACTGACTAATGTTCACTGCTGAC 1320
1261 AAGCATGAAAGTAAATATGTTGGGATTAATGAAGAACTGACTAATGTTCACTGCTGAC 1320
1321 AATGCTGATTAATGATTAATCTCTCAAGGAAAGCAGAACCTGAAATATCAGCAATTT 1380
1321 AATGCTGATTAATGATTAATCTCTCAAGGAAAGCAGAACCTGAAATATCAGCAATTT 1380
1381 CCTGACAAAGAAAGTAAAGATATCAAGAAATTTGCGAATTTGTTCTGACTACAAAGAA 1440
1381 CCTGACAAAGAAAGTAAAGATATCAAGAAATTTGCGAATTTGTTCTGACTACAAAGAA 1440
1441 AAACAGATGCCAAATTAATCTCTGAAACAGCAACCCAGAACAGACTTAAGAGTGACA 1500
1441 AAACAGATGCCAAATTAATCTCTGAAACAGCAACCCAGAACAGACTTAAGAGTGACA 1500
1501 TACAGAGAGAGATGTCACAAAGGCTTGAGGCACTGAAATATGCGCAGCAGAG 1551
1501 TACAGAGAGAGATGTCACAAAGGCTTGAGGCACTGAAATATGCGCAGCAGAG 1551

RESULT 40
US-09-198-303
; Sequence 303, Application US/09289198
; GENERAL INFORMATION:

APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE REFERENCE: 210121.419C5
CURRENT APPLICATION NUMBER: US/09/289,198
EARLIER FILING DATE: 1999-04-09
EARLIER FILING DATE: 1998-04-17
EARLIER FILING DATE: 1997-12-11
EARLIER FILING DATE: 1997-12-11
EARLIER FILING DATE: 1997-04-09
EARLIER APPLICATION NUMBER: PCT/US97/00485
EARLIER FILING DATE: 1997-01-10
EARLIER APPLICATION NUMBER: US 08/700,014
EARLIER FILING DATE: 1996-08-20
EARLIER APPLICATION NUMBER: US 08/585,392
EARLIER FILING DATE: 1996-01-01
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 303
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-289-198-303

Query Match 77.5%; Score 1551; DB 16; Length 2040;
Best Local Similarity 100.0%; Pred. No. 1.9e-173;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGCTGTTGAGTTTATTCATGCGCGCTGCTCTTCTGTGAAAGACCATTTGCTCTC 60
1 ATGCTGTTGAGTTTATTCATGCGCGCTGCTCTTCTGTGAAAGACCATTTGCTCTC 60
61 AGGAGCAAGTGGGCAAGGATGCTGCGCTGCTGCTGCTGCGAGAGAGCGGCAAG 120
61 AGGAGCAAGTGGGCAAGGATGCTGCGCTGCTGCTGCTGCGAGAGAGCGGCAAG 120
121 AGCAACGTGGGCACTTCTGAGACCAAGAGACTGCTATGAAGACACTCAGAGCAAG 180
121 AGCAACGTGGGCACTTCTGAGACCAAGAGACTGCTATGAAGACACTCAGAGCAAG 180
181 ATGGGCAAGTGGGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
181 ATGGGCAAGTGGGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
241 GGGCTTCTGAGACCAAGAGACTGCTGCTATGAAGACACTCAGAGCAAGATGGCAAG 300
241 GGGCTTCTGAGACCAAGAGACTGCTGCTATGAAGACACTCAGAGCAAGATGGCAAG 300
301 TGGTGTGCACTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
301 TGGTGTGCACTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
361 GAGAGTACAGTACAGTGGCTTCTGAGAGCCAGAGTACCACTCCGTTGGAGAGATCTG 420
361 GAGAGTACAGTACAGTGGCTTCTGAGAGCCAGAGTACCACTCCGTTGGAGAGATCTG 420
421 GACAGCTCAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
421 GACAGCTCAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
481 CTCAGGAGACACTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
481 CTCAGGAGACACTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
541 TCTGCCAATGGGAATTCAGAAAGTAGTAAACCTCTGCTGAGACAGATGTCACCTTAAT 600
541 TCTGCCAATGGGAATTCAGAAAGTAGTAAACCTCTGCTGAGACAGATGTCACCTTAAT 600

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QY 601 GTCTTGACAAACAAAAGAGACAGCTCTGATTAAGGCCGTACCAATGCCAGGAAGATGA 660
Db 601 GTCTTGACAAACAAAAGAGAGAGCTCTGATTAAGGCCGTACCAATGCCAGGAAGATGA 660
QY 661 TGTGGTAAATGTGTGGTGAACATGGCCTGATCCAAATATTTCCAGATGAGATGGAAT 720
Db 661 TGTGGTAAATGTGTGGTGAACATGGCCTGATCCAAATATTTCCAGATGAGATGGAAT 720
QY 721 ACCACTGCACTACGCTATCTATATGAATTAATGATGATGATGATGATGATGATGATGAT 780
Db 721 ACCACTGCACTACGCTATCTATATGAATTAATGATGATGATGATGATGATGATGATGAT 780
QY 781 TATGGTGTGATATGCAATCAAAAACAAAGCATGGCTCACACCACTGTACTGTGTGTA 840
Db 781 TATGGTGTGATATGCAATCAAAAACAAAGCATGGCTCACACCACTGTACTGTGTGTA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATATATATGAGAGAGAGCTCTCTACTCTGCTGATGATGATGATGATGATGATGATGAT 960
Db 901 CTGATATATATGAGAGAGAGCTCTCTACTCTGCTGATGATGATGATGATGATGATGATGAT 960
QY 961 GTGAGCCTTCTACTGAGCAAAATATTGATGATCTTCTCAAGATCTATCTGAGACAGC 1020
Db 961 GTGAGCCTTCTACTGAGCAAAATATTGATGATCTTCTCAAGATCTATCTGAGACAGC 1020
QY 1021 GCCAGAGATATGCTGTTCTAGTCATCATGATGATGATGATGATGATGATGATGATGATGAT 1080
Db 1021 GCCAGAGATATGCTGTTCTAGTCATCATGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1081 AAAGAAAAACAGATGCTAAATATCTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
Db 1081 AAAGAAAAACAGATGCTAAATATCTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGAGCTCAAAAGTTCAAGGCACTGAAATAGCCAGCCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGAGCTCAAAAGTTCAAGGCACTGAAATAGCCAGCCAGAGAAA 1200
QY 1201 ATGCTCTAGAGAGAGAGAGATTAAGATGATGATGATGATGATGATGATGATGATGATGAT 1260
Db 1201 ATGCTCTAGAGAGAGAGAGATTAAGATGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 1261 AAGCATGAAATTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
Db 1261 AAGCATGAAATTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
QY 1321 AATGGTATTAATGATTAATCTCTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1321 AATGGTATTAATGATTAATCTCTCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 CCTGACAGAGAGAGAGAGATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
Db 1381 CCTGACAGAGAGAGAGAGATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 1441 AAACAGATGCAAAATATCTCTGAAAAACAGCAATCCAGAACAGACTTAAAGTGA 1500
Db 1441 AAACAGATGCAAAATATCTCTGAAAAACAGCAATCCAGAACAGACTTAAAGTGA 1500
QY 1501 TCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1551
Db 1501 TCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1551

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RESULT 41
US-09-429-755-303

; Sequence 303, Application US/09429755A
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda

```

; APPLICANT: Reller, Marc W.  
; APPLICANT: Dillon, Devin C.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER  
; FILE REFERENCE: 210121.419C6  
; CURRENT APPLICATION NUMBER: US/09/429,755A  
; CURRENT FILING DATE: 1999-10-28  
; NUMBER OF SEQ ID NOS: 315  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 303  
; LENGTH: 2040  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-429-755-303  
  
Query Match 77.5%; Score 1551; DB 18; Length 2040;  
Best Local Similarity 100.0%; Pred. No. 1,9e-173;  
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ATGGGTGTTGAGGTGATTCATGCGCGCTGCTCTCTGTGAAGAACCAATTTGCTC 60  
Db 1 ATGGGTGTTGAGGTGATTCATGCGCGCTGCTCTCTGTGAAGAACCAATTTGCTC 60  
QY 61 AGAGCAAGATGGCAAGTGTGCTGCGTTCCTCTGCGAGGAGAGCGGCAAG 120  
Db 61 AGAGCAAGATGGCAAGTGTGCTGCGTTCCTCTGCGAGGAGAGCGGCAAG 120  
QY 121 AGCAAGTGGGCACTTCTGGAGACACAGACAGCTCTGTAGAAGACCTGAGAGCA 180  
Db 121 AGCAAGTGGGCACTTCTGGAGACACAGACAGCTCTGTAGAAGACCTGAGAGCA 180  
QY 181 ATGGCAAGTGGTGGCGGCACTGCTTCCCTGTCTGACAGGGGAGTGGCAAGACG 240  
Db 181 ATGGCAAGTGGTGGCGGCACTGCTTCCCTGTCTGACAGGGGAGTGGCAAGACG 240  
QY 241 GGCGCTTGTGAGACACAGAGACTCTGTATGAAGACCTCAGAACAGATGGGCAAG 300  
Db 241 GGCGCTTGTGAGACACAGAGACTCTGTATGAAGACCTCAGAACAGATGGGCAAG 300  
QY 301 TGGTGTCTGCCACTGCTTCCCTGCTGCGAGGGGAGCGGCAAGAGAGTGGGCTGG 360  
Db 301 TGGTGTCTGCCACTGCTTCCCTGCTGCGAGGGGAGCGGCAAGAGAGTGGGCTGG 360  
QY 361 GGAGACTACGATGACAGAGCTGCTTCATGAGGCCAGGTACCACTCCGTGGAGAAATCTG 420  
Db 361 GGAGACTACGATGACAGAGCTGCTTCATGAGGCCAGGTACCACTCCGTGGAGAAATCTG 420  
QY 421 GACAAAGCTCCACAGAGCTGCTGCTGGGTAAAGTCCCAAGAAAGATCTCATGTG 480  
Db 421 GACAAAGCTCCACAGAGCTGCTGCTGGGTAAAGTCCCAAGAAAGATCTCATGTG 480  
QY 481 CTCAGGGGACATGACGTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
Db 481 CTCAGGGGACATGACGTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
QY 541 TCTGCAATGGGAATTCAGAAATAGTAATACTCTGCTGAGACAGATGTCAACTTAAT 600  
Db 541 TCTGCAATGGGAATTCAGAAATAGTAATACTCTGCTGAGACAGATGTCAACTTAAT 600  
QY 601 GTCTTGACAAACAAAAGAGAGAGCTCTGATTAAGGCGCTGACATGAGAGATGA 660  
Db 601 GTCTTGACAAACAAAAGAGAGAGCTCTGATTAAGGCGCTGACATGAGAGATGA 660  
QY 661 TGTGGTAAATGTGTGGTGAACATGGCCTGATCCAAATATTTCCAGATGAGATGGAAT 720  
Db 661 TGTGGTAAATGTGTGGTGAACATGGCCTGATCCAAATATTTCCAGATGAGATGGAAT 720  
QY 721 ACCACTGCACTACGCTATCTATATGAATTAATGATGATGATGATGATGATGATGATGAT 780  
Db 721 ACCACTGCACTACGCTATCTATATGAATTAATGATGATGATGATGATGATGATGATGAT 780  
QY 781 TATGGTGTGATATGCAATCAAAAACAAAGCATGGCTCACACCACTGTACTGTGTGTA 840  
Db 781 TATGGTGTGATATGCAATCAAAAACAAAGCATGGCTCACACCACTGTACTGTGTGTA 840

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Db 781 TATGTCGTATATGCAATCAAAAAACAAGCATGGCTTCACCACTGTACTGGTGTGA 840
Oy 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCGAATTTAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCGAATTTAATGCA 900
Oy 901 CTGATAGATATGGAAGAGCTGCTCATCTACTCTGTATGTTGTGGATCAGCAAGTATA 960
Db 901 CTGATAGATATGGAAGAGCTGCTCATCTACTCTGTATGTTGTGGATCAGCAAGTATA 960
Oy 961 GTCACACCTTCTACTTGAGCAAAATATTTGATGTATCTTCCAAAGATCTATCTGGACAGAG 1020
Db 961 GTCACACCTTCTACTTGAGCAAAATATTTGATGTATCTTCCAAAGATCTATCTGGACAGAG 1020
Oy 1021 GCCAGAGATATGTTTCTATGATCATCATGTATTTGGCAGTTACTTCTGACTC 1080
Db 1021 GCCAGAGATATGTTTCTATGATCATCATGTATTTGGCAGTTACTTCTGACTC 1080
Oy 1081 AAAGAAAAACAGATCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
Db 1081 AAAGAAAAACAGATCTAAAAATCTCTTCTGAAAAACAGCAATCCAGAACAGACTTAAAG 1140
Oy 1141 CTGACATCAGAGAGAGAGTCAACAAAGTTCAAAAGCAGTGAATAATAGCCAGCCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGAGTCAACAAAGTTCAAAAGCAGTGAATAATAGCCAGCCAGAGAA 1200
Oy 1201 ATGTCTCAAGAACAGAAATATAATAGGATGATAGAGAGTGAAGAAAGAAATAGAG 1260
Db 1201 ATGTCTCAAGAACAGAAATATAATAGGATGATAGAGAGTGAAGAAAGAAATAGAG 1260
Oy 1261 AAGCATGAAAGTAATATGTGGGATTAAGAAAACTGACTAATGTGTCTACTGTGGC 1320
Db 1261 AAGCATGAAAGTAATATGTGGGATTAAGAAAACTGACTAATGTGTCTACTGTGGC 1320
Oy 1321 AATGTGTAATATGATTAATTTCTCAAAAGAGACAGAACCTGAAATATAGCAATTT 1380
Db 1321 AATGTGTAATATGATTAATTTCTCAAAAGAGACAGAACCTGAAATATAGCAATTT 1380
Oy 1381 CCGTCAACAGAAAGTGAAGATATCAGAGAAATTTGGAATTTCTGACTACCAAGAA 1440
Db 1381 CCGTCAACAGAAAGTGAAGATATCAGAGAAATTTGGAATTTCTGACTACCAAGAA 1440
Oy 1441 AAACGATGCCAAATACTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db 1441 AAACGATGCCAAATACTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Oy 1501 TCAGAGGAAGAGTCAACAAAGCTTGAAGGCACTGAAATGGCCAGCCAGAG 1551
Db 1501 TCAGAGGAAGAGTCAACAAAGCTTGAAGGCACTGAAATGGCCAGCCAGAG 1551
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RESULT 42

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US-09-443-686-375
; Sequence 375, Application US/09443686
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitchem, Jennifer L.
; APPLICANT: Hatlocke, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Soik, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9A
; CURRENT APPLICATION NUMBER: US/09/443.686
; CURRENT FILING DATE: 1999-11-18
; NUMBER OF SEQ ID NOS: 151
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-443-686-375

Query Match          77.5%; Score 1551; DB 18; Length 2040;
Best Local Similarity 100.0%; Pred. No. 1.9e-173;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGTGTTGAGTGTGATTCATGCCGCTCTTCTGTGAAGAAGCAATTTGGTCTC 60
Db 1 ATGTGTTGAGTGTGATTCATGCCGCTCTTCTGTGAAGAAGCAATTTGGTCTC 60
Oy 61 AGAGCAATATGGCAAGTGTGCTGCTTCTTCCCTGCTGCGAGAGAGCGGCAAG 120
Db 61 AGAGCAATATGGCAAGTGTGCTGCTTCTTCCCTGCTGCGAGAGAGCGGCAAG 120
Oy 121 AGCAACGTGGGCACTTCTGAGACACAGACAGACTGCTATGAAGCACTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTGAGACACAGACAGACTGCTATGAAGCACTCAGAGCAAG 180
Oy 181 ATGGGCAAGTGTGCCGCACTGCTTCCCTGCTGCGAGGAGAGTGGCAAGCAAGT 240
Db 181 ATGGGCAAGTGTGCCGCACTGCTTCCCTGCTGCGAGGAGAGTGGCAAGCAAGT 240
Oy 241 GCGGCTTCTGGAGACACAGACAGACTGCTATGAAGCACTGAGAAAGATGGGCAAG 300
Db 241 GCGGCTTCTGGAGACACAGACAGACTGCTATGAAGCACTGAGAAAGATGGGCAAG 300
Oy 301 TGGTGTGCACTGCTTCCCTGCTGCGAGGAGAGCGCAAGAGTGGGCGCTTGG 360
Db 301 TGGTGTGCACTGCTTCCCTGCTGCGAGGAGAGCGCAAGAGTGGGCGCTTGG 360
Oy 361 GGAGACTACGATGACAGTCCCTTCAAGAGCCAGGATACAGCTCCGTGGAGAAATCTG 420
Db 361 GGAGACTACGATGACAGTCCCTTCAAGAGCCAGGATACAGCTCCGTGGAGAAATCTG 420
Oy 421 GCAAGCTCCACAGAGCTGCTGAGGAGTAAAGTCCCAAGAAAGATGCTCATGCTGAG 480
Db 421 GCAAGCTCCACAGAGCTGCTGAGGAGTAAAGTCCCAAGAAAGATGCTCATGCTGAG 480
Oy 481 CTCAGGAGACACTGAGCTGAACAAGAGCAAGCAAAAGAGACTGCTTACATCTGGCC 540
Db 481 CTCAGGAGACACTGAGCTGAACAAGAGCAAGCAAAAGAGACTGCTTACATCTGGCC 540
Oy 541 TCTGCCAATGGGAATTCAGAAATGATGTAATCTCTGAGACAGAGATGTCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATGATGTAATCTCTGAGACAGAGATGTCAACTTAAT 600
Oy 601 GTCTTTGACAAACAAAAAGAGACAGCTCTGATTAAGGCCGTACATGCCAGAAATGAA 660
Db 601 GTCTTTGACAAACAAAAAGAGACAGCTCTGATTAAGGCCGTACATGCCAGAAATGAA 660
Oy 661 TGTGCGTTAATGTGCTGAGACATGGCACTGATCCAAATATTCAGATGATGAGAAAT 720
Db 661 TGTGCGTTAATGTGCTGAGACATGGCACTGATCCAAATATTCAGATGATGAGAAAT 720
Oy 721 ACCACTCTGCACTAGCGTATCTATATGAAGATTAATTAATGAGCAAGCACTGCTTA 780
Db 721 ACCACTCTGCACTAGCGTATCTATATGAAGATTAATTAATGAGCAAGCACTGCTTA 780
Oy 781 TATGTCGTGATATGCAATCAAAAAACAAGCATGGCTTCACCACTGTACTGGTGTGA 840
Db 781 TATGTCGTGATATGCAATCAAAAAACAAGCATGGCTTCACCACTGTACTGGTGTGA 840
Oy 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCGAATTTAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCGAATTTAATGCA 900
Oy 901 CTGATAGATATGGAAGAGCTGCTCATCTACTCTGTATGTTGTGGATCAGCAAGTATA 960
Db 901 CTGATAGATATGGAAGAGCTGCTCATCTACTCTGTATGTTGTGGATCAGCAAGTATA 960
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|||||
Db 1021 GCCAAGAGTATGCTGTTCTAGTCATCATGTAATTTGCCAGTACTTCTGACTAC 1080
Qy 1081 AAGAAAAACAGATGCTAAATCTCTTCTGAAAACAGAAATCCAGAAACAACCTTAAAG 1140
Db 1081 AAGAAAAACAGATGCTAAATCTCTTCTGAAAACAGAAATCCAGAAACAACCTTAAAG 1140
Qy 1141 CTGACATCAGAGAGAGTACCAAAAGTTCAAGAGCAGTGAATAATAGCCAGCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTACCAAAAGTTCAAGAGCAGTGAATAATAGCCAGCAGAGAA 1200
Qy 1201 ATGTTCTCAAGAACAGAAATTAATAGATGTTGATAGAGAGTTGGAAGAAATGAAG 1260
Db 1201 ATGTTCTCAAGAACAGAAATTAATAGATGTTGATAGAGAGTTGGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAGTAATTAATGTTGATTAAGTAAACCTGACTAAAGTGTCTACTGTGGC 1320
Db 1261 AAGCATGAAGTAATTAATGTTGATTAAGTAAACCTGACTAAAGTGTCTACTGTGGC 1320
Qy 1321 AATGTTGATTAATGATTAATTCCTCAAAAGAGAGAGAGAAACCTGAAATAGCAATTT 1380
Db 1321 AATGTTGATTAATGATTAATTCCTCAAAAGAGAGAGAGAAACCTGAAATAGCAATTT 1380
Qy 1381 CCTGACAAACGAAAGTGAAGAGTATCAAGAAATTTGGCAATTTCTGACTACAAAGAA 1440
Db 1381 CCTGACAAACGAAAGTGAAGAGTATCAAGAAATTTGGCAATTTCTGACTACAAAGAA 1440
Qy 1441 AAGCATGTCCTCAAAATCTCTGAAAACAGCAACCCAGAAACAGACTTAAAGCTGACA 1500
Db 1441 AAGCATGTCCTCAAAATCTCTGAAAACAGCAACCCAGAAACAGACTTAAAGCTGACA 1500
Qy 1501 TCAGAGAGAGAGTCAACAAAGCTTGAGGAGTGAATAATGGCCAGCAGAG 1551
Db 1501 TCAGAGAGAGAGTCAACAAAGCTTGAGGAGTGAATAATGGCCAGCAGAG 1551

RESULT 44

US-09-534-825A-303

Sequence 303, Application US/09534825A

GENERAL INFORMATION:

APPLICANT: Fridakis, Tony N.

APPLICANT: Smith, John M.

APPLICANT: Reed, Steven G.

APPLICANT: Misher, Lynda

APPLICANT: Rether, Marc W.

APPLICANT: Dillon, David C.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TREATMENT AND DIAGNOSIS OF BREAST CANCER

FILE REFERENCE: 210121.419C7

CURRENT APPLICATION NUMBER: US/09/534,825A

CURRENT FILING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 317

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 303

LENGTH: 2040

TYPE: DNA

ORGANISM: Homo sapien

US-09-534-825A-303

Query Match 77.5%; Score 1551; DB 20; Length 2040;
Beat Local Similarity 100.0%; Pred. No. 1.9e-173;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTGGTTGAGTGTGATTCATGCCGCTGCTCTTCTGTGAAGAGCCATTTGGTCTC 60
Db 1 ATGGTGGTTGAGTGTGATTCATGCCGCTGCTCTTCTGTGAAGAGCCATTTGGTCTC 60
Qy 61 AGGACCAAGATGGCAAGTGTGCTGCGTGTGCTCCCTGGTGCAGGGAGAGCGGCAAG 120
Db 61 AGGACCAAGATGGCAAGTGTGCTGCGTGTGCTCCCTGGTGCAGGGAGAGCGGCAAG 120
Qy 121 AGCAACGTGGGCACTTCTGAGACCAAGAGACTGTCTATGAAGACTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTGAGACCAAGAGACTGTCTATGAAGACTCAGAGCAAG 180

Db 121 AGCAACGTGGGCACTTCTGAGACCAAGAGACTGTCTATGAAGACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGGTGGCGGCACATGCTTCCCTGCTGAGGGGAGTGGCAAGCAACGTG 240
Db 181 ATGGGCAAGTGGTGGCGGCACATGCTTCCCTGCTGAGGGGAGTGGCAAGCAACGTG 240
Qy 241 GGCCTTCTGAGAGACAGCAGTCTGCTATGAAGACACTGAGAACAAAGATGGGCAAG 300
Db 241 GGCCTTCTGAGAGACAGCAGTCTGCTATGAAGACACTGAGAACAAAGATGGGCAAG 300
Qy 301 TGGTGTGCTGCTGCTTCCCTGCTGCTGAGGGGAGCGGCAAGAGCAAGTGGGCTTGG 360
Db 301 TGGTGTGCTGCTGCTTCCCTGCTGCTGAGGGGAGCGGCAAGAGCAAGTGGGCTTGG 360
Qy 361 GGAGACTACGATGACAGTCCCTTCATGAGCCAGGTACAGTCCGTGGAGAAATCTG 420
Db 361 GGAGACTACGATGACAGTCCCTTCATGAGCCAGGTACAGTCCGTGGAGAAATCTG 420
Qy 421 GACAAAGCTCCAGAGAGCTGCTGTTGGGTTAAAGTCCCGAAAGAGATCTCATGCTATG 480
Db 421 GACAAAGCTCCAGAGAGCTGCTGTTGGGTTAAAGTCCCGAAAGAGATCTCATGCTATG 480
Qy 481 CTCAGGAGACCTGACGTGAACAAGAAAGCAAGCAAAAGAGAGACTGCTTACATCTGGCC 540
Db 481 CTCAGGAGACCTGACGTGAACAAGAAAGCAAGCAAAAGAGAGACTGCTTACATCTGGCC 540
Qy 541 TCTGCCAATGGGAATTCAGAAATGATTAATCTCTGCTGAGAGAGATGATCAACTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAATGATTAATCTCTGCTGAGAGAGATGATCAACTAAT 600
Qy 601 GTCCCTTGACAAACAAAGAGAGAGAGTGTATGAAGGCGGTACAAATGCCAGAAATGAA 660
Db 601 GTCCCTTGACAAACAAAGAGAGAGAGTGTATGAAGGCGGTACAAATGCCAGAAATGAA 660
Qy 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
Qy 721 ACCACTCTGCTAGCTATCTATTAATGAAGATTAATTAATGGCCAAACACTGCTCTTA 780
Db 721 ACCACTCTGCTAGCTATCTATTAATGAAGATTAATTAATGGCCAAACACTGCTCTTA 780
Qy 781 TATGGTGTGATATCAATCAAAAAACAAGCATAGGCTCAGACACTGTTACTGGTGA 840
Db 781 TATGGTGTGATATCAATCAAAAAACAAGCATAGGCTCAGACACTGTTACTGGTGA 840
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Db 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAATCAAGAAAAAGCGAATTTAAATGCA 900
Qy 901 CTGGATAGATGAAGAGAGCTGCTCTCATACTTGTCTGTATGTTGTGATCAGCAAGTATA 960
Db 901 CTGGATAGATGAAGAGAGCTGCTCTCATACTTGTCTGTATGTTGTGATCAGCAAGTATA 960
Qy 961 GTGAGCCTTCTACTTGAAGAAATATTTGATGATCTTCAAGATCTATCTGGACAGAG 1020
Db 961 GTGAGCCTTCTACTTGAAGAAATATTTGATGATCTTCAAGATCTATCTGGACAGAG 1020
Qy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTCTGACTAC 1080
Qy 1081 AAGAAAAACAGATGCTAAATCTCTTCTGAAAACAGAAATCCAGAAACAACCTTAAAG 1140
Db 1081 AAGAAAAACAGATGCTAAATCTCTTCTGAAAACAGAAATCCAGAAACAACCTTAAAG 1140
Qy 1141 CTGACATCAGAGAGAGTACCAAAAGTTCAAGAGCAGTGAATAATAGCCAGCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTACCAAAAGTTCAAGAGCAGTGAATAATAGCCAGCAGAGAA 1200
Qy 1201 ATGTTCTCAAGAACAGAAATTAATAGATGTTGATAGAGAGTTGGAAGAAATGAAG 1260
Db 1201 ATGTTCTCAAGAACAGAAATTAATAGATGTTGATAGAGAGTTGGAAGAAATGAAG 1260

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DB 1441 AAACAGATGCCAAATATCTCTTCTGAAAACAGAACCCAGAACAGACTTAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGTACACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551
DB 1501 TCAGAGAGAGAGTACACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCCAGAG 1551

RESULT 45

US-09-536-857-375
Sequence 375, Application US/09536857
GENERAL INFORMATION:
APPLICANT: Xu, Jlangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jlang, Yuqi
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42712C12
CURRENT APPLICATION NUMBER: US/09/536, 857
NUMBER OF SEQ ID NOS: 592
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-536-857-375

Query Match 77.5%; Score 1551; DB 20; Length 2040;
Best Local Similarity 100.0%; Pred. No. 1.9e-173;
Matches 1551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 AGGAGCAAGATGGGCAAGTGTGCTGCGTTGCTCCCTGCTCAGGGAGAGGGGCAAG 120
QY 121 AGCAAGCTGGGCACTTCTGAGACACAGACACTCTGTATGAAGACACTCAGAGCAAG 180
DB 121 AGCAAGCTGGGCACTTCTGAGACACAGACACTCTGTATGAAGACACTCAGAGCAAG 180
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DB 181 ATGGGCAAGTGTGCTGCGCTGCTCCCTGCTGCAAGGGGAGTGGCAAGCAACGTG 240
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DB 241 GGCGCTTCTGAGACACAGACACTCTGTATGAAGACACTCAGAGAACAGATGGCAAG 300

QY 301 TGTGCTGCGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGAGTGGCGCTTGG 360
DB 301 TGTGCTGCGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGAGTGGCGCTTGG 360
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DB 781 TATGCTGCTATATGATGATCAAAAACAGAGATGGCTCACACACATGTTACTTGGTGA 840
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DB 841 CATGAGCAAAAACAGCAAGTGTGAAAATTTTAATCAAGAAAAAGCAATTTAATATGA 900
QY 901 CTGATGATATGGAAGAGACGCTCTCATCTTCTGTATGTTGGATGACGAAGTATA 960
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DB 961 GTGACCTTCTACTTGAAGCAAAATATGATGATCTCTCAAGATCTATCTGACAGAGC 1020
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DB 1261 AAGCATGAAAGTAATATGTTGGGATTAATCTGAAAACCTGACTAATGTTGTCAGCTGGC 1320
QY 1321 AATGTTGTAATGATTAATTTCTCAAGAGAGAGCAAGCAACCTGAAAATTCAGCAATTT 1380
DB 1321 AATGTTGTAATGATTAATTTCTCAAGAGAGAGCAAGCAACCTGAAAATTCAGCAATTT 1380

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QY 1501 TCAGAGGAGAGTCAACAAGGCTTGAGGGCAGTGAATAATGCCAGCCAGAG 1551
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Search completed: November 8, 2002, 15:48:01
 Job time : 3957.07 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 8, 2002, 02:07:38 : Search time 4020.92 Seconds
(without alignments)
12755.953 Million cell updates/sec

Title: US-09-924-400-303
Perfect score: 2040
Sequence: 1 atggttggtgaggttgatc.....aaaaaaaaaaaaaaaaaaaaa 2040

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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4	2040	100.0	2040	18	US-09-429-755-303
5	2040	100.0	2040	18	US-09-443-686-375
6	2040	100.0	2040	18	US-09-483-672A-375
7	2040	100.0	2040	20	US-09-534-825A-303
8	2040	100.0	2040	20	US-09-536-857-375
9	2040	100.0	2040	22	US-09-568-100A-375
10	2040	100.0	2040	22	US-09-577-505B-303
11	2040	100.0	2040	22	US-09-590-583-303
12	2040	100.0	2040	22	US-09-593-793A-375
13	2040	100.0	2040	23	US-09-636-215-375
14	2040	100.0	2040	25	US-09-651-236-375
15	2040	100.0	2040	25	US-09-657-279-375
16	2040	100.0	2040	26	US-09-679-272-375
17	2040	100.0	2040	26	US-09-679-426-375
18	2040	100.0	2040	27	US-09-685-166-375
19	2040	100.0	2040	27	US-09-685-166A-375
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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38 1940 95.1 2000 16 PCT-US02-24917-302 Sequence 302, App
39 1940 95.1 2000 16 US-09-288-946-374 Sequence 374, App
40 1940 95.1 2000 16 US-09-289-198-302 Sequence 302, App
41 1940 95.1 2000 18 US-09-429-755-302 Sequence 302, App
42 1940 95.1 2000 18 US-09-443-686-374 Sequence 374, App
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44 1940 95.1 2000 20 US-09-534-825A-302 Sequence 302, App
45 1940 95.1 2000 20 US-09-536-857-374 Sequence 374, App
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ALIGNMENTS

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RESULT 1
PCT-US02-24917-303
; Sequence 303, Application PC/TUS0224917
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, Davin C.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.41931PC
; CURRENT APPLICATION NUMBER: PCT/US02/24917
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-24917-303
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Query Match 100.0%; Score 2040; DB 1; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 ATGGTGGTGGAGTTGATTCATGCGGGCTCTTGTGTAAGAACCATTTGTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTCCGTTGCTCCCTGCTGACAGGAGACG 120
Db 61 AGGAGCAAGATGGGCAAGTGTGCTCCGTTGCTCCCTGCTGACAGGAGACG 120
QY 121 AGCAAGTGGGCACTTGTGAGACACGACGACTGTGTATGAAGACACTCAG 180
Db 121 AGCAAGTGGGCACTTGTGAGACACGACGACTGTGTATGAAGACACTCAG 180
QY 181 ATGGGCAATGTGGTCCGCCACTGCTCCCTGCTGACAGGAGAGTGGCAAG 240
Db 181 ATGGGCAATGTGGTCCGCCACTGCTCCCTGCTGACAGGAGAGTGGCAAG 240
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QY 241 GGGCTTCTGAGAGCCAGCAGACTGTGATGAAACATCAGAAAGATGGGCAAG 300
Db 241 GGGCTTCTGAGAGCCAGCAGACTGTGATGAAACATCAGAAAGATGGGCAAG 300
QY 301 TGTGCTGCACTGCTTCCCTGCTGACAGGAGAGCGGCAAGCAAGTGGCGCT 360
Db 301 TGTGCTGCACTGCTTCCCTGCTGACAGGAGAGCGGCAAGCAAGTGGCGCT 360
QY 361 GAGACTAGATGACAGTGCCTTCATGAGCCAGGTACACAGCTCGTGGAGATCT 420
Db 361 GAGACTAGATGACAGTGCCTTCATGAGCCAGGTACACAGCTCGTGGAGATCT 420
QY 421 GACAACTCCACAGACTGCTGCTGGTAAAGTCCCAAGAAAGATCTCATG 480
Db 421 GACAACTCCACAGACTGCTGCTGGTAAAGTCCCAAGAAAGATCTCATG 480
QY 481 CTCAGGACACTGACGTGAACAAAGAACACAAAGAGACTGCTTACATCTGCC 540
Db 481 CTCAGGACACTGACGTGAACAAAGAACACAAAGAGACTGCTTACATCTGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAACCTCTGAGACAGATGTCACCTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAACCTCTGAGACAGATGTCACCTTAAT 600
QY 601 GTCCCTGACAAACAAAAGAGACAGCTGTATTAAGCCGTACATGCCAGAAATGA 660
Db 601 GTCCCTGACAAACAAAAGAGAGAGAGCTGTATTAAGCCGTACATGCCAGAAATGA 660
QY 661 TGTGCTTAATGTGCTGCAACATGCGACTGATCCAAATATTCAGATAGTGAAT 720
Db 661 TGTGCTTAATGTGCTGCAACATGCGACTGATCCAAATATTCAGATAGTGAAT 720
QY 721 ACCACTGACACTGACGTATTAATGAAGAAATTAATGAGCCAAAGACTGCTTA 780
Db 721 ACCACTGACACTGACGTATTAATGAAGAAATTAATGAGCCAAAGACTGCTTA 780
QY 781 TATGCTGATATTCGAATCAAAAACAAAGATGCCACACACTGTTACTGGTGA 840
Db 781 TATGCTGATATTCGAATCAAAAACAAAGATGCCACACACTGTTACTGGTGA 840
QY 841 CATGACAAAACAGCAAGTGTGAATTTTATATCAAGAAAACGAATTTAATGCA 900
Db 841 CATGACAAAACAGCAAGTGTGAATTTTATATCAAGAAAACGAATTTAATGCA 900
QY 901 CTGGATAGATGAGAGAGAGCTGCTCATACCTTGCTGATGTTGTGATCAGCAAT 960
Db 901 CTGGATAGATGAGAGAGAGCTGCTCATACCTTGCTGATGTTGTGATCAGCAAT 960
QY 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAG 1020
Db 961 GTGAGCTTCTACTTGAAGCAAAATATGATGATCTTCTCAAGATCTATCTGACAG 1020
QY 1021 GCCAGAGATATGCTTCTGATCATCATCATATTAATTTGCCAGTACTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTTCTGATCATCATCATATTAATTTGCCAGTACTTCTGACTAC 1080
QY 1081 AAAGAAAACAGATGCTAAATAATCTCTGAAAACAGCAATCCAGAAAGCTTAAG 1140
Db 1081 AAAGAAAACAGATGCTAAATAATCTCTGAAAACAGCAATCCAGAAAGCTTAAG 1140
QY 1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAGGAGTGAATAATGACAGCCAGAAA 1200
Db 1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAGGAGTGAATAATGACAGCCAGAAA 1200
QY 1201 ATGTCTCAAGAACAGAAATTAATGAATGATGATGAGAGTGAACAAAGATGAAG 1260
Db 1201 ATGTCTCAAGAACAGAAATTAATGAATGATGATGAGAGTGAACAAAGATGAAG 1260
QY 1261 AAGCATGAAGTAATTAATGATGATTAATTAATTAATTAATTAATTAATTAAT 1320
Db 1261 AAGCATGAAGTAATTAATGATGATTAATTAATTAATTAATTAATTAATTAAT 1320
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QY 1321 AATGGTAAATGATTAATTCCTCAAGAGACAGACACCTGAATAATCAGCAATTT 1380
|||||
Db 1321 AATGGTAAATGATTAATTCCTCAAGAGAGACAGACACCTGAATAATCAGCAATTT 1380
QY 1381 CCTGACAAACGAAAGTGAAGAGTATCAGCAATTTGCGAATTAATGTTCTGACTACAAAGAA 1440
|||||
Db 1381 CCTGACAAACGAAAGTGAAGAGTATCAGCAATTTGCGAATTAATGTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAATATCTCTTGAAGAAACGACAAACCAAGCAACAGATTAAAGCTGACA 1500
|||||
Db 1441 AAACAGATGCCAAATATCTCTTGAAGAAACGACAAACCAAGCAACAGATTAAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGTACAAAGGCTTGAGGGCAGTGAATAATGGCCAGACCCAGAGAAAGATCT 1560
|||||
Db 1501 TCAGAGAGAGAGTACAAAGGCTTGAGGGCAGTGAATAATGGCCAGACCCAGAGAAAGATCT 1560
QY 1561 CAAGAACCGAATAATTAATAGGATGCTGATAGAGAGCTAGAAATTTTATGGCTATCGAA 1620
|||||
Db 1561 CAAGAACCGAATAATTAATAGGATGCTGATAGAGAGCTAGAAATTTTATGGCTATCGAA 1620
QY 1621 GAATGAAAGAGACGAGAACTCATGTCCGATTCCAGAAACCTGACTAATGCTGCC 1680
|||||
Db 1621 GAATGAAAGAGACGAGAACTCATGTCCGATTCCAGAAACCTGACTAATGCTGCC 1680
QY 1681 ACTGCTGCAATGGTATGATGATGATTAATTCCTCCAGAGAGAGAGCAACCTGAAAGC 1740
|||||
Db 1681 ACTGCTGCAATGGTATGATGATGATTAATTCCTCCAGAGAGAGAGCAACCTGAAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCAGACTGACGAAACCAAAATGATACTGAG 1800
|||||
Db 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCAGACTGACGAAACCAAAATGATACTGAG 1800
QY 1801 AAGCAATTTTGTGAAGAACACAAACACTGGAATATTACAGCATGAGATTCTGATTATGAA 1860
|||||
Db 1801 AAGCAATTTTGTGAAGAACACAAACACTGGAATATTACAGCATGAGATTCTGATTATGAA 1860
QY 1861 GAAAGACGATAGAAAGTGGTGAAGAAATGAAATCTGAGCTTCTTCTAGTTGTAAAGAA 1920
|||||
Db 1861 GAAAGACGATAGAAAGTGGTGAAGAAATGAAATCTGAGCTTCTTCTAGTTGTAAAGAA 1920
QY 1921 GAAAGACGATAGAAAGTGGTGAAGAAATGAAATCTGAGCTTCTTCTAGTTGTAAAGAA 1980
|||||
Db 1921 GAAAGACGATAGAAAGTGGTGAAGAAATGAAATCTGAGCTTCTTCTAGTTGTAAAGAA 1980
QY 1981 GAGCTAGACAAATGAAGAACATCAGAGCCAGCTAAATGATGATGATGATGATGATGATGAT 2040
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Db 1981 GAGCTAGACAAATGAAGAACATCAGAGCCAGCTAAATGATGATGATGATGATGATGATGAT 2040

RESULT 2

US-09-288-946-375
: Sequence 375, Application US/09288946
: GENERAL INFORMATION:
: APPLICANT: Xu, Jlangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer Lynn
: TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
: FILE REFERENCE: 210121.427C7
: CURRENT APPLICATION NUMBER: US/09/288, 946
: NUMBER OF SEQ ID NOS: 381
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 375
: LENGTH: 2040
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-288-946-375

Query Match 100.0%; Score 2040; DB 16; Length 2040;
Best Local Similarity 100.0%; Pired. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGGTTGATTCATAGCCGGCTGCGCTCTTCTGTGAAGAACCATTTGGTCTC 60
|||||
Db 1 ATGGTGGTTGAGGTTGATTCATAGCCGGCTGCGCTCTTCTGTGAAGAACCATTTGGTCTC 60
QY 61 AGGACCAAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGAGGAGAGCGGCAAG 120
|||||
Db 61 AGGACCAAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGAGGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTCTTGGAGACACAGACAGCTGCTGTATGAACACTCAGAGCAAG 180
|||||
Db 121 AGCAACGTGGGCACTCTTGGAGACACAGACAGCTGCTGTATGAACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGAGGAGAGTGGCAAGACAGT 240
|||||
Db 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGAGGAGAGTGGCAAGACAGT 240
QY 241 GGGCGTTTGGAGACACAGACAGCTCTGTATGAAGACACTCAGAGCAAGTGGGCAAG 300
|||||
Db 241 GGGCGTTTGGAGACACAGACAGCTCTGTATGAAGACACTCAGAGCAAGTGGGCAAG 300
QY 301 TGGTCTGCGCACTGCTTCCCTGCTGAGGAGAGCGGCAAGAGTGGGCGCTTGG 360
|||||
Db 301 TGGTCTGCGCACTGCTTCCCTGCTGAGGAGAGCGGCAAGAGTGGGCGCTTGG 360
QY 361 GAGAGCTACGATGACAGTGGCTTCAATGAGCCAGGTAACAGTCCGCTGGAGAGATCTG 420
|||||
Db 361 GAGAGCTACGATGACAGTGGCTTCAATGAGCCAGGTAACAGTCCGCTGGAGAGATCTG 420
QY 421 GACCAAGCTCCACAGAGAGCTGCTGGTGAAGTCCCGAGAAAGATCTCATCTCATG 480
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Db 421 GACCAAGCTCCACAGAGAGCTGCTGGTGAAGTCCCGAGAAAGATCTCATCTCATG 480
QY 481 CTCAGGAGACACTGACGTGAACAAGAGCAAGCAAAAGAGAGCTGCTTACATCTGGCC 540
|||||
Db 481 CTCAGGAGACACTGACGTGAACAAGAGCAAGCAAAAGAGAGCTGCTTACATCTGGCC 540
QY 541 TCTGCGAATGGGAATTCGAAGTACTTAAATCCGCTGGAGACAGATGTCATCTTAT 600
|||||
Db 541 TCTGCGAATGGGAATTCGAAGTACTTAAATCCGCTGGAGACAGATGTCATCTTAT 600
QY 601 GTCTTGAACACAAAAGAGAGACAGCTCTGATTAAGGCGCTGCAATGGCCAGAGATGAA 660
|||||
Db 601 GTCTTGAACACAAAAGAGAGAGCTCTGATTAAGGCGCTGCAATGGCCAGAGATGAA 660
QY 661 TGTGCGTTAATGTTCTGTAACATGCACTGATCCAAATATTCAGATGAGTGAAT 720
|||||
Db 661 TGTGCGTTAATGTTCTGTAACATGCACTGATCCAAATATTCAGATGAGTGAAT 720
QY 721 ACCACTGCACTAGGCTATCATTAAGTAAGTAATTAATGAGCAAGCACTGCTCTTA 780
|||||
Db 721 ACCACTGCACTAGGCTATCATTAAGTAAGTAATTAATGAGCAAGCACTGCTCTTA 780
QY 781 TATGGTGTGATATGCAATCAAAAAACAAGCATGGGCTCACACCACTGTACTTGGTGA 840
|||||
Db 781 TATGGTGTGATATGCAATCAAAAAACAAGCATGGGCTCACACCACTGTACTTGGTGA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCGAATTTAATGCA 900
|||||
Db 841 CATGAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCGAATTTAATGCA 900
QY 901 CTGGATAGATATGAAGAGAGCTGCTCATACTGCTGTATGTTGGATGACAGATGTA 960
|||||
Db 901 CTGGATAGATATGAAGAGAGCTGCTCATACTGCTGTATGTTGGATGACAGATGTA 960
QY 961 GTACAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGACAGAG 1020
|||||
Db 961 GTACAGCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGAGACAGAG 1020
QY 1021 GCGAGAGAGTATGCTGTTTCTAGTATCATCATGTAATTTGGCAATCTTTCTACTATC 1080
|||||
Db 1021 GCGAGAGAGTATGCTGTTTCTAGTATCATCATGTAATTTGGCAATCTTTCTACTATC 1080
QY 1081 AAAGAAAAACAGATGCTTAAATATCTTCTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
|||||

|||||
Db 1081 AAGAGAAAAACATGCTAAATAATCTCTGAAAACGCAATCCAGAACAGCTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGACACAAAGGTTCAAAAGCAGTGAATAATGCACGACAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGACACAAAGGTTCAAAAGCAGTGAATAATGCACGACAGAGAA 1200
QY 1201 ATGTCTCAAGAACACAGAAATTAATAGATGATGATAGAGAGTGGTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACACAGAAATTAATAGATGATGATAGAGAGTGGTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAAGATATATATGATGGATTACTAGAAAACCTGATATATGTTGCTGCTGCG 1320
Db 1261 AAGCATGAAAAGATATATATGATGGATTACTAGAAAACCTGATATATGTTGCTGCTGCG 1320
QY 1321 AATGGGATATGATATATATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
Db 1321 AATGGGATATGATATATATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 CCTGACACAGAAAGTGAAGATATACAGAAATTTGCGAAATTTGATCTGATCAAGAA 1440
Db 1381 CCTGACACAGAAAGTGAAGATATACAGAAATTTGCGAAATTTGATCTGATCAAGAA 1440
QY 1441 AAGCATGCTCAAAATATCTCTCTGAAAACGCAACCCAGAACAGAGATTTAAAGTGA 1500
Db 1441 AAGCATGCTCAAAATATCTCTCTGAAAACGCAACCCAGAACAGAGATTTAAAGTGA 1500
QY 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGAGAGTGAAGAAATGGCCAGAGAGAGAGAGAT 1560
Db 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGAGAGTGAAGAAATGGCCAGAGAGAGAGAT 1560
QY 1561 CAAGAACACAGAAATTAATAGATGATAGAGATGAGAGATGAGAGATTTATGGCTATCGAA 1620
Db 1561 CAAGAACACAGAAATTAATAGATGATAGAGATGAGAGATGAGAGATTTATGGCTATCGAA 1620
QY 1621 GAAATTAAGAGACAGAGAGTACTCTATGTCGATTTCCAGAGAAACCTGACTAATGGTGC 1680
Db 1621 GAAATTAAGAGACAGAGAGTACTCTATGTCGATTTCCAGAGAAACCTGACTAATGGTGC 1680
QY 1681 ACTGCTGGCAATGATGATGATGATTAATTTCTCAAGAGAGAGAGAGAGAGAGAGAG 1740
Db 1681 ACTGCTGGCAATGATGATGATGATTAATTTCTCAAGAGAGAGAGAGAGAGAGAGAG 1740
QY 1741 CAGCAATTTCTGACACATGAGATGAGAGATATCACAGTGAAGCAAAATGATCTGAG 1800
Db 1741 CAGCAATTTCTGACACATGAGATGAGAGATATCACAGTGAAGCAAAATGATCTGAG 1800
QY 1801 AAGCAATTTTGTGAGAGACAGAACTGGAATTTACAGATGAGATTTGATTCATGAA 1860
Db 1801 AAGCAATTTTGTGAGAGACAGAACTGGAATTTACAGATGAGATTTGATTCATGAA 1860
QY 1861 GAAAGACAGATGAGATGAGTGAAGAAATGAAATTTGAGTTCTGTTAGTGAAGAA 1920
Db 1861 GAAAGACAGATGAGATGAGTGAAGAAATGAAATTTGAGTTCTGTTAGTGAAGAA 1920
QY 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTGCGGAGAAATTTCCATGCTAAGACTG 1980
Db 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTGCGGAGAAATTTCCATGCTAAGACTG 1980
QY 1981 GAGCTTAGACAAATGAAACATCAGAGCCAGCTRAAAAAAATTTTTTTTTTTTTTTTT 2040
Db 1981 GAGCTTAGACAAATGAAACATCAGAGCCAGCTRAAAAAAATTTTTTTTTTTTTTTTT 2040

RESULT 3

US-09-289-198-303

; Sequence 303, Application US/09289198

; GENERAL INFORMATION:

; APPLICANT: Frudakis, Tony N.

; APPLICANT: Smith, John M.

; APPLICANT: Reed, Steven G.

; APPLICANT: Misher, Lynda

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

;; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
;; FILE REFERENCE: 210121.419C5
;; CURRENT APPLICATION NUMBER: US/09/289,198
;; CURRENT FILING DATE: 1999-04-09
;; EARLIER APPLICATION NUMBER: US 09/062,451
;; EARLIER FILING DATE: 1998-04-17
;; EARLIER APPLICATION NUMBER: US 08/991,789
;; EARLIER FILING DATE: 1997-12-11
;; EARLIER APPLICATION NUMBER: US 08/838,762
;; EARLIER FILING DATE: 1997-04-09
;; EARLIER APPLICATION NUMBER: PCT/US97/00485
;; EARLIER FILING DATE: 1997-01-10
;; EARLIER APPLICATION NUMBER: US 08/700,014
;; EARLIER FILING DATE: 1996-08-20
;; EARLIER APPLICATION NUMBER: US 08/585,392
;; EARLIER FILING DATE: 1996-01-01
;; NUMBER OF SEQ ID NOS: 312
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 303
;; LENGTH: 2040
;; TYPE: DNA
;; ORGANISM: Homo sapien
US-09-289-198-303

Query Match 100.0%; Score 2040; DB 16; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGTTGAGGTGATTCATTCATGCGGCGCTCTCTGTTGTAAGAAAGCATTTGGTCTC 60
Db 1 ATGCTGTTGAGGTGATTCATTCATGCGGCGCTCTCTCTGTTGTAAGAAAGCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGCTGCTCCGTTGCTCCCTGCTGCAAGGAGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGGCAAGTGTGCTGCTCCGTTGCTCCCTGCTGCAAGGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACACAGAGACTCTGCTATGAAAGACACTCAGAGACAAG 180
Db 121 AGCAAGTGGGCACTTCTGAGACACAGAGACTCTGCTATGAAAGACACTCAGAGACAAG 180
QY 181 ATGGGCAAGTGGGCGGCACTGCTCCCTGCTGCAAGGAGAGTGGCAAGACCAAGCTG 240
Db 181 ATGGGCAAGTGGGCGGCACTGCTCCCTGCTGCAAGGAGAGTGGCAAGACCAAGCTG 240
QY 241 GCGCTTCTGAGAGACACAGAGACTCTGCTATGAAAGACACTCAGAAAGATGGGCAAG 300
Db 241 GCGCTTCTGAGAGACACAGAGACTCTGCTATGAAAGACACTCAGAAAGATGGGCAAG 300
QY 301 TGGTGTGCCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGCAAGGTGGCGCTTGG 360
Db 301 TGGTGTGCCACTGCTTCCCTGCTGCAAGGAGAGCGGCAAGAGCAAGGTGGCGCTTGG 360
QY 361 GGAGACTAGCATGACAGTGGCTTCATGAGAGCCAGGTACCACTCGTGGAGAAATCTG 420
Db 361 GGAGACTAGCATGACAGTGGCTTCATGAGAGCCAGGTACCACTCGTGGAGAAATCTG 420
QY 421 GACCACTCCACAGAGCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 421 GACCACTCCACAGAGCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 481 CTCAGGAGACATGAGCTGAAGCAAGAGAGACAGCAAAAGAGAGAGAGAGAGAGAGAG 540
Db 481 CTCAGGAGACATGAGCTGAAGCAAGAGAGAGACAGCAAAAGAGAGAGAGAGAGAGAG 540
QY 541 TCTGCAATGGGAATTCAGAAAGTGAAGTCTCTGAGACAGAGATGCAACTTAAT 600
Db 541 TCTGCAATGGGAATTCAGAAAGTGAAGTCTCTGAGACAGAGATGCAACTTAAT 600
QY 601 GTCTTGACAAACAAAAGAGAGAGAGCTGATTAAGAGCGGTACAAATGCCAGAGAGATGAA 660
Db 601 GTCTTGACAAACAAAAGAGAGAGAGCTGATTAAGAGCGGTACAAATGCCAGAGAGATGAA 660
QY 661 TGTGCTTAATGTTGCTGGAACATGCACTGATCAAAATATTCAGATGATGGAAT 720

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Db 661 TGTGGTTAAATGTTGCTGGAACTGCACTGATCCAAATATCTCCAGATGATGGAAT 720
Qy 721 ACCACTGCACTACGCTATCTATTAATGAATAAATTAATGAGCCAAAGCACTGCTTTA 780
Db 721 ACCACTGCACTACGCTATCTATTAATGAATAAATTAATGAGCCAAAGCACTGCTTTA 780
Qy 781 TATGGTGTGATATGCAATCAAAAACAAGCATGGCTCACAACCTGTTACTGGTGA 840
Db 781 TATGGTGTGATATGCAATCAAAAACAAGCATGGCTCACAACCTGTTACTGGTGA 840
Qy 841 CATGAGCAAAAACACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGA 900
Db 841 CATGAGCAAAAACACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTAAATGA 900
Qy 901 CTGATATATATGGAAGAGAGCTGCTCATCTGCTGATATGTTGGATCAGCAAGTATA 960
Db 901 CTGATATATATGGAAGAGAGCTGCTCATCTGCTGATATGTTGGATCAGCAAGTATA 960
Qy 961 GTCAAGCTTCTACTGAGCAAAAATATATGATGATCTTCAAGATCTATCTGAGACAG 1020
Db 961 GTCAAGCTTCTACTGAGCAAAAATATATGATGATCTTCAAGATCTATCTGAGACAG 1020
Qy 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGGCAGTTACTTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGGCAGTTACTTTCTGACTAC 1080
Qy 1081 AAAGAAAAACAGATCTTAAAAATCTCTCTGAAAACAGCAATCCAGAACAGACTTAAAG 1140
Db 1081 AAAGAAAAACAGATCTTAAAAATCTCTCTGAAAACAGCAATCCAGAACAGACTTAAAG 1140
Qy 1141 CTGACATCAGAGAGAGAGCTCACAAGTTCAAGAGCAGTGAAGAAATAGCAGCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGAGCTCACAAGTTCAAGAGCAGTGAAGAAATAGCAGCAGAGAA 1200
Qy 1201 ATGTCTCAAGAACAGAAATTAATTAAGAGTGTGATAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACAGAAATTAATTAAGAGTGTGATAGAGAGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAAGTAAATATGTTGGATTAAGAAAACCTGACTAATGTTGCTGCTGCTGC 1320
Db 1261 AAGCATGAAAGTAAATATGTTGGATTAAGAAAACCTGACTAATGTTGCTGCTGCTGC 1320
Qy 1321 AATGTTGATTAATGATTAATCTCTCAAGAGAGCAGAACACCTGAAAATAGCAATTT 1380
Db 1321 AATGTTGATTAATGATTAATCTCTCAAGAGAGCAGAACACCTGAAAATAGCAATTT 1380
Qy 1381 CCTGACAAAGAAAGTGAAGAGTATCAGAAATTTGCAATTTGTTCTGACTACAAAGAA 1440
Db 1381 CCTGACAAAGAAAGTGAAGAGTATCAGAAATTTGCAATTTGTTCTGACTACAAAGAA 1440
Qy 1441 AAACGATATGCCAAATTAATCTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db 1441 AAACGATATGCCAAATTAATCTCTGAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Qy 1501 TCAGAGAGAGAGTCAAAAAGCTTGAAGGCACTGAAAATGCGCAGCAGAGAAAAGATCT 1560
Db 1501 TCAGAGAGAGAGTCAAAAAGCTTGAAGGCACTGAAAATGCGCAGCAGAGAAAAGATCT 1560
Qy 1561 CAGAAGCAGAAATTAATTAAGAGTGTGATAGAGACTAGAAAATTTTATGGCTATCGAA 1620
Db 1561 CAGAAGCAGAAATTAATTAAGAGTGTGATAGAGACTAGAAAATTTTATGGCTATCGAA 1620
Qy 1621 GAAATGAAGAGAGCAGAGAGTCTCATGTCGATATCCAGAAAACCTGACTAATGGTGC 1680
Db 1621 GAAATGAAGAGAGCAGAGAGTCTCATGTCGATATCCAGAAAACCTGACTAATGGTGC 1680
Qy 1681 ACTGCTGCAATGATGATGATGATTAATTTCTCCAAAGAGAGCAGAACACTGTAAGAC 1740
Db 1681 ACTGCTGCAATGATGATGATGATTAATTTCTCCAAAGAGAGCAGAACACTGTAAGAC 1740
Qy 1741 CAGCAATTTCTGACACTGAGAAATGAAGTATCAGAGTGAAGAACAAAATGATCTCAG 1800
Db 1741 CAGCAATTTCTGACACTGAGAAATGAAGTATCAGAGTGAAGAACAAAATGATCTCAG 1800

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Db 1741 CAGCAATTTCTGACACTGAGAAATGAAGATATCAGAGTGAAGAACAAAATGATCTCAG 1800
Qy 1801 AAGCAATTTTGGAGAAACAGAACTGGAATATTAACAGATGATGATTTGATCATGA 1860
Db 1801 AAGCAATTTTGGAGAAACAGAACTGGAATATTAACAGATGATGATTTGATCATGA 1860
Qy 1861 GAAAGCAGATGAAGTGTGAAAAATTAATGATTTCTGAGCTTTCTTATGTTGAAGAA 1920
Db 1861 GAAAGCAGATGAAGTGTGAAAAATTAATGATTTCTGAGCTTTCTTATGTTGAAGAA 1920
Qy 1921 GAAAAAGACATCTTCATGAAAAATAGTACGTTCGGGAGAGAAATTTGCCATGCTAAGACTG 1980
Db 1921 GAAAAAGACATCTTCATGAAAAATAGTACGTTCGGGAGAGAAATTTGCCATGCTAAGACTG 1980
Qy 1981 GAGCTAGACACATGAATGAATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAAATGAAAA 2040
Db 1981 GAGCTAGACACATGAATGAATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAAATGAAAA 2040

RESULT 4
US-09-429-755-303
; Sequence 303, Application US/09429755A
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, David C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C6
; CURRENT FILING DATE: US/09/429,755A
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-429-755-303

Query Match 100.0%; Score 2040; DB 18; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 421 GACAACTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAGAAAGATCTCATCGTCAG 480
DB 421 GACAACTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAGAAAGATCTCATCGTCAG 480
QY 481 CTCAGGAGACTGACGTGAACAAGAGCAAGCAAAAAGAGACTGCTTACATCTGGCC 540
DB 481 CTCAGGAGACTGACGTGAACAAGAGCAAGCAAAAAGAGACTGCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAGTACTAAACCTCTGCTGGACAGACGATGTCACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAGTACTAAACCTCTGCTGGACAGACGATGTCACTTAAT 600
QY 601 GTCTCTGACAAACAAAAGAGACAGCTCTGATTAAGGCGGTACAAATGCGAGGAATGAA 660
DB 601 GTCTCTGACAAACAAAAGAGAGAGCTCTGATTAAGGCGGTACAAATGCGAGGAATGAA 660
QY 661 TGTGCGTTAATGTGTGCTGGAACTGGACCTGATCCAAATATTCAGATGATGGAAT 720
DB 661 TGTGCGTTAATGTGTGCTGGAACTGGACCTGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTGCACTACGCTATCTATATGAAGTAAATTAATGCGCAAGACACTGCTCTTA 780
DB 721 ACCACTGCACTACGCTATCTATATGAAGTAAATTAATGCGCAAGACACTGCTCTTA 780
QY 781 TATGCTGCTGATATCGAATCAAAAAACAAGCATGGCTCACACCTGTTACTTGCTTA 840
DB 781 TATGCTGCTGATATCGAATCAAAAAACAAGCATGGCTCACACCTGTTACTTGCTTA 840
QY 841 CATAGCAAAAAACAGCAAGCTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
DB 841 CATAGCAAAAAACAGCAAGCTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATATGATATGAAGAGACTGCTCTACTTGTGTATGTTGTGAACAGATTA 960
DB 901 CTGATATGATATGAAGAGACTGCTCTACTTGTGTATGTTGTGAACAGATTA 960
QY 961 GTGAGCCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGGACAGCG 1020
DB 961 GTGAGCCTTCTACTTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGGACAGCG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATTAATTTGCGAGTTACTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATTAATTTGCGAGTTACTTCTGACTAC 1080
QY 1081 AAAGAAAAAGAGATGCTAAAAATCTCTTCTGAAAAAGCAATTCAGAAACAGACTTAAAG 1140
DB 1081 AAAGAAAAAGAGATGCTAAAAATCTCTTCTGAAAAAGCAATTCAGAAACAGACTTAAAG 1140
QY 1141 CTGACATCAGAGAAAGATCACAAGAGTTCAAAAGCAGTGAATATAGCCAGAGAGAA 1200
DB 1141 CTGACATCAGAGAAAGATCACAAGAGTTCAAAAGCAGTGAATATAGCCAGAGAGAA 1200
QY 1201 ATGCTCTAAGAACAGAAATTAATTAAGATGCTGATAGAGAGTTGGAAGAAATGAAG 1260
DB 1201 ATGCTCTAAGAACAGAAATTAATTAAGATGCTGATAGAGAGTTGGAAGAAATGAAG 1260
QY 1261 AAGCAGAAAGTAAATATGCGGATTAATCTGAAAAACCTGACTAATGCTGCTGCTG 1320
DB 1261 AAGCAGAAAGTAAATATGCGGATTAATCTGAAAAACCTGACTAATGCTGCTGCTG 1320
QY 1321 AATGCTGATATGATTAATCTCTCAAAAGAGAGAGCAACCTGAAATTCAGCAATTT 1380
DB 1321 AATGCTGATATGATTAATCTCTCAAAAGAGAGAGCAACCTGAAATTCAGCAATTT 1380
QY 1381 CCGTACAAAGAAAGTGAAGATATCAGAAATTTGCAATTTAGTTTCTGACTCAAAAGAA 1440
DB 1381 CCGTACAAAGAAAGTGAAGATATCAGAAATTTGCAATTTAGTTTCTGACTCAAAAGAA 1440
QY 1441 AAACCAATGCCAAATATCTTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
DB 1441 AAACCAATGCCAAATATCTTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500

```

```

QY 1501 TCAGAGAGAGAGTCCACAAAGCTTGAGGCACTGAAATATGCCAGCCAGAGAAAGATCT 1560
DB 1501 TCAGAGAGAGAGTCCACAAAGCTTGAGGCACTGAAATATGCCAGCCAGAGAAAGATCT 1560
QY 1561 CAAGAACCGAAATTAATTAAGATGCTGATTAAGAGAGCTGAAATTTTATGCTATGAA 1620
DB 1561 CAAGAACCGAAATTAATTAAGATGCTGATTAAGAGAGCTGAAATTTTATGCTATGAA 1620
QY 1621 GAAATGAAAGACACGGAAGTACTGATGCGGATTTCCAGAAACCTGACTAATGCTGCC 1680
DB 1621 GAAATGAAAGACACGGAAGTACTGATGCGGATTTCCAGAAACCTGACTAATGCTGCC 1680
QY 1681 ACTGCTGGCAATGATGATGATGATTAATCTCTCCAGAGAGAGCAAGAACCTGAAAGC 1740
DB 1681 ACTGCTGGCAATGATGATGATGATTAATCTCTCCAGAGAGAGCAAGAACCTGAAAGC 1740
QY 1741 CAGCAATTTCTGACACAGAGAAATGAGTATCAAGATGAGCAAGCAAAATGATCTAG 1800
DB 1741 CAGCAATTTCTGACACAGAGAAATGAGTATCAAGATGAGCAAGCAAAATGATCTAG 1800
QY 1801 AAGCAATTTTGTGAAGAACAGACACTGGAATATTACAGATGAGATTTCTGATTCATGAA 1860
DB 1801 AAGCAATTTTGTGAAGAACAGACACTGGAATATTACAGATGAGATTTCTGATTCATGAA 1860
QY 1861 GAAAAAGCAGATGAAAGTGTGAAAAATGAATTTCTGAGCTTCTCTTATGTTGAAGAA 1920
DB 1861 GAAAAAGCAGATGAAAGTGTGAAAAATGAATTTCTGAGCTTCTCTTATGTTGAAGAA 1920
QY 1921 GAAAAAGCAGATGAAAGTGTGAAAAATGATGCTGCGGGAAGAAATGCGATCTAAGACTG 1980
DB 1921 GAAAAAGCAGATGAAAGTGTGAAAAATGATGCTGCGGGAAGAAATGCGATCTAAGACTG 1980
QY 1981 GAGCTAGACACATGMAATGMAATGATGCTGCGGGAAGAAATGCGATCTAAGACTG 2040
DB 1981 GAGCTAGACACATGMAATGMAATGATGCTGCGGGAAGAAATGCGATCTAAGACTG 2040

```

```

RESULT 5
US-09-443-686-375
; Sequence 375, Application US/09443686
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Reiter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9A
; CURRENT APPLICATION NUMBER: US/09/443,686
; CURRENT FILING DATE: 1999-11-18
; NUMBER OF SEQ ID NOS: 551
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-443-686-375

```

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Query Match 100.0%; Score 2040; DB 18; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTGTTGAGTTGATTCATGCGGCTCTTCTGTAAGAACCATTTGGCTC 60
DB 1 ATGCTGTTGAGTTGATTCATGCGGCTCTTCTGTAAGAACCATTTGGCTC 60

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61 AGGACCAAGATGGGCAAGTGTGCTGCGTTCCTCCCTGCTGCAGGAGGAGCGGCAAG 120
61 AGGACCAAGATGGGCAAGTGTGCTGCGTTCCTCCCTGCTGCAGGAGGAGCGGCAAG 120
121 AGCAACGTGGGCACTTCTTGAGACCAACGACGCTGCTATGAAGACTCAGAGCAAG 180
121 AGCAACGTGGGCACTTCTTGAGACCAACGACGCTGCTATGAAGACTCAGAGCAAG 180
181 ATGGGCAAGTGTGGCGGCACTGCTTCCTGCTGAGGGGAGTGGGCAAGCAACGTCG 240
181 ATGGGCAAGTGTGGCGGCACTGCTTCCTGCTGAGGGGAGTGGGCAAGCAACGTCG 240
241 GCGGCTTGTGAGACGACGACGACTCTGCTATGAAGACACTCAGCAACGATGGGCAAG 300
241 GCGGCTTGTGAGACGACGACGACTCTGCTATGAAGACACTCAGCAACGATGGGCAAG 300
301 TGGTCTGCTGCTGCTTCCCTGCTGAGGGGAGCGGCAAGCAAGGCTGGGCGCTTGG 360
301 TGGTCTGCTGCTGCTTCCCTGCTGAGGGGAGCGGCAAGCAAGGCTGGGCGCTTGG 360
361 GGAGACTAGATGACAGTGCCTTCATGAGCCAGGTACAGTCCGTGGAGAGATCTG 420
361 GGAGACTAGATGACAGTGCCTTCATGAGCCAGGTACAGTCCGTGGAGAGATCTG 420
421 GACAAGCTCCACAGAGCTGCTGTGGGTTAAAGTCCCGAAGAGGATCTCATCTGATG 480
421 GACAAGCTCCACAGAGCTGCTGTGGGTTAAAGTCCCGAAGAGGATCTCATCTGATG 480
481 CTCAGAGGACCTGACGTGACAAAGAGCAAGCAAGAGAGAGCTGCTTACATCTGGCC 540
481 CTCAGAGGACCTGACGTGACAAAGAGCAAGCAAGAGAGAGCTGCTTACATCTGGCC 540
541 TGTGCAATGGGAATTCAGAAATAGTAAACATCCTGCTGAGAGAGATGCAACTAT 600
541 TGTGCAATGGGAATTCAGAAATAGTAAACATCCTGCTGAGAGAGATGCAACTAT 600
601 GTCTTGAACAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
601 GTCTTGAACAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
661 TGTGGCTTAAATGTCTGAGACATGGGCACTGATCCAAATATTCAGATAGATGAAAT 720
661 TGTGGCTTAAATGTCTGAGACATGGGCACTGATCCAAATATTCAGATAGATGAAAT 720
721 ACCACTGTGCACTAGGCTTCTATATGAAGATTAATTAATGAGGCAAGCACTGCTTA 780
721 ACCACTGTGCACTAGGCTTCTATATGAAGATTAATTAATGAGGCAAGCACTGCTTA 780
781 TATGCTGTGATATGGAATCAAAAAAAGAGATGGGCTCACAACACTGTTACTGGTGA 840
781 TATGCTGTGATATGGAATCAAAAAAAGAGATGGGCTCACAACACTGTTACTGGTGA 840
841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
901 CTGATAGATATGGAAGAGCTGCTCATACTTGTGCTATGTTGGATGACAGAGTATA 960
901 CTGATAGATATGGAAGAGCTGCTCATACTTGTGCTATGTTGGATGACAGAGTATA 960
961 GTGAGCCTTCTACTTGAAGCAAAATATGATGTATCTTCAAGATCTATCTGAGACAG 1020
961 GTGAGCCTTCTACTTGAAGCAAAATATGATGTATCTTCAAGATCTATCTGAGACAG 1020
1021 GCCAAGAGTATGCTGTTTCTGATCATCATATTAATTTGCCAGTTACTTTCTGACTAC 1080
1021 GCCAAGAGTATGCTGTTTCTGATCATCATATTAATTTGCCAGTTACTTTCTGACTAC 1080
1081 AAGAGAAAAACAGATCTAAATCTCTTCTGAAAAACAGAAATCCAGAAACAACTTAAAG 1140
1081 AAGAGAAAAACAGATCTAAATCTCTTCTGAAAAACAGAAATCCAGAAACAACTTAAAG 1140
1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAGAGCAATGAAATAGCCAGCCAGAGAAA 1200

1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAGAGCAATGAAATAGCCAGCAGAGAAA 1200
1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGTGATAGAGAGTGAACAAAGATGAG 1260
1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGTGATAGAGAGTGAACAAAGATGAG 1260
1261 AAGCATGAAGATTAATTAATGAGATTAATTAAGAAACCTGACTAATGTTCTCATCTG 1320
1261 AAGCATGAAGATTAATTAATGAGATTAATTAAGAAACCTGACTAATGTTCTCATCTG 1320
1321 AATGCTGAATATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
1321 AATGCTGAATATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
1381 CCTGACAAAGAGAGAGATATCACAATTTTGGGAAATTTAGTTTCTGACTACAAAGAA 1440
1381 CCTGACAAAGAGAGATATCACAATTTTGGGAAATTTAGTTTCTGACTACAAAGAA 1440
1441 AAGCATGATCCAAATATCTCTCTGAAACAGCAACCCAGAAACAGACTTAAAGCTGACA 1500
1441 AAGCATGATCCAAATATCTCTCTGAAACAGCAACCCAGAAACAGACTTAAAGCTGACA 1500
1501 TCAGAGAGAGAGTCAACAAAGGCTTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAT 1560
1501 TCAGAGAGAGAGTCAACAAAGGCTTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAT 1560
1561 CAAGAACCAAGAAATTAATTAAGATGTGATAGAGAGTGAAGAAATTTTATGCTATCGAA 1620
1561 CAAGAACCAAGAAATTAATTAAGATGTGATAGAGAGTGAAGAAATTTTATGCTATCGAA 1620
1621 GAAATGAAGAGAGAGAGATCTCATGTCGAGTTCCAGAAACCTGACTAATGAGTGGC 1680
1621 GAAATGAAGAGAGAGAGATCTCATGTCGAGTTCCAGAAACCTGACTAATGAGTGGC 1680
1681 ACTGCTGGCAATGTGATGATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAG 1740
1681 ACTGCTGGCAATGTGATGATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAG 1740
1741 CAGCAATTTTCTGACACTGAGAAATGAAGATATCAGAGTGAAGCAAAAAATGATCTCAG 1800
1741 CAGCAATTTTCTGACACTGAGAAATGAAGATATCAGAGTGAAGCAAAAAATGATCTCAG 1800
1801 AAGCAATTTTGAAG 1860
1801 AAGCAATTTTGAAG 1860
1861 AAGCAATTTTGAAG 1920
1861 AAGCAATTTTGAAG 1920
1921 GAAAAAGACATCTGATGAGAAATAGTACGTTGGGAGAGAAATTTCCATGCTAAGACTG 1980
1921 GAAAAAGACATCTGATGAGAAATAGTACGTTGGGAGAGAAATTTCCATGCTAAGACTG 1980
1981 GAGCTAGACACATGAATCATCAGAGCCAGCTTAAAAAAGAGAGAGAGAGAGAGAG 2040
1981 GAGCTAGACACATGAATCATCAGAGCCAGCTTAAAAAAGAGAGAGAGAGAGAGAG 2040

RESULT 6
US-09-483-672A-375
; Sequence 375, Application US/09483672A
; GENERAL INFORMATION:
; APPLICANT: Xu, JIANGCHUN
; APPLICANT: Dillon, DAVID C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang YUQU
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.

APPLICANT: Solk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Wang, Aijun
APPLICANT: Meagher, Madeleine
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.42711C1
CURRENT APPLICATION NUMBER: US/09/483.672A
NUMBER OF SEQ ID NOS: 390
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-483-672A-375

Query Match 100.0% Score 2040: DB 18: Length 2040:
Best Local Similarity 100.0% Pred. No. 0;
Matches 2040: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGGTTGAGGTGATTCATGCGGCTGCTCTTCTGTGAAGAACCATTTGGTCTC 60
DB 1 ATGGTGGTTGAGGTGATTCATGCGGCTGCTCTTCTGTGAAGAACCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAATGGTGGTGGCTGCTCTTCTGCTGAGGAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAATGGTGGTGGCTGCTCTTCTGCTGAGGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGACCAGCAGCTCTGCTATGAAGACCTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTGAGACCAGCAGCTCTGCTATGAAGACCTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAACGTG 240
DB 181 ATGGGCAAGTGGTGGGCGGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAACGTG 240
QY 241 GGCCCTTCTGGAGACACAGGAGCTGCTGTGAAGACACTCAGAAACATATGGGCAAG 300
DB 241 GGCCCTTCTGGAGACACAGGAGCTGCTGTGAAGACACTCAGAAACATATGGGCAAG 300
QY 301 TGGTGGTGGCACTGCTTCCCTGCTGCAAGGAGGAGCGGCAAGAGTGGGCGCTTGG 360
DB 301 TGGTGGTGGCACTGCTTCCCTGCTGCAAGGAGGAGCGGCAAGAGTGGGCGCTTGG 360
QY 361 GGAGACTACGATGACATGCTGCTTATGAGGCCAGGTAACCACTGCTGAGAAAGATCTG 420
DB 361 GGAGACTACGATGACATGCTGCTTATGAGGCCAGGTAACCACTGCTGAGAAAGATCTG 420
QY 421 GACAACTCCACAGAGCTGCTGGTGGGTAAGTCCCGCAAGAAAGATCTCATGCTATG 480
DB 421 GACAACTCCACAGAGCTGCTGGTGGGTAAGTCCCGCAAGAAAGATCTCATGCTATG 480
QY 481 CTCAGGGACACTGACGTGAACAAGAGACAAAGAGGACTGCTTACATCTGACC 540
DB 481 CTCAGGGACACTGACGTGAACAAGAGACAAAGAGGACTGCTTACATCTGACC 540
QY 541 TCTGCGCAATGGGAATTTAGAAAGTAACTCTGCTGACAGACGATGCAACTTAAT 600
DB 541 TCTGCGCAATGGGAATTTAGAAAGTAACTCTGCTGACAGACGATGCAACTTAAT 600
QY 601 GTCTTTGACAAACAAAAGAGACGCTGTATAAAGGCGGTACAAATCCAGGAAGATGAA 660
DB 601 GTCTTTGACAAACAAAAGAGACGCTGTATAAAGGCGGTACAAATCCAGGAAGATGAA 660
QY 661 TGTGCGTAAATGTTGCTGGAACATGGCACTGATCAAAATTTCCAGATGATGAAT 720
DB 661 TGTGCGTAAATGTTGCTGGAACATGGCACTGATCAAAATTTCCAGATGATGAAT 720
QY 721 ACCACTCTGACCTACGCTATCTTAAATGAAGATTAATTAAGGCCAAAGCAGCTCTTAA 780
DB 721 ACCACTCTGACCTACGCTATCTTAAATGAAGATTAATTAAGGCCAAAGCAGCTCTTAA 780

QY 781 TATGCTGCTGATATGCAATCAAAAAAAGACATGGCCTTCACACACTGTTACTGTGTGA 840
DB 781 TATGCTGCTGATATGCAATCAAAAAAAGACATGGCCTTCACACACTGTTACTGTGTGA 840
QY 841 CATGAGCAAAAACACCAAGTCTGAAATTTTAAATCAGAAAAAAGCGAATTTAAATGCA 900
DB 841 CATGAGCAAAAACACCAAGTCTGAAATTTTAAATCAGAAAAAAGCGAATTTAAATGCA 900
QY 901 CTGATATGATGGAAGAGCTGCTCATACTTGTGATGTTGGATGATGACAGATATA 960
DB 901 CTGATATGATGGAAGAGAGCTGCTCATACTTGTGATGTTGGATGATGACAGATATA 960
QY 961 GTACACCTTTACTGTTGACCAAAATTTATGATATCTTCTCAAGATCTATCTGACAGAG 1020
DB 961 GTACACCTTTACTGTTGACCAAAATTTATGATATCTTCTCAAGATCTATCTGACAGAG 1020
QY 1021 GCCAAGAGTATGCTGTTTCTAGTATCATCATGTAATTTGGCAGTACTTTGACTAC 1080
DB 1021 GCCAAGAGTATGCTGTTTCTAGTATCATCATGTAATTTGGCAGTACTTTGACTAC 1080
QY 1081 AAAGAAAAACAGATGCTTAAAAATCTCTCTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
DB 1081 AAAGAAAAACAGATGCTTAAAAATCTCTCTGAAAAACAGCAATCCAGAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGGAAGTCAACAAAGTTCAAAAGCACTGAAAAATAGCCACCAAGAGAAA 1200
DB 1141 CTGACATCAGAGGAAGTCAACAAAGTTCAAAAGCACTGAAAAATAGCCACCAAGAGAAA 1200
QY 1201 ATGCTCAGAAACCAAGAAATTAATGAAGATGCTATAGAGAGTTGAAGAAATGAAG 1260
DB 1201 ATGCTCAGAAACCAAGAAATTAATGAAGATGCTATAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGTAAATATGTTGGATTAATAGTAAACCTGACTAATGGTCTACTGCTGCG 1320
DB 1261 AAGCATGAAGTAAATATGTTGGATTAATAGTAAACCTGACTAATGGTCTACTGCTGCG 1320
QY 1321 AATGCTGTAATGATTAATTTCTTCAAAAGAGACAGACACTGAAATCAGCAATTT 1380
DB 1321 AATGCTGTAATGATTAATTTCTTCAAAAGAGAGACAGACACTGAAATCAGCAATTT 1380
QY 1381 CCTGACAAACGAAGTGAAGAGTATCAGAAATTTGGCAATTAAGTTTCTGACTACAAAAGAA 1440
DB 1381 CCTGACAAACGAAGTGAAGAGTATCAGAAATTTGGCAATTAAGTTTCTGACTACAAAAGAA 1440
QY 1441 AAACAGATGCCAAATATCTCTTCTGAAAAACAGCAACCAAGCAAGACTTAAAGCTGACA 1500
DB 1441 AAACAGATGCCAAATATCTCTTCTGAAAAACAGCAACCAAGCAAGACTTAAAGCTGACA 1500
QY 1501 TCAAGAGAGAGTACAAAGGCTTGAAGGCAAGTGAAGTGAAGGCGCAGCAAGAAAAAGATCT 1560
DB 1501 TCAAGAGAGAGTACAAAGGCTTGAAGGCAAGTGAAGTGAAGGCGCAGCAAGAAAAAGATCT 1560
QY 1561 CAAGAACAGAAATTAATGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 1620
DB 1561 CAAGAACAGAAATTAATGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 1620
QY 1621 GAAATGAAGAGAGAGAGTACTCATGTGGAATTTCCCAAGAAACCTGACTAATGAGTGC 1680
DB 1621 GAAATGAAGAGAGAGAGTACTCATGTGGAATTTCCCAAGAAACCTGACTAATGAGTGC 1680
QY 1681 ACTGCTGGCAATGATGATGATTAATTTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
DB 1681 ACTGCTGGCAATGATGATGATTAATTTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
QY 1741 CAGCAATTTCTGACACTGGAATGAAGAGTATACAGAGTGAAGAGAGAGAGAGAGAGAGAGAG 1800
DB 1741 CAGCAATTTCTGACACTGGAATGAAGAGTATACAGAGTGAAGAGAGAGAGAGAGAGAGAGAG 1800
QY 1801 AAGCAATTTTGTGAAG 1860
DB 1801 AAGCAATTTTGTGAAG 1860

[illegible]

```

RESULT 7
US-09-534-825A-303
Sequence 303, Application US/09534825A
GENERAL INFORMATION:
APPLICANT: Fridakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
APPLICANT: Misher, Lynda
APPLICANT: Retter, Marc W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE REFERENCE: 210121.419C7
CURRENT APPLICATION NUMBER: US/09/534, 825A
NUMBER OF SEQ ID NOS: 317
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 303
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-534-825A-303

```

Query Match	100.0%	Score 2040;	DB 20;	Length 2040;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2040;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

D _b	1	ATGGTGGTTGAGGTTGATTCATCATGCGCGGCTGCCCTTCTGTGAAGAAGCATTTGGGTCTC	60
Q _y	61	AGGAGCAAGATGGGCAAGTGGTGTGCTGCCGTTGCTTCCCTGCTGCAAGGAGACGGCCAAg	120
D _b	61	AGGAGCAAGATGGGCAAGTGGTGTGCTGCCGTTGCTTCCCTGCTGCAAGGAGACGGCCAAg	120
Q _y	121	AGCAACCTGGGCACTTCTGTGGAGACACAGACACTCTCTATGAAGACACTCAGAGACAAG	180
D _b	121	AGCAACCTGGGCACTTCTGTGGAGACACAGACACTCTCTATGAAGACACTCAGAGACAAG	180
Q _y	181	ATTGGGCAAGTGTGTCGCCGCACTGTTCCCTGCTGCAAGGGGAGTGGCAAGACCAACGTg	240
D _b	181	ATTGGGCAAGTGTGTCGCCGCACTGTTCCCTGCTGCAAGGGGAGTGGCAAGACCAACGTg	240
Q _y	241	GGGCCTTCTGTGAGACACAGACACTGCTATGAAGACACTCAGAAACAAGATGGGCAAG	300
D _b	241	GGGCCTTCTGTGAGACACAGACACTGCTATGAAGACACTCAGAAACAAGATGGGCAAG	300
Q _y	301	TGGTGTCCGCACTCTTCCCTGCTGTGAGGGGGGAGCGGCAAGCAAGGTGGGCGCTTGG	360
D _b	301	TGGTGTCCGCACTCTTCCCTGCTGTGAGGGGGGAGCGGCAAGCAAGGTGGGCGCTTGG	360
Q _y	361	GGAGACTACGATGACACTGTGCTTCATGAGAGCCAGTACCACGTCGGTGAGAGAAGATCTg	420
D _b	361	GGAGACTACGATGACACTGTGCTTCATGAGAGCCAGTACCACGTCGGTGAGAGAAGATCTg	420
Q _y	421	GACAAAGTCCCAAGAGTGGCTGGTGGGGTAAAGTCCCCAGAAAGAAATCTCATGCTCATAG	480
D _b	421	GACAAAGTCCCAAGAGTGGCTGGTGGGGTAAAGTCCCCAGAAAGAAATCTCATGCTCATAG	480
Q _y	481	CTCAGGACACTGCAGTGAACAAGAAAGACAAAGCAAAAAGAGAGACTGTCTACATCTGGGC	540

Dd	481	CTCAGGACACTGACGTGAACAGAAAGAGACAGCAAAAGAGACAGCTGCTCTACATCTGGCC	540
Oy	541	TCCTGCATGGGAATTTCAGAAAGTAAATACTCTGCTGCAGACAGATGTCAACTTAAT	600
Dd	541	TCCTGCATGGGAATTTCAGAAAGTAAATACTCTGCTGCAGACAGAGATGTCAACTTAAT	600
Oy	601	GTCCTTGACAACAATAAAGAGACAGCTCTGATTAAGAGCCGTCAATTGCCAGAGATGAA	660
Dd	601	GTCCTTGACAACAATAAAGAGACAGCTCTGATTAAGAGCCGTCAAAATGCCAGAGATGAA	660
Oy	661	TGTGGTAAATGTTGGCGGGAACATGGCAGCTGATCCAAATATTCCAGATGAGATGGAAT	720
Dd	661	TGTGGTAAATGTTGGCGGGAACATGGCAGCTGATCCAAATATTCCAGATGAGATGGAAT	720
Oy	721	ACCACCTGACACTACGCTATCTTAATTAAGAATAAATTAATGCCAAAGCACTGCTCTTA	780
Dd	721	ACCACCTGACACTACGCTATCTTAATTAAGAATAAATTAATGCCAAAGCACTGCTCTTA	780
Oy	781	TATGGTGTGATATCGAATCAAAAACAGCAATGCGCTCACACCACTGTTACTTGGTGTA	840
Dd	781	TATGGTGTGATATCGAATCAAAAACAGCAATGCGCTCACACCACTGTTACTTGGTGTA	840
Oy	841	CATAGCAAAAAACAGCAATGCGTAATTTTAACTCAAAAAAAGCGAATTTAATATCA	900
Dd	841	CATAGCAAAAAACAGCAATGCGTAATTTTAACTCAAAAAAAGCGAATTTAATATCA	900
Oy	901	CTGGATGATATGGAAGAGACTGCTCTCATCTCTGATGTTGGTGGATCAGCAAGTTA	960
Dd	901	CTGGATGATATGGAAGAGACTGCTCTCATCTCTGATGTTGGTGGATCAGCAAGTTA	960
Oy	961	GTCAGCCTTACTTGTGAGCAAAATATTGATGATATCTTCTCAAGATCTATCTGGACAGC	1020
Dd	961	GTCAGCCTTACTTGTGAGCAAAATATTGATGATATCTTCTCAAGATCTATCTGGACAGC	1020
Oy	1021	GCCAGAGAGTATGCTGTTTCTAATCATCATATGTAATTTGCCAGTACTTCTACATAC	1080
Dd	1021	GCCAGAGAGTATGCTGTTTCTAATCATCATATGTAATTTGCCAGTACTTCTACATAC	1080
Oy	1081	AAAGAAAAACAGATGCTTAATAATCTCTTGAAACAGCAATCCAGAACAACTTAAAG	1140
Dd	1081	AAAGAAAAACAGATGCTTAATAATCTCTTGAAACAGCAATCCAGAACAACTTAAAG	1140
Oy	1141	CTGACATCAGAGGAAGATCACAAGGTTCAAAAGGCAAGTGAATAATAGCCAGCCAGAGAA	1200
Dd	1141	CTGACATCAGAGGAAGATCACAAGGTTCAAAAGGCAAGTGAATAATAGCCAGCCAGAGAA	1200
Oy	1201	ATGCTCTCAAGAACCAAGAAATTAATTAAGATGTTGATAGAGAGTTGAAAGAAATGAAG	1260
Dd	1201	ATGCTCTCAAGAACCAAGAAATTAATTAAGATGTTGATAGAGAGTTGAAAGAAATGAAG	1260
Oy	1261	AAGCATGAACCTAATTAATGTTGGGTTAATCTTGAAACCTGACATTAATGTTGCTCAGCTGCG	1320
Dd	1261	AAGCATGAACCTAATTAATGTTGGGTTAATCTTGAAACCTGACATTAATGTTGCTCAGCTGCG	1320
Oy	1321	AATGGTGAATTAATGATTAATTCCTCAAAAGCAAGACAGAAACCTGTAATAATAGCAATTT	1380
Dd	1321	AATGGTGAATTAATGATTAATTCCTCAAAAGCAAGACAGAAACCTGTAATAATAGCAATTT	1380
Oy	1381	CTGTGCAACGAAGTGAAGATATCACAAGATTTGCGAATTAAGTTTCTGATCTACAAAGAA	1440
Dd	1381	CTGTGCAACGAAGTGAAGATATCACAAGATTTGCGAATTAAGTTTCTGATCTACAAAGAA	1440
Oy	1441	AAACAGATGCCAAATATCTCTTGAAACAGCAACCCAGAAACAAAGACTTAAGCTGACAA	1500
Dd	1441	AAACAGATGCCAAATATCTCTTGAAACAGCAACCCAGAAACAAAGACTTAAGCTGACAA	1500
Oy	1501	TCAGAGGAAGATGACAAAGGCTTTGAAGGCACTGAATAATGGCCAGCAGAGAAAGATCT	1560
Dd	1501	TCAGAGGAAGATGACAAAGGCTTTGAAGGCACTGAATAATGGCCAGCAGAGAAAGATCT	1560
Oy	1561	CAAGAACCCAGAAATTAATTAAGATGTTGATAGAGACTAGAAAATTTATGGCTATCGAA	1620
Dd	1561	CAAGAACCCAGAAATTAATTAAGATGTTGATAGAGACTAGAAAATTTATGGCTATCGAA	1620

Db 1561 CAAGACCAGAAATTAATAGCATGTGATAGAGAGCTAGAAAAATTTTATGCTATCGAA 1620
QY 1621 GAAATGAAAGACACGGAAGTACTCATGTGCGATTCGCCAGAAAACTGACTAATGTGCGC 1680
Db 1621 GAAATGAAAGACACGGAAGTACTCATGTGCGATTCGCCAGAAAACTGACTAATGTGCGC 1680
QY 1681 ACTGCTGGCAATGTGTGATGATGATTAATTCCTCCAGAGAGACAGAACCTGGAAGC 1740
Db 1681 ACTGCTGGCAATGTGTGATGATGATTAATTCCTCCAGAGAGACAGAACCTGGAAGC 1740
QY 1741 CAGCAATTCCTGACACGAGATGAAGAGATATCAAGTGCAGAACAAAAATGATATCTAG 1800
Db 1741 CAGCAATTCCTGACACGAGATGAAGAGATATCAAGTGCAGAACAAAAATGATATCTAG 1800
QY 1801 AAGCAATTTTGTGAAGAACACAGACCTGGAATTTACAGATGAGATCTGATTCATGAA 1860
Db 1801 AAGCAATTTTGTGAAGAACACAGACCTGGAATTTACAGATGAGATCTGATTCATGAA 1860
QY 1861 GAAAAGCAGATGAAAGTGTGTTGAAAAATGAAATTCGTGAGCTTCTGATGTTAGAAA 1920
Db 1861 GAAAAGCAGATGAAAGTGTGTTGAAAAATGAAATTCGTGAGCTTCTGATGTTAGAAA 1920
QY 1921 GAAAAGCAGATGAAAGTGTGTTGAAAAATGAAATTCGTGAGCTTCTGATGTTAGAAA 1980
Db 1921 GAAAAGCAGATGAAAGTGTGTTGAAAAATGAAATTCGTGAGCTTCTGATGTTAGAAA 1980
QY 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAAATGAAAA 2040
Db 1981 GAGCTAGACACATGAAACATCAGAGCCAGCTAAAAAATGAAAAAATGAAAAAATGAAAA 2040

RESULT 8

US-09-536-857-375

: Sequence 375, Application US/09536857

: GENERAL INFORMATION:

: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jians, Yuhui
: APPLICANT: Reed, Steven G.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Reiter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.42712C12
: CURRENT APPLICATION NUMBER: US/09/536,857
: NUMBER OF SEQ ID NOS: 592
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 375
: LENGTH: 2040
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-536-857-375

Query Match 100.0%; Score 2040; DB 20; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTGTTGAGTTGATTCATCGCGTCCCTCTCTGTGGAAGAGCCATTGGTCTC 60
Db 1 ATGTGTGTTGAGTTGATTCATCGCGTCCCTCTCTGTGGAAGAGCCATTGGTCTC 60
QY 61 AGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTCAGGAGAGCGGCAAG 120
Db 61 AGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTCAGGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTGTGAGACCAAGACAGACACTCTGATGAAGACATCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTGTGAGACCAAGACAGACACTCTGATGAAGACATCAGAGCAAG 180

Db 121 AGCAAGTGGGCACTTGTGAGACCAAGACAGACACTCTGATGAAGACATCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGCGCACTGCTTCCCTGCTGTCAGAGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGTGCGCGCACTGCTTCCCTGCTGTCAGAGGGAGTGGCAAGCAAGCTG 240
QY 241 GGGCTTCTGAGAGACACAGACACTGCTATGAAGACACTCAGAGAACAGATGGGCAAG 300
Db 241 GGGCTTCTGAGAGACACAGACACTGCTATGAAGACACTCAGAGAACAGATGGGCAAG 300
QY 301 TGGTGTCCCACTGCTTCCCTGCTGTCAGAGGGAGGAGGCAAGAGTGGGCTTGG 360
Db 301 TGGTGTCCCACTGCTTCCCTGCTGTCAGAGGGAGGAGGCAAGAGTGGGCTTGG 360
QY 361 GGAGACTACATGACAGTGCCTTCATGAGGCCAGGTACACAGTCCGCGAGAGATCTG 420
Db 361 GGAGACTACATGACAGTGCCTTCATGAGGCCAGGTACACAGTCCGCGAGAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGCTGAGGGAAGTCCCAAGAAAGATCTCATGTCATG 480
Db 421 GACAAGCTCCACAGAGCTGCTGCTGAGGGAAGTCCCAAGAAAGATCTCATGTCATG 480
QY 481 CTCAGGGACACTGACGTGTAACAAGAGCAAGCAAGAAAGAGACTGCTCATCTGCCC 540
Db 481 CTCAGGGACACTGACGTGTAACAAGAGCAAGCAAGAAAGAGACTGCTCATCTGCCC 540
QY 541 TCTCCATGAGGAATTCAGAGTAGTAATACTCGCTGTCAGACAGATGTCACATTAAT 600
Db 541 TCTCCATGAGGAATTCAGAGTAGTAATACTCGCTGTCAGACAGATGTCACATTAAT 600
QY 541 TCTCCATGAGGAATTCAGAGTAGTAATACTCGCTGTCAGACAGATGTCACATTAAT 600
Db 541 TCTCCATGAGGAATTCAGAGTAGTAATACTCGCTGTCAGACAGATGTCACATTAAT 600
QY 601 GTCCCTTGACAAACAAAAGAGAGCAGCTCTGATTAAGGCCCTACATGACAGGAAGATGA 660
Db 601 GTCCCTTGACAAACAAAAGAGAGCAGCTCTGATTAAGGCCCTACATGACAGGAAGATGA 660
QY 661 TGTGCGTTAATGTGCTGGAACATGGGACGTGATCCAAATATTCAGATGAGTATGGAAT 720
Db 661 TGTGCGTTAATGTGCTGGAACATGGGACGTGATCCAAATATTCAGATGAGTATGGAAT 720
QY 721 ACCACTGTGACACTGATATCTATATGATGAAGATTAATGAGCCAAAGCACTGCTCTTA 780
Db 721 ACCACTGTGACACTGATATCTATATGATGAAGATTAATGAGCCAAAGCACTGCTCTTA 780
QY 781 TATGTGCTGATATGCAATCAAAAAACAGATGGCCACACCACTGTACTGTGCTGA 840
Db 781 TATGTGCTGATATGCAATCAAAAAACAGATGGCCACACCACTGTACTGTGCTGA 840
QY 841 CATGAGCAAAACAGCAAGTGTGAATTTTATTAACAAGAAAGAAATTAATTAATGA 900
Db 841 CATGAGCAAAACAGCAAGTGTGAATTTTATTAACAAGAAAGAAATTAATTAATGA 900
QY 901 CTGATAGATATGGAAGAGACTGCTCATACTGCTGATGTTGTGATCGCAAGTATA 960
Db 901 CTGATAGATATGGAAGAGACTGCTCATACTGCTGATGTTGTGATCGCAAGTATA 960
QY 961 GTCAAGCTTCTACTGAGCAAAATATGATGATCTCTCAAGATCTATCTGAGCAGAG 1020
Db 961 GTCAAGCTTCTACTGAGCAAAATATGATGATCTCTCAAGATCTATCTGAGCAGAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGATTAATTTCCAGTAACTTCTGACATC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGATTAATTTCCAGTAACTTCTGACATC 1080
QY 1081 AAAAAAAGCAGATGTAAATAATCTCTTCTGAAAGACAGCAATCCAGAAACAGATTAAG 1140
Db 1081 AAAAAAAGCAGATGTAAATAATCTCTTCTGAAAGACAGCAATCCAGAAACAGATTAAG 1140
QY 1141 CTGACATCAGAGAAAGTGTCAAAAGGTCAAAAGGAGTGAATAATAGCAGCCAGAGAAA 1200
Db 1141 CTGACATCAGAGAAAGTGTCAAAAGGTCAAAAGGAGTGAATAATAGCAGCCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATAGAGTGTATAGAGAGTTGAAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAGAAATTAATAGAGTGTATAGAGAGTTGAAAGAAATGAAG 1260

```

QY 1261 AACATGAAAGTAATATGTGGATTACTAGAAAACTGACTAATGTGTCACTGTC 1320
    |||||||
DB 1261 AAGCATGAAAGTAATATGTGGATTACTAGAAAACTGACTAATGTGTCACTGTC 1320
QY 1321 AATGTGTAATATGATTAATTCCTCAAGAGAGCAGAAACCTGAAAAATCAGCAATTT 1380
    |||||||
DB 1321 AATGTGTAATATGATTAATTCCTCAAGAGAGCAGAAACCTGAAAAATCAGCAATTT 1380
QY 1381 COTGCAACGAAAGTAAGAGTATACACAGAAATTTGGCAATTTAGTTTCTACTACAAAGAA 1440
    |||||||
DB 1381 COTGCAACGAAAGTAAGAGTATACACAGAAATTTGGCAATTTAGTTTCTACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAATTAATCTCTGAAACACAGAACCCAGAACAGACTTAAGAGTGACA 1500
    |||||||
DB 1441 AAACAGATGCCAAATTAATCTCTGAAACACAGAACCCAGAACAGACTTAAGAGTGACA 1500
QY 1501 TCAGAGAGAAAGTCAACAAAGCCTTGAGGGCAGTGAATAATGGCCAGCAGAGAAAGATCT 1560
    |||||||
DB 1501 TCAGAGAGAAAGTCAACAAAGCCTTGAGGGCAGTGAATAATGGCCAGCAGAGAAAGATCT 1560
QY 1561 CAAGAACCAAGAAATTAATAGAGTGTGATAGAGACTAGAAATTTTATGCTATCGAA 1620
    |||||||
DB 1561 CAAGAACCAAGAAATTAATAGAGTGTGATAGAGACTAGAAATTTTATGCTATCGAA 1620
QY 1621 GAAATGAAGAAAGCAGGAAGTCTCATGTCGATTCGCCGAAACCTGACTAATGCTGCC 1680
    |||||||
DB 1621 GAAATGAAGAAAGCAGGAAGTCTCATGTCGATTCGCCGAAACCTGACTAATGCTGCC 1680
QY 1681 ACTGCTGGCAATGTGATGATGATTAATTCCTCCAGAGAAAGCAGAACACCTGTAAGC 1740
    |||||||
DB 1681 ACTGCTGGCAATGTGATGATGATTAATTCCTCCAGAGAAAGCAGAACACCTGTAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGATGAAGATTCACAGTGCAGAACAAATGATACTCAG 1800
    |||||||
DB 1741 CAGCAATTTCTGACACTGAGATGAAGATTCACAGTGCAGAACAAATGATACTCAG 1800
QY 1801 AAGCAATTTTGTGAAGAACAGAACTGGAATATTACAGATGAGATTCGATTCATGAA 1860
    |||||||
DB 1801 AAGCAATTTTGTGAAGAACAGAACTGGAATATTACAGATGAGATTCGATTCATGAA 1860
QY 1861 GAAAGCAGATGAAGTGGTTGAAAAAATGAATTCGACCTTCTTCTAGTTGAAGAA 1920
    |||||||
DB 1861 GAAAGCAGATGAAGTGGTTGAAAAAATGAATTCGACCTTCTTCTAGTTGAAGAA 1920
QY 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTGCGGGAAGAAATTCCTAGACTG 1980
    |||||||
DB 1921 GAAAAAGACATCTTGCATGAAAAATAGTACGTTGCGGGAAGAAATTCCTAGACTG 1980
QY 1981 GAGCTAGACACAATGAACATCAGAGCCGACTAAAAAATGAAAAAAAAAAAAAAAAAAAA 2040
    |||||||
DB 1981 GAGCTAGACACAATGAACATCAGAGCCGACTAAAAAATGAAAAAAAAAAAAAAAAAAAA 2040

```

RESULT 9
US-09-568-100A-375
Sequence 375. Application US/09568100A

GENERAL INFORMATION:

```

: APPLICANT: Xu, JIANGCHUN
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitchem, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yugu
: APPLICANT: Reed, Steven G.
: APPLICANT: Kalos, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darriek
: APPLICANT: Li, Samuel
: APPLICANT: Wang, Aljun

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: APPLICANT: Skelky, Yasir A.N.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
: FILE REFERENCE: 210121.42713c13
: CURRENT APPLICATION NUMBER: US/09/568,100A
: NUMBER OF SEQ ID NOS: 701
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO: 375
: LENGTH: 2040
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-568-100A-375

Query Match      100.0%; Score 2040; DB 22; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGTGTTGAGTGTGATTCATGCGGCTGCTCTTGTGAAGAACCATTTGGTCTC 60
    |||||||
DB 1 ATGGTGTGTTGAGTGTGATTCATGCGGCTGCTCTTGTGTGAAGAACCATTTGGTCTC 60
QY 61 AGAGAGCAAGATGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGAGAGCGGCAAG 120
    |||||||
DB 61 AGAGAGCAAGATGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGACACGACGACTGCTATGAAACACTCAGAGCAAG 180
    |||||||
DB 121 AGCAACGTGGGCACTTCTGAGACACGACGACTGCTATGAAACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAAGAGGAGTGGCAAGACGTG 240
    |||||||
DB 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGCAAGAGGAGTGGCAAGACGTG 240
QY 241 GCGGCTTCTGAGACACGACGACTGCTATGAAACACTCAGAAACAAGATGGGCAAG 300
    |||||||
DB 241 GCGGCTTCTGAGACACGACGACTGCTATGAAACACTCAGAAACAAGATGGGCAAG 300
QY 301 TGGTGTGCTGCTGCTTCCCTGCTGCAAGAGGAGGAGGCAAGCAAGTGGGCGTGG 360
    |||||||
DB 301 TGGTGTGCTGCTGCTTCCCTGCTGCAAGAGGAGGAGGCAAGCAAGTGGGCGTGG 360
QY 361 GGAGACTAGACAGTGCCTTCATGAGCCAGGATACAGTCCCTGGAGAAGATCTG 420
    |||||||
DB 361 GGAGACTAGACAGTGCCTTCATGAGCCAGGATACAGTCCCTGGAGAAGATCTG 420
QY 421 GACAAAGCTCCACAGAGCTGCTGTTGAGGATTAAGTCCCGAAGAAAGATCTCATG 480
    |||||||
DB 421 GACAAAGCTCCACAGAGCTGCTGTTGAGGATTAAGTCCCGAAGAAAGATCTCATG 480
QY 481 CTCAGGAGACACTGAGTGAACAAGAACGAAAGAAAGAGACTGCTTACATCTGGCC 540
    |||||||
DB 481 CTCAGGAGACACTGAGTGAACAAGAACGAAAGAAAGAGACTGCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAAGTCTGCTGAGACAGAGATGCAACTTAAT 600
    |||||||
DB 541 TCTGCCAATGGGAATTCAGAAAGTAAAGTCTGCTGAGACAGAGATGCAACTTAAT 600
QY 601 GTCTCTTGACAAACAAAAGAGACAGCTGTGATTAAGGCGGTACAAATGCCAGAAAGTGA 660
    |||||||
DB 601 GTCTCTTGACAAACAAAAGAGAGAGCTGTGATTAAGGCGGTACAAATGCCAGAAAGTGA 660
QY 661 TGTGCGTTAATGTGTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
    |||||||
DB 661 TGTGCGTTAATGTGTGCTGGAACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTGCTAGCTAGCTATCTATATGAAGTAAATTAATGAGCCAAAGCACTGCTTA 780
    |||||||
DB 721 ACCACTGCTAGCTAGCTATCTATATGAAGTAAATTAATGAGCCAAAGCACTGCTTA 780
QY 781 TATGTGTCTGATATGAAATCAAAAAACAAGCATGGGCTGCACACACTGTTACTGTGTA 840
    |||||||
DB 781 TATGTGTCTGATATGAAATCAAAAAACAAGCATGGGCTGCACACACTGTTACTGTGTA 840

```


QY 541 TCTGCAATGGGAATTCAGAAAGTAAACTCTGCTGGACAGAGATGCACTTAAT 600
 |||||
 Db 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGGACAGAGATGCACTTAAT 600
 QY 601 GTCCCTTGACACAAAAGAGGACAGCTGTGATAAAGCCGTACAAATGCCAGAAATGAA 650
 |||||
 Db 601 GTCCCTTGACACAAAAGAGGACAGCTGTGATAAAGCCGTACAAATGCCAGAAATGAA 650
 QY 661 TGTGCTTAATGTTGCTGGACATGGCAGTATCCAAATATTCAGATGATGTGAAT 720
 |||||
 Db 661 TGTGCTTAATGTTGCTGGACATGGCAGTATCCAAATATTCAGATGATGTGAAT 720
 QY 721 AACACCTGACATGACCTATCTAATTAATGAAGATTAATGAGCAAGACAGCTCTTA 780
 |||||
 Db 721 AACACCTGACATGACCTATCTAATTAATGAAGATTAATGAGCAAGACAGCTCTTA 780
 QY 781 TATGCTGTGATATCGAATCAAAAAACAAGCATGGCCTCACACAGCTGTACTGTGTA 840
 |||||
 Db 781 TATGCTGTGATATCGAATCAAAAAACAAGCATGGCCTCACACAGCTGTACTGTGTA 840
 QY 841 CATGACACAAAACAGCAAGTCTGAAATTTTATCAGAAAAAGCGAATTTAAATGCA 900
 |||||
 Db 841 CATGACACAAAACAGCAAGTCTGAAATTTTATCAGAAAAAGCGAATTTAAATGCA 900
 QY 901 CTGATAGATATGAGAGAGCTGCTCATCTGCTGATGTTGGATGAGCAAGTATA 960
 |||||
 Db 901 CTGATAGATATGAGAGAGCTGCTCATCTGCTGATGTTGGATGAGCAAGTATA 960
 QY 961 GTGAGCCTTACTTACGACAAAATATTTGATGATCTTCTCAAGATCTATCTGACAGACG 1020
 |||||
 Db 961 GTGAGCCTTACTTACGACAAAATATTTGATGATCTTCTCAAGATCTATCTGACAGACG 1020
 QY 1021 GCCAGAGATATGCTGTTCTAGTCAATCATGTAATTTGCCAGTTACTTTGTGACTAC 1080
 |||||
 Db 1021 GCCAGAGATATGCTGTTCTAGTCAATCATGTAATTTGCCAGTTACTTTGTGACTAC 1080
 QY 1081 AAGAAACACAGATGCTAAAAATCTCTTCGAAAACAGCAATTCAGAAAGACTTAAAG 1140
 |||||
 Db 1081 AAGAAACACAGATGCTAAAAATCTCTTCGAAAACAGCAATTCAGAAAGACTTAAAG 1140
 QY 1141 CTGACATCAGAGAGAGAGTCAACAAGGTTCAAGAGCAGTGAATATGCCAGCAGAGAAA 1200
 |||||
 Db 1141 CTGACATCAGAGAGAGAGTCAACAAGGTTCAAGAGCAGTGAATATGCCAGCAGAGAAA 1200
 QY 1201 ATGTCTCAAGACCAAGAAATTAATTAAGATGTTGATAGAGAGGTTGAAGAAATGAAAG 1260
 |||||
 Db 1201 ATGTCTCAAGACCAAGAAATTAATTAAGATGTTGATAGAGAGGTTGAAGAAATGAAAG 1260
 QY 1261 AAGCATGAAGATTAATTAATGAGATATCTAAGAAACCTGACTAATGTTGCTGCTGGC 1320
 |||||
 Db 1261 AAGCATGAAGATTAATTAATGAGATATCTAAGAAACCTGACTAATGTTGCTGCTGGC 1320
 QY 1321 AATGCTGATATGATTAATTTCTCAAGAGAGAGCAGACACTGAAATTCAGCAATTT 1380
 |||||
 Db 1321 AATGCTGATATGATTAATTTCTCAAGAGAGAGCAGACACTGAAATTCAGCAATTT 1380
 QY 1381 CCTGACACAGAAAGTGAAGATATCAAGAAATTTGCGAATTTGCTGACTCAAAAGAA 1440
 |||||
 Db 1381 CCTGACACAGAAAGTGAAGATATCAAGAAATTTGCGAATTTGCTGACTCAAAAGAA 1440
 QY 1441 AAACATGATGCAAAATACTCTTCTGAAAACAGAACCCAGAACCAAGCTTAAAGCTGACA 1500
 |||||
 Db 1441 AAACATGATGCAAAATACTCTTCTGAAAACAGAACCCAGAACCAAGCTTAAAGCTGACA 1500
 QY 1501 TCAGAGAGAGTACACAAAGGCTTGAGGGCAGTGAATATGCCAGCAGAGAAAGATCT 1560
 |||||
 Db 1501 TCAGAGAGAGTACACAAAGGCTTGAGGGCAGTGAATATGCCAGCAGAGAAAGATCT 1560
 QY 1561 CAAGAACAGAAATTAATTAAGATGTTGATAGAGAGCTAGAAAAATTTTATGCTATCGAA 1620
 |||||
 Db 1561 CAAGAACAGAAATTAATTAAGATGTTGATAGAGAGCTAGAAAAATTTTATGCTATCGAA 1620

QY 1621 GAATGAGAGACGAGGAAGTACTCATGTCGATATCCAGAAAACTGATTAATGCTGCC 1680
 |||||
 Db 1621 GAATGAGAGACGAGGAAGTACTCATGTCGATATCCAGAAAACTGATTAATGCTGCC 1680
 QY 1681 ACTGTGGCAATGTTGATGATGATTAATTTCTCCAGAGAGCAGAACCTGAAAGC 1740
 |||||
 Db 1681 ACTGTGGCAATGTTGATGATGATTAATTTCTCCAGAGAGCAGAACCTGAAAGC 1740
 QY 1741 CAGCAATTTCTTACACTGTGAATGAAAGTATCACAGTCAGCAACAAAATGATACTCAG 1800
 |||||
 Db 1741 CAGCAATTTCTTACACTGTGAATGAAAGTATCACAGTCAGCAACAAAATGATACTCAG 1800
 QY 1801 AAGCAATTTCTTACACTGTGAATGAAAGTATCACAGTCAGCAACAAAATGATACTCAG 1860
 |||||
 Db 1801 AAGCAATTTCTTACACTGTGAATGAAAGTATCACAGTCAGCAACAAAATGATACTCAG 1860
 QY 1861 GAAAGCAGATGAGAGTGTGAAAAATGAAATTTCTGAGTTCTTAAGTAAAGAA 1920
 |||||
 Db 1861 GAAAGCAGATGAGAGTGTGAAAAATGAAATTTCTGAGTTCTTAAGTAAAGAA 1920
 QY 1921 GAAAAAGACATCTTGCATGAAATTAATGATGCTGCGGAGAGAAATTTGCCATGCTAAGACTG 1980
 |||||
 Db 1921 GAAAAAGACATCTTGCATGAAATTAATGATGCTGCGGAGAGAAATTTGCCATGCTAAGACTG 1980
 QY 1981 GAGCTGACACATGAAACATCAGAGCAGCTAAAAAATGAAAAAATGAAAAAATGAAAAA 2040
 |||||
 Db 1981 GAGCTGACACATGAAACATCAGAGCAGCTAAAAAATGAAAAAATGAAAAAATGAAAAA 2040

RESULT 11
 US-09-583-303
 ; Sequence 303, Application us/09590583
 ; GENERAL INFORMATION:
 ; APPLICANT: Frudakis, Tony N.
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Smith, John M.
 ; APPLICANT: Misher, Linda E.
 ; APPLICANT: Dillon, David C.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Wang, Aljun
 ; APPLICANT: Skelky, Yasir A.W.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 ; FILE REFERENCE: 210121.419C9
 ; CURRENT APPLICATION NUMBER: US/09/590,583
 ; CURRENT FILING DATE: 2000-06-08
 ; NUMBER OF SEQ ID NOS: 324
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 303
 ; LENGTH: 2040
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-09-590-583-303
 Query Match 100.0%; Score 2040; DB 22; Length 2040;
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 2040; Conservative 0;

QY 1 ATGTGTTGAGTTGATTCATGCGGCTGCTTCTGTGAAGAACCATTTGCTC 60
 |||||
 Db 1 ATGTGTTGAGTTGATTCATGCGGCTGCTTCTGTGAAGAACCATTTGCTC 60
 QY 61 AGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
 |||||
 Db 61 AGAGCAAGATGGGCAAGTGTGCTGCTGCTTCCCTGCTGCAAGGAGAGCGGCAAG 120
 QY 121 AGCAAGTGGGCACTTCTGAGACCAAGAGACTGCTTGAAGACTCAGAGCAAG 180
 |||||
 Db 121 AGCAAGTGGGCACTTCTGAGACCAAGAGACTGCTTGAAGACTCAGAGCAAG 180
 QY 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGT 240
 |||||
 Db 181 ATGGGCAAGTGTGCGGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGT 240

OY	24.1	GGCCTTCTGGAGACCAAGCAAGCACTGCGTATGAAAGAACACTGAGAAACAAGTGGGCAAG	300
Db	24.1	GGCCCTTCTGGAGACCAAGCAAGCACTGCGTATGAAAGAACACTGAGAAACAAGTGGGCAAG	300
OY	30.1	TGTGTCTGCACACTGCTCTCCCTGCTCAGGGGAGCGGCAAGAGCAAGGTGGGCGCTTGG	360
Db	30.1	TGTGTCTGCACACTGCTCTCCCTGCTCAGGGGAGCGGCAAGAGCAAGGTGGGCGCTTGG	360
OY	36.1	GGAGACTACGATGATGACAGTGGCTTTCATGGAAGCCAGGTACCGACGTCCGTGGAGAAATCTG	420
Db	36.1	GGAGACTACGATGATGACAGTGGCTTTCATGGAAGCCAGGTACCGACGTCCGTGGAGAAATCTG	420
OY	42.1	GACAAAGTCCACAGAGCTGGCTGGTGGGGTAAAGTGTCCCAAGAAAGATTCATTCGTATG	480
Db	42.1	GACAAAGTCCACAGAGCTGGCTGGTGGGGTAAAGTGTCCCAAGAAAGATTCATTCGTATG	480
OY	48.1	CTCAGGACACTGACGTGAACAAGAGAGCAACCAAAAGAGAGTGCCTACATGTGGCC	540
Db	48.1	CTCAGGACACTGACGTGAACAAGAGAGCAACCAAAAGAGAGTGCCTACATGTGGCC	540
OY	54.1	TCTGCCAATGGGAATTCAGAAAGTAACTCTGCTGGACGAGAGATGTCACATTAT	600
Db	54.1	TCTGCCAATGGGAATTCAGAAAGTAACTCTGCTGGACGAGAGATGTCACATTAT	600
OY	60.1	GTCCTTGACAACAACAAAAGAGACAGCTCTGATTAAGAGCCGTACAAATGCCAGAGATGAA	660
Db	60.1	GTCCTTGACAACAACAAAAGAGACAGCTCTGATTAAGAGCCGTACAAATGCCAGAGATGAA	660
OY	66.1	TGTGCGTTAATGTTGCGGGAACAATGGCAGCTGATCCAAATATCCAGATAGATGGAAT	720
Db	66.1	TGTGCGTTAATGTTGCGGGAACAATGGCAGCTGATCCAAATATCCAGATAGATGGAAT	720
OY	72.1	ACCACTGTGCACACTACGCTATCTATTAATGAAGATTAATTAATGGCCAAAGCACTGCTCTTA	780
Db	72.1	ACCACTGTGCACACTACGCTATCTATTAATGAAGATTAATTAATGGCCAAAGCACTGCTCTTA	780
OY	78.1	TATGTGCTGATATCGATTAACAAAACAAAGCATGGCCTCACACCCTGTTACTTGGTGA	840
Db	78.1	TATGTGCTGATATCGATTAACAAAACAAAGCATGGCCTCACACCCTGTTACTTGGTGA	840
OY	84.1	CATGAGCAAAAACGCAAGTCGGAATTTTAACTAACAAAAGCGAATTTAAATGCA	900
Db	84.1	CATGAGCAAAAACGCAAGTCGGAATTTTAACTAACAAAAGCGAATTTAAATGCA	900
OY	90.1	CTGGATAGATATGGAAGAGACTGCTCTCATCTCTGCTGATGTTGGATCAGCAAGTATA	960
Db	90.1	CTGGATAGATATGGAAGAGACTGCTCTCATCTCTGCTGATGTTGGATCAGCAAGTATA	960
OY	96.1	GTCAGCCTTCTACTTGTAGCAAAAATATGATGTAATCTTCCAAAGATCTATCTGGACAGCG	1020
Db	96.1	GTCAGCCTTCTACTTGTAGCAAAAATATGATGTAATCTTCCAAAGATCTATCTGGACAGCG	1020
OY	102.1	GCCAGAGATGCGTGTCTTACTGATCAGTCAATGTAATTTGGCAGTACTTCTGACATAC	1080
Db	102.1	GCCAGAGATGCGTGTCTTACTGATCAGTCAATGTAATTTGGCAGTACTTCTGACATAC	1080
OY	108.1	AAAGAAAAACAGATGCTAAAAATCTCTTGCAAAAACAGCAATCCAGAACAGACTTAAAG	1140
Db	108.1	AAAGAAAAACAGATGCTAAAAATCTCTTGCAAAAACAGCAATCCAGAACAGACTTAAAG	1140
OY	114.1	CTGACATCAGAGAGAGTGCATCAAAAAGTTCAAAAGGACAGTAAATATAGCCAGCAGAGAA	1200
Db	114.1	CTGACATCAGAGAGAGTGCATCAAAAAGTTCAAAAGGACAGTAAATATAGCCAGCAGAGAA	1200
OY	120.1	ATGTCTCAAGAACCAAGAAATTAATTAAGGATGGTGATAGAGAGTTGAAGAGAAATGAAG	1260
Db	120.1	ATGTCTCAAGAACCAAGAAATTAATTAAGGATGGTGATAGAGAGTTGAAGAGAAATGAAG	1260
OY	126.1	AAGCATGAAAGTAAATATGTGGGATTAATGAGAAAACCTGACTAATAGGTGCTACCTGCTGC	1320
Db	126.1	AAGCATGAAAGTAAATATGTGGGATTAATGAGAAAACCTGACTAATAGGTGCTACCTGCTGC	1320

Oy	1321	AATGCTATTAATGATTAATTTCTTCCAAAGAGAGAGAAACCTGAAAATTCACAAATTT	1380
Oy	1321	AATGCTATTAATGATTAATTTCTTCCAAAGAGAGAGAAACCTGAAAATTCACAAATTT	1380
Db	1321	AATGCTATTAATGATTAATTTCTTCCAAAGAGAGAGAAACCTGAAAATTCACAAATTT	1380
Oy	1381	CCTGACACAGAAAGTGAAGATATCACAAGATTTTGGAAATTAATGTTCTGTACTACAAAGAA	1440
Db	1381	CCTGACACAGAAAGTGAAGATATCACAAGATTTTGGAAATTAATGTTCTGTACTACAAAGAA	1440
Oy	1441	AAACAGATGCCAAATTAATCTTTCTTGAAAACACGACACCCAGAACAAAGACTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAATTAATCTTTCTTGAAAACACGACACCCAGAACAAAGACTTAAAGCTGACA	1500
Oy	1501	TCACAGGAAAGTCCACAAAGGCTTTGGAGGAGTGAAGAAATGGCCACGACAGAGAAAAGATCT	1560
Db	1501	TCACAGGAAAGTCCACAAAGGCTTTGGAGGAGTGAAGAAATGGCCACGACAGAGAAAAGATCT	1560
Oy	1561	CAAGAACACAGAAATTAATTAAGATGGTGTAGTAGAGACTAGAAAATTTTATGGCTATCGAA	1620
Db	1561	CAAGAACACAGAAATTAATTAAGATGGTGTAGTAGAGACTAGAAAATTTTATGGCTATCGAA	1620
Oy	1621	GAATTAAGAAAGCACGGAAGTACTCATGTCCGATTCGCCAGAAAACCTGACTAATGATGCC	1680
Db	1621	GAATTAAGAAAGCACGGAAGTACTCATGTCCGATTCGCCAGAAAACCTGACTAATGATGCC	1680
Oy	1681	ACTGCTGGCAATGGTGTATGTATGATTAATTTCTCCAAAGAAAGGAGAAACCTGTGAAGC	1740
Db	1681	ACTGCTGGCAATGGTGTATGTATGATTAATTTCTCCAAAGAAAGGAGAAACCTGTGAAGC	1740
Oy	1741	CAGCAATTCCTGTACACTGTGAATGAAGATATCAGTGCAGCAACAAATGATACTGAG	1800
Db	1741	CAGCAATTCCTGTACACTGTGAATGAAGATATCAGTGCAGCAACAAATGATACTGAG	1800
Oy	1801	AAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAGATTTCTGATTCATGAA	1860
Db	1801	AAGCAATTTTGTGAAGAACAGAACACTGGAATATTAACAGATGAGATTTCTGATTCATGAA	1860
Oy	1861	GAAGAAAGAGATAGAAAGTGTTGAAAAAATGAATTCGACCTTCTTGAATGTAAGAA	1920
Db	1861	GAAGAAAGAGATAGAAAGTGTTGAAAAAATGAATTCGACCTTCTTGAATGTAAGAA	1920
Oy	1921	GAAGAAAGCATCTTGCAATGAATTAAGTACGTGGCGGAAGAAATGGCATGCTAAGACTG	1980
Db	1921	GAAGAAAGCATCTTGCAATGAATTAAGTACGTGGCGGAAGAAATGGCATGCTAAGACTG	1980
Oy	1981	GAGCTAGACACAAATGAACATCTGAGCCAGCTAAAAAATTTTTTTTTTTTTTTTTTTTTT	2040
Db	1981	GAGCTAGACACAAATGAACATCTGAGCCAGCTAAAAAATTTTTTTTTTTTTTTTTTTTTT	2040
RESULT 12			
US-09-593-793A-375			
: Sequence 375, Application US/09593793A			
: GENERAL INFORMATION:			
: APPLICANT: Xu, Jiangchun			
: APPLICANT: Dillon, David C.			
: APPLICANT: Mitcham, Jennifer L.			
: APPLICANT: Harlocker, Susan L.			
: APPLICANT: Jiang, Youqi			
: APPLICANT: Reed, Steven G.			
: APPLICANT: Kalos, Michael D.			
: APPLICANT: Fanger, Gary R.			
: APPLICANT: Retter, Marc W.			
: APPLICANT: Stolk, John A.			
: APPLICANT: Day, Craig H.			
: APPLICANT: Vedvick, Thomas S.			
: APPLICANT: Carter, Darrick			
: APPLICANT: Li, Samuel			
: APPLICANT: Wang, Aijun			
: APPLICANT: Skeiky, Yasir A.W.			
: APPLICANT: Helper, William			
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND			
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER			
: FILE REFERENCE: 210121.4215015			

; CURRENT APPLICATION NUMBER: US/09/593,793A
; CURRENT FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 814
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-593-793A-375

Query Match 100.0%; Score 2040; DB 22; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGGGTTGAGGTGATTCATGCGCGGCTCTCTCTGTGAAGAGCATTTGGTCTC 60
DB 1 ATGGTGGTTGAGGTGATTCATGCGCGGCTCTCTCTGTGAAGAGCATTTGGTCTC 60
QY 61 AGGAGCAAGATGGGCAAGTGTGTGCTGCTTCCCTGCTGCAAGAGAGCGGCAAG 120
DB 61 AGGAGCAAGATGGGCAAGTGTGTGCTGCTTCCCTGCTGCAAGAGAGCGGCAAG 120
QY 121 AGCAACGTGGGCACTTGTGAGACCAACGACACTGCTATGAGACACTCAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTGTGAGACCAACGACACTGCTATGAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAACGTG 240
DB 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGAGGGGAGTGGCAAGCAACGTG 240
QY 241 GCGGCTTGTGAGACCAACGACACTGCTATGAGACACTCAGAGCAAGTGGGCAAG 300
DB 241 GCGGCTTGTGAGACCAACGACACTGCTATGAGACACTCAGAGCAAGTGGGCAAG 300
QY 301 TGGTGTGCTGCACTGCTTCCCTGCTGAGGGGAGCGGCAAGAGCAAGTGGGCTTG 360
DB 301 TGGTGTGCTGCACTGCTTCCCTGCTGAGGGGAGCGGCAAGAGCAAGTGGGCTTG 360
QY 361 GGAGACTACGATGACAGTGCCTTCATGAGCCAGGTACAGTCCGTGGAGAGATCTG 420
DB 361 GGAGACTACGATGACAGTGCCTTCATGAGCCAGGTACAGTCCGTGGAGAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAGATCTCATCTCATG 480
DB 421 GACAAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCGAAGAGATCTCATCTCATG 480
QY 481 CTCAGGAGACACTGACGTGAACAAGAACCAAGAGAGAGACTGCTTACATCTGGCC 540
DB 481 CTCAGGAGACACTGACGTGAACAAGAACCAAGAGAGAGACTGCTTACATCTGGCC 540
QY 541 TCTGCCAATGGGAATTCAGAACTAGTAAAGTCTGCTGACAGACGATGTCAACTTAAT 600
DB 541 TCTGCCAATGGGAATTCAGAACTAGTAAAGTCTGCTGACAGACGATGTCAACTTAAT 600
QY 601 GTCTCTTGACAAACAAAAGAGACAGCTGTATAAAGCCGTACAAATGCCAGAGATGAA 660
DB 601 GTCTCTTGACAAACAAAAGAGAGACAGCTGTATAAAGCCGTACAAATGCCAGAGATGAA 660
QY 661 TGTGCGTTAATGTGTGCTGAGACATGGCACTGATCCAAATATTTCCAGATGATGGAAT 720
DB 661 TGTGCGTTAATGTGTGCTGAGACATGGCACTGATCCAAATATTTCCAGATGATGGAAT 720
QY 721 ACCACTGTGCACTAGGCTATCTATATGAAGATAAATTAATGGCCAAACACTGCTTAA 780
DB 721 ACCACTGTGCACTAGGCTATCTATATGAAGATAAATTAATGGCCAAACACTGCTTAA 780
QY 781 TATGTTGCTGATATGAATCAAAAAACAAGCATGGCCTCACACACTGTTACTTGGTGA 840
DB 781 TATGTTGCTGATATGAATCAAAAAACAAGCATGGCCTCACACACTGTTACTTGGTGA 840
QY 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAACGAATTTAAATGCA 900
DB 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAACGAATTTAAATGCA 900

QY 901 CTGGATGATATGGAAGACCTGCTCATACCTTGCATGATGTTGGATCAGCAAGTATA 960
DB 901 CTGGATGATATGGAAGACCTGCTCATACCTTGCATGATGTTGGATCAGCAAGTATA 960
QY 961 GTGAGCCTTCTAGTGGCAAAATATGATGATCTTCTCAAGATCTATCTGGACAGC 1020
DB 961 GTGAGCCTTCTAGTGGCAAAATATGATGATCTTCTCAAGATCTATCTGGACAGC 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGCTATCATATGTAATTTGCCAGTTACTTTCTGACTAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGCTATCATATGTAATTTGCCAGTTACTTTCTGACTAC 1080
QY 1081 AAAGAAAACAGATGCTAAAAATCTTGTGAAAACAGCAATCCAGAACACTTAAAG 1140
DB 1081 AAAGAAAACAGATGCTAAAAATCTTGTGAAAACAGCAATCCAGAACACTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGTCCACAAAGCTTCAAGGCAAGTGAATAATAGCCAGCCAGAAA 1200
DB 1141 CTGACATCAGAGAGAGTCCACAAAGCTTCAAGGCAAGTGAATAATAGCCAGCCAGAAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGGTATGAGAGGTTGAGAGCAATGAAG 1260
DB 1201 ATGTCTCAAGAACCAAGAAATTAATTAAGATGGTATGAGAGGTTGAGAGCAATGAAG 1260
QY 1261 AAGCATGAAGTAAATTAATGGGATTAAGTGAAGAAACCTGACTAATGGTGCATGCTGGC 1320
DB 1261 AAGCATGAAGTAAATTAATGGGATTAAGTGAAGAAACCTGACTAATGGTGCATGCTGGC 1320
QY 1321 AATGGTATATGATTAATTTCTCAAGGAGAGCAGAACACTGAAAAATCAGCAATTT 1380
DB 1321 AATGGTATATGATTAATTTCTCAAGGAGAGCAGAACACTGAAAAATCAGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTAAAGATATCACAGAAATTTGGCAATTTAGTTTCTGACTACAAAGAA 1440
DB 1381 CCTGACAAAGAAAGTAAAGATATCACAGAAATTTGGCAATTTAGTTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAAATAGCTTCTGAAAACAGCAACCCGAAACAAAGCTTAAAGCTGACA 1500
DB 1441 AAACAGATGCCAAAATAGCTTCTGAAAACAGCAACCCGAAACAAAGCTTAAAGCTGACA 1500
QY 1501 TCAGAGAGAGTACACAAAGGCTTGAAGGCAAGTGAATAATGGCCAGCAGAGAAAGATCT 1560
DB 1501 TCAGAGAGAGTACACAAAGGCTTGAAGGCAAGTGAATAATGGCCAGCAGAGAAAGATCT 1560
QY 1561 CAAGAAACCAAAATTAATTAAGATGGTATAGAGACTTGAATAATTTATGGCTATCGAA 1620
DB 1561 CAAGAAACCAAAATTAATTAAGATGGTATAGAGACTTGAATAATTTATGGCTATCGAA 1620
QY 1621 GAAATGAAGACAGGAAGTACTCATGTGCGATTCCAGAAAACCTGACTAATGGTGCC 1680
DB 1621 GAAATGAAGACAGGAAGTACTCATGTGCGATTCCAGAAAACCTGACTAATGGTGCC 1680
QY 1681 ACTGCTGGCAATGGTATGATGATTAATTTCCCAAGGAGAGCAACACCTGGAAGC 1740
DB 1681 ACTGCTGGCAATGGTATGATGATTAATTTCCCAAGGAGAGCAACACCTGGAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGAAATGAAGATACACAGTCAACAAATAATGATCTCAG 1800
DB 1741 CAGCAATTTCTGACACTGAGAAATGAAGATACACAGTCAACAAATAATGATCTCAG 1800
QY 1801 AAGCAATTTTGAAGAAACAGAACTGGAATTTACAGATGAGATTTGATCTTCAATGAA 1860
DB 1801 AAGCAATTTTGAAGAAACAGAACTGGAATTTACAGATGAGATTTGATCTTCAATGAA 1860
QY 1861 GAAAAGCAGATGAAGTGTGAAAAATGAATTTGAGACTTTCTTATGTTTAAGAAA 1920
DB 1861 GAAAAGCAGATGAAGTGTGAAAAATGAATTTGAGACTTTCTTATGTTTAAGAAA 1920
QY 1921 GAAAAAGACATCTTGCAATGAATAATGATGCTGGGGAAGAAATTCATGCTTAAGACTG 1980
DB 1921 GAAAAAGACATCTTGCAATGAATAATGATGCTGGGGAAGAAATTCATGCTTAAGACTG 1980


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QY 1981 GAGCTAGACACATGAAATCAGAGCCAGCTAATAAAAAAAAAAAAAAAAAAAA 2040
|
Db 1981 GAGCTAGACACATGAAATCAGAGCCAGCTAATAAAAAAAAAAAAAAAAAAAA 2040

RESULT 13
US-09-605-783A-375
; Sequence 375, Application US/09605783A
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605.783A
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-605-783A-375

Query Match 100.0%; Score 2040; DB 23; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 421 GACAAGCTCCACAGAGCTGCTGGGGTAAAGTCCCAAGAAAGATCTCATCTCATG 480
QY 481 CTCAGGACACTGACGTGAACAAAGAGACAAAGCAAGAGAGACTGCTACATCTGACC 540
|
Db 481 CTCAGGACACTGACGTGAACAAAGAGACAAAGCAAGAGAGACTGCTCATCTGACC 540
QY 541 TCTGCCAATGGGAATTCAGAAATGTAATAACTCTGCTGACAGACAGATGTCAACTTAAT 600
|
Db 541 TCTGCCAATGGGAATTCAGAAATGTAATAACTCTGCTGACAGACAGATGTCAACTTAAT 600
QY 601 GTCTTTCACAAACAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
|
Db 601 GTCTTTCACAAACAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGACATGATCCAAATATTTCCAGATGATGAAAT 720
|
Db 661 TGTGCGTTAATGTTGCTGGAACATGACATGATCCAAATATTTCCAGATGATGAAAT 720
QY 721 ACCACTGTCACATACGCTATCTAATAGAGATTAATTAATGATGATGATGATGATGAT 780
|
Db 721 ACCACTGTCACATACGCTATCTAATAGAGATTAATTAATGATGATGATGATGATGAT 780
QY 781 TATGTCGTGATATCGAATCAAAAACAGATGCGCCACAGCAGTGTACTTGGTGA 840
|
Db 781 TATGTCGTGATATCGAATCAAAAACAGATGCGCCACAGCAGTGTACTTGGTGA 840
QY 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
|
Db 841 CATGAGCAAAAACAGCAAGTGTGAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
QY 901 CTGATAGATATGGAAGAGACTGCTCTCATCTTCTGATATGTTGGATCAGCAAGTATA 960
|
Db 901 CTGATAGATATGGAAGAGACTGCTCTCATCTTCTGATATGTTGGATCAGCAAGTATA 960
QY 961 GTCAAGCCCTTACTGAGCAAAATATGATGATGATGATGATGATGATGATGATGATGATG 1020
|
Db 961 GTCAAGCCCTTACTGAGCAAAATATGATGATGATGATGATGATGATGATGATGATGATG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTATCATCATCATGTAATTTGCCAGTACTTCTGATAC 1080
|
Db 1021 GCCAGAGATATGCTGTTTCTAGTATCATCATCATGTAATTTGCCAGTACTTCTGATAC 1080
QY 1081 AAAGAAAAAGATGCTTAATAATCTCTTCTGAAAAACAGCAATCCAGAAACAGACTTAAG 1140
|
Db 1081 AAAGAAAAAGATGCTTAATAATCTCTTCTGAAAAACAGCAATCCAGAAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTCAAAAGTTCAAGAGAGTGAATAATAGCAGCAGAGAGAA 1200
|
Db 1141 CTGACATCAGAGAGAGAGTCAAAAGTTCAAGAGAGTGAATAATAGCAGCAGAGAGAA 1200
QY 1201 ATGTCTCAAGAACGAAATTAATTAAGATGATGATGATGATGATGATGATGATGATG 1260
|
Db 1201 ATGTCTCAAGAACGAAATTAATTAAGATGATGATGATGATGATGATGATGATGATG 1260
QY 1261 AAGCATGAAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
|
Db 1261 AAGCATGAAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
QY 1321 AATGCTGATTAATGATTAATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
|
Db 1321 AATGCTGATTAATGATTAATCTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 CCTGACAAAGAAATGAAAGATATCACGAATTTGCCAATTAATGTTTCTGACTACAAAGAA 1440
|
Db 1381 CCTGACAAAGAAATGAAAGATATCACGAATTTGCCAATTAATGTTTCTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAATTAATCTCTTCTGAAAAACAGCAATCCAGAAACAGACTTAAGCTGCA 1500
|
Db 1441 AAACAGATGCCAAATTAATCTCTTCTGAAAAACAGCAATCCAGAAACAGACTTAAGCTGCA 1500
QY 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGGCAGTGAATAATGSCAGCCAGAGAAAAAGATCT 1560
|
Db 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGGCAGTGAATAATGSCAGCCAGAGAAAAAGATCT 1560
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QY 1561 CAAGAACCAGAAATAATAAGATGCTGATAGAGACTAGAAATTTTATGCTATCGAA 1620
|||||
Db 1561 CAGAAGCCAGAAATAATAAGATGCTGATAGAGACTAGAAATTTTATGCTATCGAA 1620
|||||
QY 1621 GAAATGAGAGACGCGAAGTACTCATGTGCTGATCCAGAAAACTGACTAATGCTGCC 1680
|||||
Db 1621 GAAATGAGAGACGCGAAGTACTCATGTGCTGATCCAGAAAACTGACTAATGCTGCC 1680
|||||
QY 1681 ACTGCGCAATGCTATGATGATTAATTCCTCCAGAGAGACGAGACCTGAAAGC 1740
|||||
Db 1681 ACTGCGCAATGCTATGATGATTAATTCCTCCAGAGAGACGAGACCTGAAAGC 1740
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QY 1741 CAGCAATTTCTGACACTGAGATGAAAGATACAGATGACGAGCAAAATGATCTAG 1800
|||||
Db 1741 CAGCAATTTCTGACACTGAGATGAAAGATACAGATGACGAGCAAAATGATCTAG 1800
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QY 1801 AAGCAATTTTGTGAGACAGAACACTGCAATATACAGATGAGATTTCTGATTCATGAA 1860
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Db 1801 AAGCAATTTTGTGAGACAGAACACTGCAATATACAGATGAGATTTCTGATTCATGAA 1860
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QY 1861 GAAAGCAGATGAGTGTGAAAAATGCAATTCGAGCTTCTCTAGTTGTAAGAA 1920
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Db 1861 GAAAGCAGATGAGTGTGAAAAATGCAATTCGAGCTTCTCTAGTTGTAAGAA 1920
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QY 1921 GAAAAAGACATCTTGATGAAATAGTACCTGCGGAGAGAAATGCGATGTAAGCTG 1980
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Db 1921 GAAAAAGACATCTTGATGAAATAGTACCTGCGGAGAGAAATGCGATGTAAGCTG 1980
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QY 1981 GAGCTAGACATGAAACATCAGAGCCAGCTAAAAAATTTTAAAAAATTTTAAAAA 2040
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Db 1981 GAGCTAGACATGAAACATCAGAGCCAGCTAAAAAATTTTAAAAAATTTTAAAAA 2040
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RESULT 14

US-09-636-215-375
; Sequence 375, Application US/09636215
; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvyck, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636, 215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-636-215-375

Query Match 100.0%; Score 2040; DB 24; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGTTAGGTTGATTCATGCGGCTGCTTCTGTGAAGAACATTTGCTC 60

|||||
Db 1 ATGCTGTTAGGTTGATTCATGCGGCTGCTTCTGTGAAGAACATTTGCTC 60
|||||
QY 61 AGAGAGCAAGTGGGCAAGTGTGCTGCTTCTGCTCCCTGCTGAGAGGAGACGGCAG 120
|||||
Db 61 AGAGAGCAAGTGGGCAAGTGTGCTGCTTCTGCTCCCTGCTGAGAGGAGACGGCAG 120
|||||
QY 121 AGCAAGTGGGCACTTCTGAGAGCCAGAGACTCTGATGAAGACTCAGAGAGCAAG 180
|||||
Db 121 AGCAAGTGGGCACTTCTGAGAGCCAGAGACTCTGATGAAGACTCAGAGAGCAAG 180
|||||
QY 181 ATGGGCAAGTGTGCGCCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGT 240
|||||
Db 181 ATGGGCAAGTGTGCGCCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGT 240
|||||
QY 241 GGGGCTTCTGAGAGCCAGAGACTCTGCTATGAAGACTCAGAGCAAGATGGGCAAG 300
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Db 241 GGGGCTTCTGAGAGCCAGAGACTCTGCTATGAAGACTCAGAGCAAGATGGGCAAG 300
|||||
QY 301 TGGTGTGCTGCTGCTTCCCTGCTGAGGGGAGGCAAGAGCAAGTGGGCGCTTG 360
|||||
Db 301 TGGTGTGCTGCTGCTTCCCTGCTGAGGGGAGGCAAGAGCAAGTGGGCGCTTG 360
|||||
QY 361 GGAAGTACAGATGACAGTGCCTTCATGAGCCAGAGTACCAAGTCCGTGAGAGATCTG 420
|||||
Db 361 GGAAGTACAGATGACAGTGCCTTCATGAGCCAGAGTACCAAGTCCGTGAGAGATCTG 420
|||||
QY 421 GACAGCTCCACAGAGTGCCTGCTGAGGAGTAAAGTCCCAAGAGATCTCATGCTATG 480
|||||
Db 421 GACAGCTCCACAGAGTGCCTGCTGAGGAGTAAAGTCCCAAGAGATCTCATGCTATG 480
|||||
QY 481 CTCAGGAGACTGACGTAAGCAAGAGAGCAAGAGAGAGAGTGTCTACATCTGCGC 540
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Db 481 CTCAGGAGACTGACGTAAGCAAGAGAGCAAGAGAGAGAGTGTCTACATCTGCGC 540
|||||
QY 541 TCTGCCAATGGGAATTCAGAGTGTAAATCTCTGCTGAGAGAGACTGCAATTAAT 600
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Db 541 TCTGCCAATGGGAATTCAGAGTGTAAATCTCTGCTGAGAGAGACTGCAATTAAT 600
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QY 601 GTCCCTTGACAAACAAAAGAGACAGCTCTGATTAAGGCGCTACAGTCCAGAGATGAA 660
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Db 601 GTCCCTTGACAAACAAAAGAGAGACAGCTCTGATTAAGGCGCTACAGTCCAGAGATGAA 660
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QY 661 TGTGCGTTAATGTGCTGGAACATGGCAGTGTCCAAATTTCCAGATGATGAAT 720
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Db 661 TGTGCGTTAATGTGCTGGAACATGGCAGTGTCCAAATTTCCAGATGATGAAT 720
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QY 721 ACCACTCTGACATACGCTATCTAATGAAGATTAATTAAGGCAAGAGACTGCTTGA 780
|||||
Db 721 ACCACTCTGACATACGCTATCTAATGAAGATTAATTAAGGCAAGAGACTGCTTGA 780
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QY 781 TATGCTGCTATATCGAATCAAAAACACAGATGCGCTCACACACTGTTACTTGCTGA 840
|||||
Db 781 TATGCTGCTATATCGAATCAAAAACACAGATGCGCTCACACACTGTTACTTGCTGA 840
|||||
QY 841 CATGAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGGAAATTTTAAATGCA 900
|||||
Db 841 CATGAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGGAAATTTTAAATGCA 900
|||||
QY 901 CTGATGATATGAGAGAGTGTCTCATCTGCTTATGTTGTGATCAGCAAGATATA 960
|||||
Db 901 CTGATGATATGAGAGAGTGTCTCATCTGCTTATGTTGTGATCAGCAAGATATA 960
|||||
QY 961 GTGAGCTTCTACTGAGCAAAATATGATGTATCTTCAAGATCTATCTGAGCAGAG 1020
|||||
Db 961 GTGAGCTTCTACTGAGCAAAATATGATGTATCTTCAAGATCTATCTGAGCAGAG 1020
|||||
QY 1021 GCGAGAGATGCTGTTCTATGATCATCATGATTAATGCGAGTACTTCTGATAC 1080
|||||
Db 1021 GCGAGAGATGCTGTTCTATGATCATCATGATTAATGCGAGTACTTCTGATAC 1080
|||||
QY 1081 AAGGAAAAACAGATGCTAAAAATCTTCTGAAAAACAGATCCAGAAACACTTGAAG 1140
|||||

Db 1081 AAGAAAAAGATGCTAATAAATCTCTTGAATAAAGCAGCAATCCAGAAACCAAGCTTAAAG 1140
Qy 1141 CTGACATCAGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAGAA 1200
Qy 1201 ATGCTCAGAGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 1260
Db 1201 ATGCTCAGAGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 1260
Qy 1261 AAGATGAGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 1320
Db 1261 AAGATGAGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 1320
Qy 1321 AATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
Db 1321 AATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
Qy 1381 CCGTACAGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 1440
Db 1381 CCGTACAGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 1440
Qy 1441 AAGAGATGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 1500
Db 1441 AAGAGATGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 1500
Qy 1501 TCAGAGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 1560
Db 1501 TCAGAGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 1560
Qy 1561 CAGAGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 1620
Db 1561 CAGAGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 1620
Qy 1621 GAAATGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 1680
Db 1621 GAAATGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 1680
Qy 1681 ACTGCTGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 1740
Db 1681 ACTGCTGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 1740
Qy 1741 CAGAGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 1800
Db 1741 CAGAGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 1800
Qy 1801 AAGCAATTTGTGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAG 1860
Db 1801 AAGCAATTTGTGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAG 1860
Qy 1861 GAAAGAGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 1920
Db 1861 GAAAGAGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 1920
Qy 1921 GAAAGAGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 1980
Db 1921 GAAAGAGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 1980
Qy 1981 GAGCTAGAGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 2040
Db 1981 GAGCTAGAGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 2040

RESULT 15

US-09-651-236-375

; Sequence 375, Application US/09651236

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yugu

; APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Patrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Ajun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.42718C18
CURRENT APPLICATION NUMBER: US/09/651,236
CURRENT FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 865
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-651-236-375

Query Match 100.0%; Score 2040; DB 25; Length 2040;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 ATGCTGCTGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 60
Db 1 ATGCTGCTGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 60
Qy 61 AGAGAGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 120
Db 61 AGAGAGAGAGAGAGTTCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGCAGAG 120
Qy 121 AGCAAGTGGGACTTCGAGAGCAGAGAGTTCGATGAAGACACTCAGAGAGAG 180
Db 121 AGCAAGTGGGACTTCGAGAGCAGAGAGTTCGATGAAGACACTCAGAGAGAG 180
Qy 181 ATGGGAGAGTTCGAGAGCAGAGAGTTCGATGAAGACACTCAGAGAGAG 240
Db 181 ATGGGAGAGTTCGAGAGCAGAGAGTTCGATGAAGACACTCAGAGAGAG 240
Qy 241 GGGCTTCGAGAGCAGAGAGTTCGATGAAGACACTCAGAGAGAG 300
Db 241 GGGCTTCGAGAGCAGAGAGTTCGATGAAGACACTCAGAGAGAG 300
Qy 301 TGGTGTCCACTGCTCCCTGCTGAGAGGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 301 TGGTGTCCACTGCTCCCTGCTGAGAGGAGAGAGAGAGAGAGAGAGAGAGAG 360
Qy 361 GGAGAGTTCGAGAGCAGAGAGTTCGATGAAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 361 GGAGAGTTCGAGAGCAGAGAGTTCGATGAAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Qy 421 GACAGAGTTCGAGAGCAGAGAGTTCGATGAAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 421 GACAGAGTTCGAGAGCAGAGAGTTCGATGAAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Qy 481 CTCAG 540
Db 481 CTCAG 540
Qy 541 TCTGCAATGGAGATTCAG 600
Db 541 TCTGCAATGGAGATTCAG 600
Qy 601 GTCTTGAAG 660
Db 601 GTCTTGAAG 660
Qy 661 TGTGCTTAATGTTGCTGAG 720

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Db 661 TGTGGTTAATGTCTGTGACATGGCAGTGCATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTGTGCACTAGCACTCTATATATGAAGATTAATTAATGGCCAAACACGCTCTTA 780
Db 721 ACCACTGTGCACTAGCACTCTATATATGAAGATTAATTAATGGCCAAACACGCTCTTA 780
QY 781 TATGGTGTGATATGGAATCAAAAAACAAGCATGGCCCTCACACACTGTTACTTGGTGA 840
Db 781 TATGGTGTGATATGGAATCAAAAAACAAGCATGGCCCTCACACACTGTTACTTGGTGA 840
QY 841 CATGAGCAAAAAACAGCAAGTGTGAAATTTTAAATCAGAAAAAAGCGAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTGTGAAATTTTAAATCAGAAAAAAGCGAATTTAAATGCA 900
QY 901 CTGGATAGATATGGAAGAGCTGCTCTCATATCTTCCAGATCTATCTGGACAGAG 960
Db 901 CTGGATAGATATGGAAGAGCTGCTCTCATATCTTCCAGATCTATCTGGACAGAG 960
QY 961 GTACAGCCTTCTACTGAGCAAAATATGATGATCTTCCAGATCTATCTGGACAGAG 1020
Db 961 GTACAGCCTTCTACTGAGCAAAATATGATGATCTTCCAGATCTATCTGGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
QY 1081 AAGAAAAACACATGCTAAAAATCTCTTGAACACAGCATCCAGAACACACTTAAG 1140
Db 1081 AAGAAAAACACATGCTAAAAATCTCTTGAACACAGCATCCAGAACACACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAGGCAAGTGAATAATGCCAGCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTCAACAAAGTTCAAGGCAAGTGAATAATGCCAGCAGAGAA 1200
QY 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGGTATAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACCAAGAAATTAATAGATGGTATAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAAGTAATATGTGGGATTACTAGAAAACTGACTAATGTGTCTGCTGGC 1320
Db 1261 AAGCATGAAAGTAATATGTGGGATTACTAGAAAACTGACTAATGTGTCTGCTGGC 1320
QY 1321 AATGTGATATGATTAATTTCTCAAGAGAGCAGAAACCTGAAATCAGCAATTT 1380
Db 1321 AATGTGATATGATTAATTTCTCAAGAGAGCAGAAACCTGAAATCAGCAATTT 1380
QY 1381 CCTGACAAACGAAGTGAAGAGTATCAGAAATTTGGCAATTTGACTACAAAGAA 1440
Db 1381 CCTGACAAACGAAGTGAAGAGTATCAGAAATTTGGCAATTTGACTACAAAGAA 1440
QY 1441 AAACAGATGCCAAATACTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATACTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
QY 1501 TCAGAGGAAGAGTCAACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCAGAGAAAGATCT 1560
Db 1501 TCAGAGGAAGAGTCAACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCAGAGAAAGATCT 1560
QY 1561 CAAGAACCAGAAATTAATTAAGATGGTATAGAGAGCTGAAATTTTATGGCTATCGAA 1620
Db 1561 CAAGAACCAGAAATTAATTAAGATGGTATAGAGAGCTGAAATTTTATGGCTATCGAA 1620
QY 1621 GAAATGAAGAACAGGAAAGTACTCATGTGCGATTTCCAGAAAACTGACTAATGGTCCC 1680
Db 1621 GAAATGAAGAACAGGAAAGTACTCATGTGCGATTTCCAGAAAACTGACTAATGGTCCC 1680
QY 1681 ACTGCTGGCAATGTGATGATGATTAATTTCTCCAAAGAGAGCAGAACACCTGAAAGC 1740
Db 1681 ACTGCTGGCAATGTGATGATGATTAATTTCTCCAAAGAGAGCAGAACACCTGAAAGC 1740
QY 1741 CAGCAATTTCTGACACTGAGATGAAGATACACAGTACGAAACAAATGATACTCAG 1800

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Db 1741 CAGCAATTTCTGACACTGAGATGAAGATATCACAGTACGCAACCAAAATGATACTCAG 1800
QY 1801 AAGCAATTTTGTGAAGACAGAACTGGAAATTTACAGATGAGATTCGATTCATGAA 1860
Db 1801 AAGCAATTTTGTGAAGACAGAACTGGAAATTTACAGATGAGATTCGATTCATGAA 1860
QY 1861 GAAAGCAGATGAAGTGGTTGAAAAATGAAATTCGACCTTCTCTAGTTGTGAAGAA 1920
Db 1861 GAAAGCAGATGAAGTGGTTGAAAAATGAAATTCGACCTTCTCTAGTTGTGAAGAA 1920
QY 1921 GAAAAAGACATCTTGATGAAATTAAGTACGTGCGGGAAGAAATTCATGCTAAGACTG 1980
Db 1921 GAAAAAGACATCTTGATGAAATTAAGTACGTGCGGGAAGAAATTCATGCTAAGACTG 1980
QY 1981 GAGCTGACACAAATGAACATCAGACGCTTAAAAAATGAAAAAATGAAAAA 2040
Db 1981 GAGCTGACACAAATGAACATCAGACGCTTAAAAAATGAAAAAATGAAAAA 2040

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Search completed: November 8, 2002, 08:45:47
 Job time : 4025.92 secs

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APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C139
CURRENT FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 21
LENGTH: 1041
TYPE: DNA
ORGANISM: Homo Sapien
US-10-131-813A-21

Query Match 8.4%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 1,7e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;
QY 378 TGCCTTATGAGGCCAGGTACGATCGTGGAGAGATCTGGCAAGCTCCACAGGC 437
DB 300 TGGCTTCCATTTCCCATATCCCATTAACCGTATCATCTGAAGAGATCCACAGAGC 359
QY 438 TGGCTGGGGGTAAGATCCCGAGAAAGATCTCATCTGCAATGCGAGGACAGAGCT 497
DB 360 TGTCTTACATGTATTAATCTAGAGAACTGA--GTACCTTGTGCTACAGATTAATGAGCG 416
QY 498 GAACAGAGAGCAAGCAAAAGAGAGTCTCTACATCTGGCCCTTCGCAATGGGAATTC 557
DB 417 CAATTAAGAGAGCAAGAGAAAGAGAGCCGCTACATTTGGCCGTGTGCGCACTGGCAAC 476
QY 558 AGAAGTAACTAACTCTGCTGGAGACGATGTCACACTTAATGTCTTGAACAACAAAA 617
DB 477 GGAATGTGATCATCTCGCTGTGTCAGAAAGATGTGAGCTTAACCTCGACCGGTGAGA 536
QY 618 GAGAGAGCTGTGAATAAGGCCGTACATGCGCAAGAAATGAATGTGCTTAATGTCTCT 677
DB 537 CAGAGACCTCTGTATCAAGGCTGTACAACTGAGGAGGAGGCTGTGTCAACTCTTCTGCT 596

QY 678 GGAACATGACACTGTATCCAAATATTTCAGATGAGTATGAAATACCACTGCACTACGC 737
DB 597 GCAAAATGCGCGCATCCAAATATTATACGATTTCTTGAAGAGACTGCTGCACTACGC 656
QY 738 TATCTATATGAGATTAATTAATGCGCAAGACATGCTTATATGTGTGATATGGA 797
DB 657 TGTGTATATGAAATATCATCATGATAGAAAAACTTCTTTCACATGGTATCAAAATATTGA 716
QY 798 ATCAAAAAACAAG 810
DB 717 AGAATGCAAG 729

RESULT 3
US-10-131-819A-21
Sequence 21, Application US/10131819A
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C134
CURRENT FILING DATE: 2002-04-24
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 21
LENGTH: 1041
TYPE: DNA
ORGANISM: Homo Sapien
US-10-131-819A-21
Query Match 8.4%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 1,7e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;
QY 378 TGCCTTATGAGGCCAGGTACGATCGTGGAGAGATCTGGCAAGCTCCACAGGC 437

```
Db 300 TGGCTTCGGCATTTCCCAATACCCATTAACCGTATCATCTGAAAGAGATCCAGAGAGC 359
Qy 438 TGGCTTCGGGGTAAAGTCCCAAGAAAGATCTCATCTGATGCTGAGGACACTGACGT 497
Db 360 TGTCTTACATGTTAACTTGAGAAACTGAA---GTACCTTCCTGCTCAGCTATTATGACGC 416
Qy 498 GAACAGAAGAGCAAGCAAAAGAGAGAGCTGCTACATCTGGGCTGCGCAATGGGAATTC 557
Db 417 CATTAAGAGAGACAGAGAAAGAGAGCCCTTACATTTGGCCTGTGCGCACTGGCAACC 476
Qy 558 AGAAGTAGTAAACTCTCTGCTGAGACAGATGTCACTTAATGTCCTTGACAAACAAA 617
Db 477 GGAATGTGACATCTCTGCTGCTGAGAGATGTGAGCTTAACTCTGGACCGTAAGA 536
Qy 618 GAGGACAGCTCTGATTAAGGCGGTGACATGCCAGAGATGAATGTCGCTTAATGTTGCT 677
Db 537 CAGGACACCTCTGATCAACAGCTGTACACTGAGGAGGCTTGTGCAACTTCTCTGCT 596
Qy 678 GGAACATGACACTGATCCAAATATTCCAGATGATGTAAGAAATACCACTGCACTAGCC 737
Db 597 GCAAAATGGCGCCATCCAAATATTTCGATTTCTTGGAAAGAGCTGCTGTGACACTAGC 656
Qy 738 TATCTAATTAAGATTAATTAATGCGCAAGACACTGCTTATATGTCGTGATATGCA 797
Db 657 TGTGTATTAATGAAGATACATCATGATAGAAAACCTTTTCACATGATGTAACAATTTGA 716
Qy 798 ATCAAAAACAAG 810
Db 717 AGAATGACAGCAAG 729
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RESULT 4

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US-10-131-823A-21
; Sequence 21, Application US/10131823A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C143
; CURRENT APPLICATION NUMBER: US/10/131,823A
; PRIOR APPLICATION NUMBER: 60/049111
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
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; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 21
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-823A-21
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Query Match 8.4%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 1,7e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;
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Qy 378 TGGCTTCATGAGAGCCAGGTACCCAGCTCCGTGAGAGATCTGAGACAGCTCCAGAGAGC 437
Db 300 TGGCTTCGGCATTTCCCAATACCCATTAACCGTATCATCTGAAAGAGATCCAGAGAGC 359
Qy 438 TGGCTTCGGGGTAAAGTCCCAAGAAAGATCTCATCTGATGCTGAGGACACTGACGT 497
Db 360 TGTCTTACATGTTAACTTGAGAAACTGAA---GTACCTTCCTGCTCAGCTATTATGACGC 416
Qy 498 GAACAGAAGAGCAAGCAAAAGAGAGAGCTGCTACATCTGGGCTGCGCAATGGGAATTC 557
Db 417 CATTAAGAGAGACAGAGAAAGAGAGCCCTTACATTTGGCCTGTGCGCACTGGCAACC 476
Qy 558 AGAAGTAGTAAACTCTCTGCTGAGACAGATGTCACTTAATGTCCTTGACAAACAAA 617
Db 477 GGAATGTGACATCTCTGCTGCTGAGAGATGTGAGCTTAACTCTGGACCGTAAGA 536
Qy 618 GAGGACAGCTCTGATTAAGGCGGTGACATGCCAGAGATGAATGTCGCTTAATGTTGCT 677
Db 537 CAGGACACCTCTGATCAACAGCTGTACACTGAGGAGGCTTGTGCAACTTCTCTGCT 596
Qy 678 GGAACATGACACTGATCCAAATATTTCAGATGATGTAAGAAATACCACTGCACTAGCC 737
Db 597 GCAAAATGGCGCCATCCAAATATTTCGATTTCTTGGAAAGAGCTGCTGTGACACTAGC 656
Qy 738 TATCTAATTAAGATTAATTAATGCGCAAGACACTGCTTATATGTCGTGATATGCA 797
Db 657 TGTGTATTAATGAAGATACATCATGATAGAAAACCTTTTCACATGATGTAACAATTTGA 716
Qy 798 ATCAAAAACAAG 810
Db 717 AGAATGACAGCAAG 729
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RESULT 5

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US-10-131-824A-21
; Sequence 21, Application US/10131824A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C143
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FILE REFERENCE: P3330R1C126
CURRENT APPLICATION NUMBER: US/10/131,824A
CURRENT FILING DATE: 2002-04-29
PRIORITY APPLICATION NUMBER: 60/049111
PRIORITY FILING DATE: 1997-06-18
PRIORITY APPLICATION NUMBER: 60/056974
PRIORITY FILING DATE: 1997-08-26
PRIORITY APPLICATION NUMBER: 60/055113
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059115
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059117
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/053122
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/059184
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/052653
PRIORITY FILING DATE: 1997-09-18
PRIORITY APPLICATION NUMBER: 60/059352
PRIORITY FILING DATE: 1997-09-19
PRIORITY APPLICATION NUMBER: 60/059588
PRIORITY FILING DATE: 1997-09-19
Remaining PRIORITY application data removed - See File Wrapper or PALM
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 21
LENGTH: 1041
TYPE: DNA
ORGANISM: Homo Sapien
US-10-131-824A-21

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Query Match	8.4%;	Score 170.6;	DB 6;	Length 1041;
Best Local Similarity	63.7%;	Pred. No. 1.7e-32;		
Matches 276; Conservative	0;	Mismatches 154;	Indels 3;	Gaps 1

QY	378	TGCCCTCATGTGAGGCCCGACAGGTACACACGTCGCGTGAGAGAAATCTGGACAAAGCTCCACAGAGC	4373
Dp	300	TGGCTTCCCATTTTCCCAATACCCCAATTAACCGTATCATCTGAAAGAGATCCACAGAGC	355
QY	438	TGCCGTGTGGGGTAAAGTCCCCAGAAAGATCTCATGCTCATGCTCAAGGACACTGACGT	497
Dp	360	TGCTTTACATGGTATCATGTAGAAACTGAA---GTACCTTCTGCTACGATTAATTGACGC	418
QY	498	GAACAGAAAGGACAAAGCAAAAGAGAGATGCTCTACATCTGGCCCTCTCCATGGGAATTC	555
Dp	417	CATATAGAGAGACAGGAAGAAAGACCGCCCTCATTTTGGCTGTGCTCACTGGCCAAAC	478
QY	558	AGAACTACTAAAACTCCTCGCTGGACAGACGATGTCAACTATATCTCCTGCAACAACAAAA	6173
Dp	477	GGAATTGGTACATCTGCTCGTGTCGCAAGAAATGTAGACTTAACCTCTGGCAGCGGTGAAA	538
QY	618	GAGGACACTCTGATTAAGGCCGTACAAATGCCAGGAAGATGAATGTGCGTTATGTTGCT	6777
Dp	537	CAGGACACCTCTGTATCAACAGCTGTACAACATGAGGACAGAGGCTTGTGCAACTCTTCGTCT	598
QY	678	GGAACATGCGACTGTGCCAAATATTTCCGATGAGATGAGGAATATCCACTGTGCACTACGC	737
Dp	597	GCAAAATGCGCCCAATCCAAATTTATAGGATTTCTTTGGAAGGACGTGCTGTGCACTACGC	658
QY	738	TATCTATATTAAGATAATTAATTTATGGCCAAAGCACTGCTCTTATATGATGCTGATATCGA	797
Dp	657	TGTGTATTAATGAAGTATACATCCATGATGAGAAAACTTCTTCACATGATGTACAAATATTGA	718
QY	798	ATCAAAAAACAAG 810	
Dp	717	AGAAATGCAGCAAG 729	

RESULT 6
US-10-131-826A-21
; Sequence 21, Application US/10131826A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.

```

APPLICANT: Beresini, Laureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Flivaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remaining SEQ ID Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 21
LENGTH: 1041
TYPE: DNA
ORGANISM: Homo Sapien
US-10-131-826A-21

```

Query Match	8.4%;	Score 170.6;	DB 6;	Length 1041;
Best Local Similarity	63.7%;	Pred. No. 1.7e-32;		
Matches 276;	Conservative	0;	Mismatches 154;	Indels 3;
				Gaps 1.

Oy	378	TGCCCTCAATGGAGCCCGAAGTACACACGTCCTCGGAGAAGATGTGGACAAGCCTCACAGGC	433
Dd	300	TGGCTTGCCATTTCGCCCATATACCOCATTTAAACCGATCATCTGAAAGAGATCCACAGGC	355
Oy	438	TGCCGTGTGGGATAAGTCCCAGAAAGATCTCATGTCTACTGCTCAAGGACACTGACGT	497
Dd	360	TGCTTTACATGGTAATCTAGAGAAACTGA---GTACCTTCCTGCTCAGATTTATTTGACGC	418
Oy	498	GACACGAAGAAGCAACGAAAAGAGACTCTCTACATCTGGCCCTGSCAATGGGAATTC	557
Dd	417	CATATAGAGARCAAGAAAGAAAGAACCCGCTTACATTTTGGCCTGTGCACTGGCCAAAC	476
Oy	558	AGAACTACTAAACTCCTGCTGACAGACAGATGTCACCTTAATGTCTTGACAAACAAAA	617
Dd	477	GGAAATGSTATATCTCCTCGGTGTCACAGAAAGATGTAGACTTAACCTCTGCAGCCGTGAAGA	536
Oy	618	GAGGACACCTCTGATTAAGGCGCGATCAATGCCAGAGAAGATCAATGTGCGTTAAATGTGCT	677
Dd	537	CAGGACACCTCTGATCAACAGCTGTACACACTGAGCAGAGAGGCTTGTGCAACTCTTGTGCT	596

OY	678	GGAAACATGGCAGCTGATCCAAATATTCAGATGAGTATGSAAAATACACGCTGACATACGC	737
Db	597	GCAAAATGGGCCCATCTCCAAATATTTACGAGTTCTTTGGAAAGGCGTGGCTTGACATACGC	656
OY	738	TATCTATATGATGAATTAATTAATGGCCAAAGCAGCTCTTATATGTCGCTATATCGA	797
Db	657	TGTGTATATGATGATACATCCATCATGATAGAAAACTTCTTACCATGGTACAAATATGGA	716
OY	798	ATCAAAAAACAG	810
Db	717	AGAAATGACGACAG	729

RESULT 7
US-10-131-829A-21
; Sequence 21, Application US/10131829A
; GENERAL INFORMATION:

1 APPLICANT: Baker, Kevin P.
 2 APPLICANT: Beresini, Maureen
 3 APPLICANT: DeForge, Laura
 4 APPLICANT: Desnoyers, Luc
 5 APPLICANT: Filvaroff, Ellen
 6 APPLICANT: Gao, Wei-Qiang
 7 APPLICANT: Gerlitsen, Mary E.
 8 APPLICANT: Goddard, Audrey
 9 APPLICANT: Godowski, Paul J.
 10 APPLICANT: Gurney, Austin L.
 11 APPLICANT: Sherwood, Steven
 12 APPLICANT: Smith, Victoria
 13 APPLICANT: Stewart, Timothy A.
 14 APPLICANT: Tumas, Daniel
 15 APPLICANT: Watanabe, Collin K
 16 APPLICANT: Wood, William
 17 APPLICANT: Zhang, Zemin
 18 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 19 ACIDS ENCODING THE SAME
 20 TITLE OF INVENTION: ACIDS ENCODING THE SAME
 21 FILE REFERENCE: P3330R1C138
 22 CURRENT APPLICATION NUMBER: US/10/131,829A

```

? PRIOR APPLICATION NUMBER: 60/049911
? PRIOR FILING DATE: 1997-06-18
? PRIOR APPLICATION NUMBER: 60/056974
? PRIOR FILING DATE: 1997-08-26
? PRIOR APPLICATION NUMBER: 60/059113
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059115
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059117
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059122
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059184
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059263
? PRIOR FILING DATE: 1997-09-18
? PRIOR APPLICATION NUMBER: 60/059352
? PRIOR FILING DATE: 1997-09-19
? PRIOR APPLICATION NUMBER: 60/059588
? PRIOR FILING DATE: 1997-09-19
? Remaining Prior Application data removed - See File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 550
? SEQ ID NO 21
? LENGTH: 1041
? TYPE: DNA
? ORGANISM: Homo Sapien
US-10-131-829A-21

```

Query Match	8.44;	Score 170.6;	DB 6;	Length 1041;
Best Local Similarity	63.78;	Pred. No. 1.7e-32;		
Matches 276;	Conservative	0;	Mismatches 154;	Indels 3;
				Gaps
QY	378	TGCCTTCATGAGCCCACTACCAACGTCCTGGAGAAATGTGACACAGCTCCACAAGC	437	

Db 300 TGGCTTGCCATTTCGCCCAATTCGCCCAATTAACGCTATCATCTGMAAGAGATCCACAGAG 359

Qy 438 TGCCTGGTGGGGTAAGTCTCCCGACAAAGATCTTCATGTCATGCTCAGGACACTGACGT 497

Db 360 TGTCTTACATGTAATGCTAGAGAAACTGAA---GTACCTCTTGCTGCACGTATATGACGC 416

Qy 498 GACACAGAAGGACACAGCAAGCAAAAGAGAGACTGCTTTCATCTGCGCTCTGCCAATGGGAATTC 557

Db 417 CAATTAAGAGACAGCAAGAAAGGACCGCCCTCATTTTGGCCGTGCGCACTGGCCAAACC 476

Qy 558 AGAAGTAGTAATAACTCTCTGCTGGACACACACATGTGCACATTAAATGTCTTTACACAACAAAA 617

Db 477 GGAATGGTAGATCTCCTGGGTGTCCAAAGATGTGACCTTAACCTCGACCGGTGAAGA 536

Qy 618 GAGGACACCTGTGATTAAGGCGGTGACCAATGGCAGAGAAGATGAATGTGCGTAAATGTGCT 677

Db 537 CAGGACACCTGTGATCAAGGCTGTACAACTGAGGACAGAGGCGTTGTCCAACCTCTTGCT 586

Qy 678 GGACATGCGACATCAATCAAAATATTCAGATGATGATGGAATACACTCTGGCACTACGC 737

Db 557 GCMAATATGGCCCAATCCAAATATATTACGAGATTTTGGGAAGGACCTCTGTGCACATACGC 656

Qy 738 TATCTATATGATGAATTAATTAATGAGCCAAAGACACTGCTCTTATATGCTGCTGATATGGA 797

Db 657 TGTGTATATATGAAGTACATCCATGATAGAAAACCTCTTCACATGCTACAAATATTTGA 716

Qy 798 ATCAAAAAACAAG 810

Db 717 AGAATGCGCAAG 729

RESULT 8
US-10-125-926A-21
; Sequence 21, Application US/10125926A

1 APPLICANT: Baker, Kevin P.
2 APPLICANT: Beresini, Maureen
3 APPLICANT: Beresini, Laura
4 APPLICANT: Desnoyers, Luc
5 APPLICANT: Filvaroff, Ellen
6 APPLICANT: Gao, Wei-Qiang
7 APPLICANT: Gerritsen, Mary E.
8 APPLICANT: Goddard, Audrey
9 APPLICANT: Godowski, Paul J.
10 APPLICANT: Gurney, Austin L.
11 APPLICANT: Sherwood, Steven
12 APPLICANT: Smith, Victoria
13 APPLICANT: Stewart, Timothy A.
14 APPLICANT: Tumas, Daniel
15 APPLICANT: Watanabe, Colin K
16 APPLICANT: Wood, William
17 APPLICANT: Zhang, Zhenli
18 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
19 TITLE OF INVENTION: ACIDS ENCODING THE SAME
20 FILE REFERENCE: P3330R1C80
21 CURRENT APPLICATION NUMBER: US/10/125,926A
22 CURRENT FILING DATE: 2002-10-15
23 PRIOR APPLICATION NUMBER: 60/049911
24 PRIOR FILING DATE: 1997-06-18
25 PRIOR APPLICATION NUMBER: 60/056974
26 PRIOR FILING DATE: 1997-08-26
27 PRIOR APPLICATION NUMBER: 60/059113
28 PRIOR FILING DATE: 1997-09-17
29 PRIOR APPLICATION NUMBER: 60/059115
30 PRIOR FILING DATE: 1997-09-17
31 PRIOR APPLICATION NUMBER: 60/059117
32 PRIOR FILING DATE: 1997-09-17
33 PRIOR APPLICATION NUMBER: 60/059122
34 PRIOR FILING DATE: 1997-09-17
35 PRIOR APPLICATION NUMBER: 60/059184
36 PRIOR FILING DATE: 1997-09-17
37 PRIOR APPLICATION NUMBER: 60/059263
38 PRIOR FILING DATE: 1997-09-18

```
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PAM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 21
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-125-926A-21

Query Match      8.4%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 1.7e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 378 TGCGTTCATGAGACCCAGTACACGTCCTCGAGAAAGATCTGGACAAGCTCCACAGAGC 437
DB 300 TGCGTTCGATTTCCCAATACCCCATTAACCGTATCATCTGAAGGATCCACAGAGC 359
QY 438 TGCGTGTGGGTAAGTCCCGCAGAAAGATCTCATGCTGCTCAGAGCACTGACGT 497
DB 360 TGCTTACATGTAATCTAGAGAACTGAA---GTACCTTCTGCTCAGCTATATGACGC 416
QY 498 GAACAAGAGAGACAAAGAGAGACTGCTTACATCTGGCTTCCCATGGGAATTC 557
DB 417 CAATAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 476
QY 558 AGAAGTAGTAATTAACCTGCTGAGACAGAGATGCAACTTAATGCTTACACAAAAA 617
DB 477 GGAATAGTACATCTCTGCTGTCAGAGAGATGAGCTTAACCTGCGACCGTGAAGA 536
QY 618 GAGGACAGCTCTGATTAAGGCCCTTACATGCTCAGAGAGATGAATGTCCTTAATGTTGCT 677
DB 537 CAGGACACCTCTGATCAAGGCTGTACACACAGAGAGAGAGAGAGAGAGAGAGAGAG 596
QY 678 GGAACATGCGCATGATCCAAATATTCAGATGATGATGAATACACACTGTGACCTACG 737
DB 597 GCAAAATGGGCCCAATCCAAATATTAAGGATTTCTTTGGAAGAGACGCTCTGACCTACG 656
QY 738 TATCTTAATGAAGATTAATTAATGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 797
DB 657 TGCTTAATGAAGATCAATCATCATGATAGAAAACCTTCTTACATGATGATCAAAATTTGA 716
QY 798 ATCAAAAACAG 810
DB 717 AGAATGAGAGAG 729

RESULT 9
US-10-127-829A-21
; Sequence 21, Application US/10127829A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C85
```

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; CURRENT APPLICATION NUMBER: US/10/127, 829A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PAM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 21
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-829A-21

Query Match      8.4%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 1.7e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 378 TGCGTTCATGAGACCCAGTACACGTCCTCGAGAAAGATCTGGACAAGCTCCACAGAGC 437
DB 300 TGCGTTCGATTTCCCAATACCCCATTAACCGTATCATCTGAAGGATCCACAGAGC 359
QY 438 TGCGTGTGGGTAAGTCCCGCAGAAAGATCTCATGCTGCTCAGAGCACTGACGT 497
DB 360 TGCTTACATGTAATCTAGAGAACTGAA---GTACCTTCTGCTCAGCTATATGACGC 416
QY 498 GAACAAGAGAGACAAAGAGAGACTGCTTACATCTGGCTTCCCATGGGAATTC 557
DB 417 CAATAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 476
QY 558 AGAAGTAGTAATTAACCTGCTGAGACAGAGATGCAACTTAATGCTTACACAAAAA 617
DB 477 GGAATAGTACATCTCTGCTGTCAGAGAGATGAGCTTAACCTGCGACCGTGAAGA 536
QY 618 GAGGACAGCTCTGATTAAGGCCCTTACATGCTCAGAGAGATGAATGTCCTTAATGTTGCT 677
DB 537 CAGGACACCTCTGATCAAGGCTGTACACACAGAGAGAGAGAGAGAGAGAGAGAGAG 596
QY 678 GGAACATGCGCATGATCCAAATATTCAGATGATGATGAATACACACTGTGACCTACG 737
DB 597 GCAAAATGGGCCCAATCCAAATATTAAGGATTTCTTTGGAAGAGACGCTCTGACCTACG 656
QY 738 TATCTTAATGAAGATTAATTAATGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 797
DB 657 TGCTTAATGAAGATCAATCATCATGATAGAAAACCTTCTTACATGATGATCAAAATTTGA 716
QY 798 ATCAAAAACAG 810
DB 717 AGAATGAGAGAG 729

RESULT 10
US-10-127-831A-21
; Sequence 21, Application US/10127831A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
```


QY	438	TGCCGTGGGGGTAAAGCCCCACAAGAGATCTCATGCTATGCTGACGGACATGACGT	497
Db	360	TGCTCTTACATGTAATCTAGAGAACTGAA---GTACCTTCTGCTACGATTTATATGACG	416
QY	498	GAAACAAGAGACAAGCAAGAAAAGAGACTGCTTACATCTGGCCCTGACCANTGGGAATTC	557
Db	417	CAATTAAGAGACAGAGAAAGGAAAGACCGCCCTTACATTTGGCCGTGCTCCACTGGCAAC	476
QY	558	AGAAGTACTAAACTCCTGCTGGACACACGATGTGCAACTTAATGTCTTACACACAAAA	617
Db	477	GGAATATGTTACATCTCCGTGGTGTCCAAAGATGTGACCTTAACCTTGCACCCGTGAGA	536
QY	618	GAGGACACCTCTGATPAAAGGCGGTACAAATGCGACGAGAAATGAATGTGCCGTAAATGTTGCT	677
Db	537	CAGGACACCTCTGTATCAAGGCTGTACACTGAGGCAAGAGCGTTGTCCAACTTCTGCT	596
QY	678	GGAACATGGCATCTANTCCAAATATTTCCAGATGAGTATGAGAAATACCACTCTGCATACGC	737
Db	597	GCAAAATGGCCCAATCCAAATATTTACGGAATTTCTTTGGAAAGGACGTCTGTGCACATACG	656
QY	738	TATCTATATGAAAGATTAATTAATGSCCAAACCACTGCTTTATATGCTGCTATATCGA	797
Db	657	TGTGTATATGAAATATCATCATCATGATAGAAAACTCTTTCACATGCTCAATAATATTGA	716
QY	798	ATCAAAAAACAAG 810	
Db	717	AGAAATGCAGCAAG 729	

RESULT 12
US-10-127-837A-21
; Sequence 21, Application US/10127837A

1 APPLICANT: Baker, Kevin P.
 2 APPLICANT: Beresini, Maureen
 3 APPLICANT: Deforge, Laura
 4 APPLICANT: Desnoyers, Luc
 5 APPLICANT: Filvaroff, Ellen
 6 APPLICANT: Gao, Wei-Qiang
 7 APPLICANT: Gerritsen, Mary E.
 8 APPLICANT: Goddard, Audrey
 9 APPLICANT: Godowski, Paul J.
 10 APPLICANT: Gurney, Austin L.
 11 APPLICANT: Sherwood, Steven
 12 APPLICANT: Smith, Victoria
 13 APPLICANT: Stewart, Timothy A.
 14 APPLICANT: Tumas, Daniel
 15 APPLICANT: Watanabe, Colin K
 16 APPLICANT: Wood, William
 17 APPLICANT: Zhang, Zemin
 18 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 19 ACIDS OF INVENTION: ACIDS ENCODING THE SAME
 20 FILE REFERENCE: P330R1C96
 21 CURRENT APPLICATION NUMBER: US/10/127,837A

1 PRIOR APPLICATION NUMBER: 60/049911
2
3 PRIOR FILING DATE: 1997-06-18
4
5 PRIOR APPLICATION NUMBER: 60/056974
6
7 PRIOR FILING DATE: 1997-08-26
8
9 PRIOR APPLICATION NUMBER: 60/059113
10
11 PRIOR FILING DATE: 1997-09-17
12
13 PRIOR APPLICATION NUMBER: 60/059115
14
15 PRIOR FILING DATE: 1997-09-17
16
17 PRIOR APPLICATION NUMBER: 60/059117
18
19 PRIOR FILING DATE: 1997-09-17
20
21 PRIOR APPLICATION NUMBER: 60/059122
22
23 PRIOR FILING DATE: 1997-09-17
24
25 PRIOR APPLICATION NUMBER: 60/059184
26
27 PRIOR FILING DATE: 1997-09-17
28
29 PRIOR APPLICATION NUMBER: 60/059283
30
31 PRIOR FILING DATE: 1997-09-18
32
33 PRIOR APPLICATION NUMBER: 60/059352

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: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/055588
: PRIOR FILING DATE: 1997-09-19
: Remaining Prior Application data removed - See File Wrapper or PALM
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 21
: LENGTH: 1041
: TYPE: DNA
: ORGANISM: Homo Sapien
US-10-127-837A-21

```

Query Match	8.4%;	Score 170.6;	DB 6;	Length 1041;
Best Local Similarity	63.7%;	Pred. No. 1.7e-32;		
Matches 276;	Conservative 0;	Mismatches 154;	Indels 3;	Gaps 1

QY	378	TGCGTCAATGGAAGCCACAGGATCCACGTCGCCGGAGAGAAGATCTGGACAAAGTCCACAGAGC	437
Db	300	TGGCTTGCCATTTTCCCAATBACCCCATTTAAACGCTATCATCTGTAAGAGATCCACAGAGC	359
QY	438	TGCGTGTGGGGTAAAGTCCCCAGAAAGATTCATCGTCATGCTCAGGGACATCGAGCT	497
Db	360	TGCTCTACATGTAATCAATGAGAAACTGAA---GTACTCTTGCTGCTACGATTAATGACGC	416
QY	498	GAAACAAGAGACAAAGCAAAAGAGACTGCTCTCATCTGCGCCCTGCTCCCAATGGGAATTC	557
Db	417	CAATBAGAGAGACAGGAAGGAAAGACCGCCCTACATTTGGCCGTGTCACACTGGCCAAAC	476
QY	558	AGAAGTAGTAAACCTCTGCTGGACAGACAGTGTCAACTTAATGTCCCTTGACAAACAAAA	617
Db	477	GGAATGCTACATCTCCTGGGTGTCAGAAAGATGTGACCTTAACCTCTGGCAGCCGTGAGA	536
QY	618	GAGGACAGCTTGATTAAGGCCCGGTACAAATGCCAGGAAGATGATGTGCTTAATGTGCT	677
Db	537	CAGGACACCTCTGTGATCAAGGCTGTACAACTGAGGACAGAGGCTTGCCCACTCTTGCT	596
QY	678	GGAACATGCGCACTGATCCAAATATTCCAGATGAGTATGAGAAATACCACTCTGGACTACGC	737
Db	597	GCAAAATGCGCCCAATCCAAATATTACGAGATTTCTTTGGAAAGAGACTCTTGCACATRGC	656
QY	738	TATCTATATGAGATAAATTAATGAGCAAGCACTGCTCTTATATGCTGCTATATGCA	797
Db	657	TGTGTATATGAATATCATCATCATGATGAGAAAACTCTTCCATGCTGATCAATAATATGA	716
QY	798	ATCAAAAAACAAG 810	
Db	717	AGAAATGCAGCAAG 729	

RESULT 13
US-10-127-842A-21
; Sequence 21, Application US/10127842A

1 APPLICANT: Baker, Kevin P.
 2 APPLICANT: Beresini, Maureen
 3 APPLICANT: DeForge, Laura
 4 APPLICANT: Desnoyers, Luc
 5 APPLICANT: Filvaroff, Ellen
 6 APPLICANT: Gao, Wei-Qiang
 7 APPLICANT: Gerritsen, Mary E.
 8 APPLICANT: Goddard, Audrey
 9 APPLICANT: Godowski, Paul J.
 10 APPLICANT: Gurney, Austin L.
 11 APPLICANT: Sherwood, Steven
 12 APPLICANT: Smith, Victoria
 13 APPLICANT: Stewart, Timothy A.
 14 APPLICANT: Tumas, Daniel
 15 APPLICANT: Watanabe, Colin K
 16 APPLICANT: Wood, William
 17 APPLICANT: Zhang, Zemin
 18 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 19 ACIDS ENCODING THE SAME
 20 FILE REFERENCE: P330R1C100
 21 CURRENT APPLICATION NUMBER: US/10/127,842A

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: CURRENT FILING DATE: 2002-10-15
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059184
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059352
: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/059588
: PRIOR FILING DATE: 1997-09-19
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 21
: LENGTH: 1041
: TYPE: DNA
: ORGANISM: Homo Sapien
US-10-127-850A-21

```

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Query Match      8.4%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 1.7e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

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OY 378 TGCCTTCATGAGCCAGGACGCTCCGTCGAGAGATCTGGCAAGCTCCACAGAGC 437
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Db 300 TGGCTTCGCAATTTCCCAATACCCATTAACCGTATCATCTGGAAGAGATCCACAGAGC 359
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 438 TGGCTGGGGTAAAGTCCAGAAAGATGTCATGTCATGTCGAGGAGACGAGAGT 497
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Db 417 CAATAGAGAGACAGAGAAAGAGACCGCCCTACATTTGGCTGTGCAACGGGCAACG 476
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OY 558 AGAGTACTAAATCTCTGCTGGAGACGATGTCACTTAATGCTTGGACACAAGAA 617
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Db 477 GGAATGTGATCATCTCTGCTGTCAGAGAGATGTGAGCTTAACCTGCGACCGTGAAGA 536
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OY 618 GAGGACACTCTGATTAAGGCGGTACATGCGAGAGATGAATGAGCTTAATGCT 677
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Db 537 CAGGACACCTCTGATCAAGGCTGTACAACTGAGCGAGAGGCTTGTGCAACTCTTCTGCT 596
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OY 678 GGAACATGCACTGATCCAAATATATCCAGATGATGGAATTAACCATCTGCACTAGCG 737
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Db 597 GCAAAATGGCGCATCCAAATATATAGGATTTCTTTGGAAGAGATGCTGCTGCACTAGCG 656
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OY 738 TATCTATATGAGATTAATTAATGAGCAAGCACTGCTTAATATGCTGATATGCA 797
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Db 657 TGTGTATATGAGATTAATTAATGAGCAAGCACTGCTTAATATGCTGATATGCA 716
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OY 798 ATCAAAAAAAG 810
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 717 AGAATGACAGCAG 729
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```

```

RESULT 14
US-10-127-850A-21
: Sequence 21, Application US/10127850A
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: Deforge, Laura

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: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P330R1C110
CURRENT FILING DATE: 2002-10-15
CURRENT FILING DATE: 2002-10-15
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 21
: LENGTH: 1041
: TYPE: DNA
: ORGANISM: Homo Sapien
US-10-127-850A-21

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Query Match      8.4%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 1.7e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

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OY 378 TGCCTTCATGAGCCAGGACGCTCCGTCGAGAGATCTGGCAAGCTCCACAGAGC 437
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 300 TGGCTTCGCAATTTCCCAATACCCATTAACCGTATCATCTGGAAGAGATCCACAGAGC 359
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OY 438 TGGCTGGGGTAAAGTCCAGAAAGATGTCATGTCATGTCGAGGAGACGAGAGT 497
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Db 360 TGTCTTACATGTAATCTAGAGAAACTGAA--GTACCTTCTGCTCAGATTAATGAGCG 416
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OY 498 GAACAAGAGAGACAAGAAAGAGAGCTGCTACATCTGGCCCTGCGCAATGGGAATTC 557
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Db 417 CAATAGAGAGACAGAGAAAGAGACCGCCCTACATTTGGCTGTGCAACGGGCAACG 476
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OY 558 AGAGTACTAAATCTCTGCTGGAGACGATGTCACTTAATGCTTGGACACAAGAA 617
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Db 477 GGAATGTGATCATCTCTGCTGTCAGAGAGATGTGAGCTTAACCTGCGACCGTGAAGA 536
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OY 618 GAGGACACTCTGATTAAGGCGGTACATGCGAGAGATGAATGAGCTTAATGCT 677
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Db 537 CAGGACACCTCTGATCAAGGCTGTACAACTGAGCGAGAGGCTTGTGCAACTCTTCTGCT 596
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OY 678 GGAACATGCACTGATCCAAATATATCCAGATGATGGAATTAACCATCTGCACTAGCG 737
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Db 597 GCAAAATGGCGCAATCCAAATATTACGATTTCTTTGGAAGGACCTCTCTGCACCTACGC 656
QY 738 TATCTATAATGAAGATAAATTATGCGCAAGACGCTGCTCTATATGTCGCTGATATCGA 797
Db 657 TGTGTATAATGAAGATACATCCATGATAGAAAACCTTCTTTCACATGTCACAAATATTGA 716
QY 798 ATCAAAAACCAAG 810
Db 717 AGAATGCAGCAAG 729

RESULT 15
US-10-127-901A-21
; Sequence 21, Application US/10127901A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Guirney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RJC86
; CURRENT APPLICATION NUMBER: US/10/127,901A
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 21
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-901A-21

Query Match 8.4%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 1.7e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 378 TGGCTTCATGAGACGACGATCCGCTGAGAAAGATCGACACAGCTCCACAGAGC 437
Db 300 TGGCTTCGATTTCCCAATACCCCATTTAAACCGTATCATCTGAGAGATCCACAGAGC 359

QY 438 TGGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATCTGATCTCAGGACACTGACGT 497
Db 360 TGTCTTACATGATGAATCTAGAGAACTGAA--GTACCTTCTGCTCAGATATTATGACGC 416
QY 498 GATCAAGAAAGACCAAGCAAGAGAGAGCTGCTACATCTGCGCTCGCAATGGGAATTC 557
Db 417 CAATTAAGAGAGACAG 476
QY 558 AGAAGTAGTAAACCTCTGCTGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 617
Db 477 GGAATGTGATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 536
QY 618 GAGGACAGCTCTGATTAAG 677
Db 537 CAGGACACCTCTGATCAAG 596
QY 678 GGAACATGAGCTGATCCAAATATTCCAGATGATGATGATGATGATGATGATGATGATGAT 717
Db 597 GCAAAATGGCGCAATCCAAATATTACGGATTTCTTTGGAAGGACCTCTGACCTACGAC 656
QY 738 TATCTATAATGAAGATAAATTATGCGCAAGACGCTGCTCTATATGTCGCTGATATCGA 797
Db 657 TGTGTATAATGAAGATACATCCATGATAGAAAACCTTCTTTCACATGTCACAAATATTGA 716
QY 798 ATCAAAAACCAAG 810
Db 717 AGAATGCAGCAAG 729

Search completed: November 8, 2002, 08:53:04
Job time : 219.594 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 8, 2002, 05:05:38 ; Search time 410.891 Seconds
(without alignments)
1726.908 Million cell updates/sec

Title: US-09-924-400-302

Perfect score: 2000

Sequence: 1 atggtgtgtgtgtgtgtgtc.....aaaaaaaaaaaaaaaaaaaa 2000

Scoring table:

Gapop 10.0 , Gapext 1.0

Searched: 320260 seqs, 177392727 residues

Total number of hits satisfying chosen parameters: 640520

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/pubpna/PCr_NEW_PUB.seq:*
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- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2000	100.0	2000	10	US-09-759-143-374
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4	2000	100.0	2000	10	US-09-810-936-302
5	2000	100.0	2000	10	US-09-822-827-314
6	2000	100.0	2000	10	US-09-429-755-302
7	1940	97.0	2040	10	US-09-825-301-7
8	1940	97.0	2040	10	US-09-759-143-375
9	1940	97.0	2040	10	US-09-780-669-375
10	1940	97.0	2040	10	US-09-810-936-303
11	1940	97.0	2040	10	US-09-822-827-315
12	1940	97.0	2040	10	US-09-429-755-303
13	1147.6	57.4	1853	10	US-09-759-143-369
14	1147.6	57.4	1853	10	US-09-780-669-369
15	1147.6	57.4	1853	10	US-09-810-936-295
16	1147.6	57.4	1853	10	US-09-822-827-309
17	1147.6	57.4	1853	10	US-09-429-755-295
18	1131.6	56.6	1155	10	US-09-825-301-5
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22	1131.6	56.6	1155	10	US-09-822-827-373	Sequence 373, App
23	1131.6	56.6	1155	10	US-09-429-755-301	Sequence 301, App
24	1129.6	56.5	1159	10	US-09-810-936-323	Sequence 323, App
25	1126.8	56.3	1155	10	US-09-810-936-328	Sequence 328, App
26	1016.4	50.8	1155	10	US-09-810-936-329	Sequence 329, App
27	1011.6	50.6	1155	10	US-09-810-936-325	Sequence 325, App
28	1010	50.5	1155	10	US-09-810-936-330	Sequence 330, App
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31	912.8	45.6	1852	10	US-09-780-669-530	Sequence 530, App
32	912.8	45.6	1852	10	US-09-810-936-313	Sequence 313, App
33	912.8	45.6	1852	10	US-09-822-827-530	Sequence 530, App
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36	900.8	45.0	1851	10	US-09-759-143-366	Sequence 366, App
37	900.8	45.0	1851	10	US-09-780-669-366	Sequence 366, App
38	900.8	45.0	1851	10	US-09-810-936-291	Sequence 291, App
39	900.8	45.0	1851	10	US-09-810-936-292	Sequence 291, App
40	900.8	45.0	1851	10	US-09-822-827-366	Sequence 366, App
41	900.8	45.0	1851	10	US-09-429-755-291	Sequence 291, App
42	900.8	45.0	1851	10	US-09-429-755-292	Sequence 291, App
43	888	44.4	2184	10	US-09-759-143-370	Sequence 370, App
44	888	44.4	2184	10	US-09-780-669-370	Sequence 370, App
45	888	44.4	2184	10	US-09-810-936-296	Sequence 296, App

ALIGNMENTS

RESULT 1
US-09-825-301-6
Sequence 6, Application US/09825301
Patent No. US20020009738A1
GENERAL INFORMATION:
APPLICANT: Houghton, Raymond L.
APPLICANT: Dillon, David C.
APPLICANT: Molesh, David A.
APPLICANT: Xu, Jianshun
APPLICANT: Zehentner, Barbara
APPLICANT: Persing, David H.
TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
OF INVENTION: AND MONITORING OF BREAST CANCER
FILE REFERENCE: 210121.513
CURRENT APPLICATION NUMBER: US/09/825,301
CURRENT FILING DATE: 2001-04-02
NUMBER OF SEQ ID NOS: 77
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-825-301-6

Query Match 100.0%; Score 2000; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTTGAGTGTATTCATGCCGCGCTCTTGTGAAGACCATTTGTC 60
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DB 1 ATGTGTTGAGTGTATTCATGCCGCGCTCTTGTGAAGACCATTTGTC 60
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QY 61 AGGAGCAAGTGGGCAAGTGTGCTCCGTTGCTGCGAGGAGCGGCAAG 120
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DB 61 AGGAGCAAGTGGGCAAGTGTGCTCCGTTGCTGCGAGGAGCGGCAAG 120
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QY 121 AGCAAGTGGGCACTTCTGAGACACGACGATCTGCTATGAAGACCTCAGAGCAAG 180
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DB 121 AGCAAGTGGGCACTTCTGAGACACGACGATCTGCTATGAAGACCTCAGAGCAAG 180
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QY 181 ATGGGCAAGTGTGCGGCACTGCTCCCTGCTGAGGGGAGTGGCAAGACGTCG 240
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Qy 301 TGTGTCTCCACTGCTTCCCTGCTGACAGGGAGCGGCAAGAGAGTGGCGCTTGG 360
Db 301 TGTGTCTCCACTGCTTCCCTGCTGACAGGGAGCGGCAAGAGAGTGGCGCTTGG 360
Qy 361 GGAGACTGACAGAGAGTCCCTTCAATGAGGCCAGGTACCGACGTCGGGAGAAATGTG 420
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Db 541 TCTGCAATGGGAATTCAGAAATGATAAACTCCGTCGACAGAGTGTCACTTAT 600
Qy 601 GTCTTCGACAAACAAAAGAGAGACGCTGTATAAAGCCGTACATGCGAGAGATGA 660
Db 601 GTCTTCGACAAACAAAAGAGAGACGCTGTATAAAGCCGTACATGCGAGAGATGA 660
Qy 661 TGTGCGTAAATGTGTGTGAGACATGGGCACTGATCCAAATATCCAGATGATGGAAT 720
Db 661 TGTGCGTAAATGTGTGTGAGACATGGGCACTGATCCAAATATCCAGATGATGGAAT 720
Qy 721 ACCACTGCACTAGCTATCTATATGAATAAATTAATGGCCAAAGCACTGCTCTTA 780
Db 721 ACCACTGCACTAGCTATCTATATGAATAAATTAATGGCCAAAGCACTGCTCTTA 780
Qy 781 TATGCTGTATATCGAATCAAAAAACAAGCATGGCCCTACACCACTGTACTGGTGA 840
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Db 841 CATGAGCAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAAGCAATTTTAAATGA 900
Qy 901 CTGATATATATGAAAGAGTGTCTCTCATCTGCTGTATGTTGGATGAGCAATATA 960
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Qy 961 GTCAGCCTTCTACTGAGCAAAATATGATATCTTCTCAAGATCTATCTGACAGAG 1020
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Qy 1561 TTTATGCTATCGAAGAAATGAAGACAGCGAAAGTACTCATGTTCGATTTCCAGAAAC 1620
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Qy 1621 CTGACTAATGGTGCACACTGCTGGCAATGTGATGATGATTAATTCCTCAAGAGAGAGC 1680
Db 1621 CTGACTAATGGTGCACACTGCTGGCAATGTGATGATGATTAATTCCTCAAGAGAGAGC 1680
Qy 1681 AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAGATACACAGTGACGAA 1740
Db 1681 AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGAAATGAAGATACACAGTGACGAA 1740
Qy 1741 CAAATGATCTACAGAACCAATTTTGTGAAGAACAGAACTGGAATATTCACAGATGAG 1800
Db 1741 CAAATGATCTACAGAACCAATTTTGTGAAGAACAGAACTGGAATATTCACAGATGAG 1800
Qy 1801 ATTCTGATTCATGAAGAAACAGATGAAATGTTGAAAAATGAAATTCGACTTCT 1860
Db 1801 ATTCTGATTCATGAAGAAACAGATGAAATGTTGAAAAATGAAATTCGACTTCT 1860
Qy 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGCATGAAAAATAGTACGTTGGGGAAGAAAT 1920
Db 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGCATGAAAAATAGTACGTTGGGGAAGAAAT 1920
Qy 1921 GCCATGCTAAGACGTGAGCTGACACAAATGAATCAGACCCAGCTRAAAAAA 1980
Db 1921 GCCATGCTAAGACGTGAGCTGACACAAATGAATCAGACCCAGCTRAAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 2
US-09-143-374
Sequence 374, Application US/09759143
Patent No. US20020022248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedivick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND


```

; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-374

Query Match      100.0%; Score 2000; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGGTGGTTGAGTTGATTCATGCGCGGCTCTTCTGTGTGAAGAGCCATTGGTCTC 60
DB      1 ATGGTGGTTGAGTTGATTCATGCGCGGCTCTTCTGTGTGAAGAGCCATTGGTCTC 60
QY      61 AGGAGCAAGATGGGCAAGTGGTGGTCCGTTGCTTCCCGTGGTGGAGGAGCGGCAAG 120
DB      61 AGGAGCAAGATGGGCAAGTGGTGGTCCGTTGCTTCCCGTGGTGGAGGAGCGGCAAG 120
QY      121 AGCAACGTTGGGCACTTCTGGAGACACAGAGACTGTGTATGAAGACACTCAGAGCAAG 180
DB      121 AGCAACGTTGGGCACTTCTGGAGACACAGAGACTGTGTATGAAGACACTCAGAGCAAG 180
QY      181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGCGAGGGGGAGTGGCAAGCAACGTG 240
DB      181 ATGGGCAAGTGGTGGCGCCACTGCTTCCCTGCTGCGAGGGGGAGTGGCAAGCAACGTG 240
QY      241 GGGGCTTTGGAGACACGACGACTGCTGTATGAAGACACTCAGAGCAAGATGGGCAAG 300
DB      241 GGGGCTTTGGAGACACGACGACTGCTGTATGAAGACACTCAGAGCAAGATGGGCAAG 300
QY      301 TGGTGGTGGCACTGCTTCCCTGCTGTCAGAGGGGAGCGGCAAGAGTGGGCGCTTGG 360
DB      301 TGGTGGTGGCACTGCTTCCCTGCTGTCAGAGGGGAGCGGCAAGAGTGGGCGCTTGG 360
QY      361 GGAAGATTACGATGACAGTGGCTTTCATGAGGCCAGGTACACGCTCCGTGGAGAAATCTG 420
DB      361 GGAAGATTACGATGACAGTGGCTTTCATGAGGCCAGGTACACGCTCCGTGGAGAAATCTG 420
QY      421 GACAACTCCACAGAGCTGCTGGTGGGGTAAAGTCCCGAAGAAAGATCTCAATCGTCAG 480
DB      421 GACAACTCCACAGAGCTGCTGGTGGGGTAAAGTCCCGAAGAAAGATCTCAATCGTCAG 480
QY      481 CTCAGGAGACACTGACGTGAACAAGAGCAACAAGAGAGACTGCTTACATCTGGCC 540
DB      481 CTCAGGAGACACTGACGTGAACAAGAGCAACAAGAGAGACTGCTTACATCTGGCC 540
QY      541 TCTGGCAATGGCAATTCAGAAAGTAAACTCTGCTGTGACAGACAGATGTCAACTTAAT 600
DB      541 TCTGGCAATGGCAATTCAGAAAGTAAACTCTGCTGTGACAGAGATGTCAACTTAAT 600
QY      601 GTCCCTTGACAACAAAAGAGAGAGCTGTGATTAAGGCGGTAAAGTCCAGAGAAAGTAA 660
DB      601 GTCCCTTGACAACAAAAGAGAGAGCTGTGATTAAGGCGGTAAAGTCCAGAGAAAGTAA 660
QY      661 TGTGCGTTAATGTGCTGGAGACATGGCACTGATCCAAATATTTCCAGATGATGGAAT 720
DB      661 TGTGCGTTAATGTGCTGGAGACATGGCACTGATCCAAATATTTCCAGATGATGGAAT 720
QY      721 ACCACCTGCACTACGCTATCTATATGAAGATTAATTAATGGCCAAAGCACTGCTTAA 780
DB      721 ACCACCTGCACTACGCTATCTATATGAAGATTAATTAATGGCCAAAGCACTGCTTAA 780
QY      781 TATGCTGTGATTCGAATCAAAAACAAAGCATGGCTCAGACACACTGTTACTTGGTGA 840
DB      781 TATGCTGTGATTCGAATCAAAAACAAAGCATGGCTCAGACACACTGTTACTTGGTGA 840
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DB      841 CATGACCAAAAACAGCAAGTCTGTAATTTTAAATCAAGAAAAAGCGAATTTAAATGCA 900
QY      901 CTGGATAGATATGGAAGAGACTGCTCATCACTGCTGTATGTTGGATCAGCAATATA 960
DB      901 CTGGATAGATATGGAAGAGACTGCTCATCACTGCTGTATGTTGGATCAGCAATATA 960
QY      961 GTCAGCCTTCTACTTGAGCAAAATATGATGTATCTTCAAGATATATCTGGACGAGC 1020
DB      961 GTCAGCCTTCTACTTGAGCAAAATATGATGTATCTTCAAGATATATCTGGACGAGC 1020
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DB      1021 GCCAGAGATATGCTGTTTCTACTCATCATCATATTAATTTGCCAGTTACTTCTGACTAC 1080
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DB      1081 AAGAAAAACAGATGCTAAAAATCTTTCTGAAAACAGCAATCAGAACAAAGCTTAAAG 1140
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DB      1141 CTGACATCAGAGAAAGATCACAAAGGTTCAAGAGCAGTGAATAATAGCCAGAGAAA 1200
QY      1201 ATGCTCAAGAACCAAGAAATAAATTAAGATGTGATAGAGAGGTTGAGAGAAATGAAG 1260
DB      1201 ATGCTCAAGAACCAAGAAATAAATTAAGATGTGATAGAGAGGTTGAGAGAAATGAAG 1260
QY      1261 AAGCATGAAGATATATATGTTGGATTTCTAGAAAACCTGACTATATGTTGCTGCTGGC 1320
DB      1261 AAGCATGAAGATATATATGTTGGATTTCTAGAAAACCTGACTATATGTTGCTGCTGGC 1320
QY      1321 AATGGTATATATGATTAATTTCTCAAGAGAAAGCAGAACACCTGAAAAATCGCAATTT 1380
DB      1321 AATGGTATATATGATTAATTTCTCAAGAGAAAGCAGAACACCTGAAAAATCGCAATTT 1380
QY      1381 CCTGACAAGAAAAGTGAAGAGTATCACAGATTTGGCAATTAATTTCTGACTCAAAAGAA 1440
DB      1381 CCTGACAAGAAAAGTGAAGAGTATCACAGATTTGGCAATTAATTTCTGACTCAAAAGAA 1440
QY      1441 AAACAGATGCCAAATATCTTCTTGAAGAACAGTACCCAGAACACTTAAAGCTGACA 1500
DB      1441 AAACAGATGCCAAATATCTTCTTGAAGAACAGTACCCAGAACACTTAAAGCTGACA 1500
QY      1501 TCAGAGAAAGATCACAAAGGCTTGAAGGGCAGTGAAGAAAGGCCAGAGCTAGAAAAT 1560
DB      1501 TCAGAGAAAGATCACAAAGGCTTGAAGGGCAGTGAAGAAAGGCCAGAGCTAGAAAAT 1560
QY      1561 TTTATGGCTATCGAAGAAATGAAGAGCAAGAGTACTCATGTCCGATTTCCAGAAAAAC 1620
DB      1561 TTTATGGCTATCGAAGAAATGAAGAGCAAGAGTACTCATGTCCGATTTCCAGAAAAAC 1620
QY      1621 CTGACTATATGTTGCCACTGCTGGCAATGTTGATGATGATTAATTTCTCCAGAGAAAGC 1680
DB      1621 CTGACTATATGTTGCCACTGCTGGCAATGTTGATGATGATTAATTTCTCCAGAGAAAGC 1680
QY      1681 AGAACAACCTGAAGAGCAGCAATTTCTGACACGTGAAGAAAGATATCAGATGAGGAA 1740
DB      1681 AGAACAACCTGAAGAGCAGCAATTTCTGACACGTGAAGAAAGATATCAGATGAGGAA 1740
QY      1741 CAAAATGATATCTCAGAGCAATTTTGTGAAGAACAGAACACTGGAATATTTACAGATGAG 1800
DB      1741 CAAAATGATATCTCAGAGCAATTTTGTGAAGAACAGAACACTGGAATATTTACAGATGAG 1800
QY      1801 ATTCTGATTCATGAAGAAAAAGCAGATAGAGTGTGAAAAAATGAATTTGAGCTTTCT 1860
DB      1801 ATTCTGATTCATGAAGAAAAAGCAGATAGAGTGTGAAAAAATGAATTTGAGCTTTCT 1860
QY      1861 CTTAGTTGTAAAGAAAAAAGACATCTTGCAATGAATAATAGTCTGTGGGGAAAGAAAT 1920
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QY      1921 GCCATCTAAGACTGAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAAAGAAAAA 1980
DB      1921 GCCATCTAAGACTGAGCTAGACACATGAAACATCAGAGCCAGCTTAAAAAAGAAAAA 1980
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Db 1921 GCCATGCTAGACTGGAGCTAGACACAATGAACATCAGACGACTAAAAAAAAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAA 2000

RESULT 3

US-09-780-669-374
Sequence 374, Application US/09780669
Patent No. US20020051977A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuxi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Wang, Aljun
APPLICANT: Li, Samuel
APPLICANT: Skeiky, Yashir A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghlon, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780.669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-780-669-374

Query Match 100.0%; Score 2000; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGTTGAGTTGATTCATGCGCGCTCTCTTCTGTGAAGAACCATTTGGTCTC 60
Db 1 ATGCTGTTGAGTTGATTCATGCGCGCTCTCTTCTGTGAAGAACCATTTGGTCTC 60
Qy 61 AGGAGCAAGATGGGCAATGGTGTGCTGCGTTCCTCCCTGCTGAGGAGAGCGGCAAG 120
Db 61 AGGAGCAAGATGGGCAATGGTGTGCTGCGTTCCTCCCTGCTGAGGAGAGCGGCAAG 120
Qy 121 AGCAACGTGGGCACTTCTGGAGACACAGACGACTCTGCTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAACGTGGGCACTTCTGGAGACACAGACGACTCTGCTATGAAGACACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGGTCCCGGCACTGCTCCCTGCTGTCAGGAGGAGTGGCAAGCAACGTG 240
Db 181 ATGGGCAAGTGGTCCCGGCACTGCTCCCTGCTGTCAGGAGGAGTGGCAAGCAACGTG 240
Qy 241 GGGCTTCTGGAGACACAGACGACTCTGCTATGAAGACACTCAGAGCAAGTGGGCAAG 300
Db 241 GGGCTTCTGGAGACACAGACGACTCTGCTATGAAGACACTCAGAGCAAGTGGGCAAG 300
Qy 301 TGGTGTGCGCACTGCTCCCTGCTGTCAGGAGGAGCGGCAAGACAGAGTGGGCTTGG 360
Db 301 TGGTGTGCGCACTGCTCCCTGCTGTCAGGAGGAGCGGCAAGACAGAGTGGGCTTGG 360

Qy 361 GGAGACTACGATGACAGTCCCTTCATGAGCCAGGTACCACTGCTCGTGAGAAATCTG 420
Db 361 GGAGACTACGATGACAGTCCCTTCATGAGCCAGGTACCACTGCTCGTGAGAAATCTG 420
Qy 421 GACAAGCTCCACAGAGCTGCTGGGTAAATGCCCAAAAGATCTCTATGCTATG 480
Db 421 GACAAGCTCCACAGAGCTGCTGGGTAAATGCCCAAAAGATCTCTATGCTATG 480
Qy 481 CTCAGGGACACTGACGTGAACAGAGGACAAAGAGAGACTGCTCATCTGACC 540
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Db 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGACAGACGATGCAACTTAAT 600
Qy 601 GTCCCTTGACAAACAAAAGAGAGAGCTCTGATTAAGGCCGTACAAATGCCAGAAATGAA 660
Db 601 GTCCCTTGACAAACAAAAGAGAGAGCTCTGATTAAGGCCGTACAAATGCCAGAAATGAA 660
Qy 661 TGTGCGTTAATGTTGCTGGAACATGCGCACTGATCCAAATATTCAGATGATGAAAT 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGCGCACTGATCCAAATATTCAGATGATGAAAT 720
Qy 721 ACCACTGTGACACTACGCTATCTATATGAAGATTAATATGATGATGATGATGATGAT 780
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Db 781 TATGCTGTGATATGCAATCAAAAAACAGAGATGGCCACACACCTGTTCTGGTGA 840
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Db 841 CATAGCAAAAACAGCAAGCTGTAATTTTAAATCAAGAAAAAGCAATTTAAATGCA 900
Qy 901 CTGATAGATATGGAAGAGCTGCTCTCATCTGATGATGATGATGATGATGATGAT 960
Db 901 CTGATAGATATGGAAGAGCTGCTCTCATCTGATGATGATGATGATGATGATGAT 960
Qy 961 GTGAGCTTCTACTGACCAAAATATGATGATGATGATGATGATGATGATGATGATGAT 1020
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Qy 1021 GCCAGAGATATGCTGTTCTAGTCATCATCATGATTAATTTCCAGTTACTTCTGATAC 1080
Db 1021 GCCAGAGATATGCTGTTCTAGTCATCATCATGATTAATTTCCAGTTACTTCTGATAC 1080
Qy 1081 AAAGAAAAACAGATGCTAAAAATCTCTGTAAGAACAGCAATCCAGAACAGACTTAAG 1140
Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTGTAAGAACAGCAATCCAGAACAGACTTAAG 1140
Qy 1141 CTGACATCAGAGAGAGTCAAAAGTTCAAGAGGTCAAGAGGTCAAGAGGTCAAGAG 1200
Db 1141 CTGACATCAGAGAGAGTCAAAAGTTCAAGAGGTCAAGAGGTCAAGAGGTCAAGAG 1200
Qy 1201 ATGCTCTAAGAACAGAAATTAATTAAGATGATGATGATGATGATGATGATGATGAT 1260
Db 1201 ATGCTCTAAGAACAGAAATTAATTAAGATGATGATGATGATGATGATGATGATGAT 1260
Qy 1261 AAGCATGAAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
Db 1261 AAGCATGAAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
Qy 1321 AATGCTATTAATGATTAATTTCTCAAAAGAGAGCAAGCACTGAAATTAATTTT 1380
Db 1321 AATGCTATTAATGATTAATTTCTCAAAAGAGAGCAAGCACTGAAATTAATTTT 1380
Qy 1381 CCTGACAAAGAAAGTGAAGATATCAGAAATTTGCGAATTTGATGATGATGATGATGAT 1440
Db 1381 CCTGACAAAGAAAGTGAAGATATCAGAAATTTGCGAATTTGATGATGATGATGATGAT 1440
Qy 1441 AAACAGATGCCAAATATCTTCTGAAAAAGCAACCCAGAACAAAGATTAAGCTGACA 1500

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Db 1441 AACAGATGCCCCAAATCTCTCTGAAACACAGCAACCCAGACAAGACTTAAAGCTGACA 1500
Qy 1501 TCAGAGGAAGAGTCAACAAAGGCTTGAAGGCATGAAATGGCCAGCCAGAGCTAGAAAT 1560
Db 1501 TCAGAGGAAGAGTCAACAAAGGCTTGAAGGCATGAAATGGCCAGCCAGAGCTAGAAAT 1560
Qy 1561 TTTATGAGTATGCAAGAAATGAAGAAGCAGGAGTACTCATGTGGATTCCAGAAAAC 1620
Db 1561 TTTATGAGTATGCAAGAAATGAAGAAGCAGGAGTACTCATGTGGATTCCAGAAAAC 1620
Qy 1621 CTGACTAATGCTGCCACTGCTGGCAATGGTGATGATGATTAATTCCTCCAGAGAAAGC 1680
Db 1621 CTGACTAATGCTGCCACTGCTGGCAATGGTGATGATGATTAATTCCTCCAGAGAAAGC 1680
Qy 1681 AGAAGACTGAAAGCCAGCAATTTCTGACACTGAGATGAAGAGTATCAGCTGACGAA 1740
Db 1681 AGAAGACTGAAAGCCAGCAATTTCTGACACTGAGATGAAGAGTATCAGCTGACGAA 1740
Qy 1741 CAAATGATCTCAGAGCAATTTTGTGAAGAAGCAACACTGSAATATTACAGATGAG 1800
Db 1741 CAAATGATCTCAGAGCAATTTTGTGAAGAAGCAACACTGSAATATTACAGATGAG 1800
Qy 1801 ATTCTGATTCAGAGAAAGCAGATAGAGTGGTTGAAAAATGAAATTCAGAGCTTCT 1860
Db 1801 ATTCTGATTCAGAGAAAGCAGATAGAGTGGTTGAAAAATGAAATTCAGAGCTTCT 1860
Qy 1861 CTTACTTGTAGAGAAAGAAAGACATCTTGCAATGAATAATGATGCTGGGAGAAAT 1920
Db 1861 CTTACTTGTAGAGAAAGAAAGACATCTTGCAATGAATAATGATGCTGGGAGAAAT 1920
Qy 1921 GCCATGCTAGAGCTGAGCTAGACAAATGAAACATCAGAGCAGCTAAAAA 1980
Db 1921 GCCATGCTAGAGCTGAGCTAGACAAATGAAACATCAGAGCAGCTAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA .2000

RESULT 4
US-09-810-936-302
; Sequence 302, Application US/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810.936
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-936-302

Query Match 100.0%; Score 2000; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGTGGTTGAGGTGATTCATGCGCGCTCTTCTGTGAAGAAGCAATTGGTCTC 60

|||||
Db 1 ATGGTGGTTGAGGTGATTCATGCGCGCTCTTCTGTGAAGAAGCAATTGGTCTC 60
Qy 61 AGAGCAAGATGGCGAAGTGGTGGCTTCTCCCTGGTGGAGGAGGCGGCAAG 120
Db 61 AGAGCAAGATGGCGAAGTGGTGGCTTCTCCCTGGTGGAGGAGGCGGCAAG 120
Qy 121 AGCAAGGTGGGCACTTCTGGAGACACGAGCACTGGCTATGAAGCACTCAGAGCAAG 180
Db 121 AGCAAGGTGGGCACTTCTGGAGACACGAGCACTGGCTATGAAGCACTCAGAGCAAG 180
Qy 181 ATGGCAAGTGGTGGCGGCACTGCTCCCTGCTCAGGGGAGTGGCAAGAGCAAGT 240
Db 181 ATGGCAAGTGGTGGCGGCACTGCTCCCTGCTCAGGGGAGTGGCAAGAGCAAGT 240
Qy 241 GCGGCTTCTGGAGACACGAGCACTGCTATGAAGCACTCAGAGCAAGTGGCAAG 300
Db 241 GCGGCTTCTGGAGACACGAGCACTGCTATGAAGCACTCAGAGCAAGTGGCAAG 300
Qy 301 TGGTGGTGGCACTGCTCCCTGCTGAGGGGAGGCGCAAGAGTGGGCGCTTGG 360
Db 301 TGGTGGTGGCACTGCTCCCTGCTGAGGGGAGGCGCAAGAGTGGGCGCTTGG 360
Qy 361 GGAGACTAGATGAGAGTGGCTTCAATGAGCCAGGTACACGCTCGTGAGAGATCTG 420
Db 361 GGAGACTAGATGAGAGTGGCTTCAATGAGCCAGGTACACGCTCGTGAGAGATCTG 420
Qy 421 GACAAAGCTCCACAGAGCTGCTGGTGGGTTAAAGTCCCGAAGAGATCTCATG 480
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Qy 481 CTCAGGAGACCTGAGGTGAAGAAAGCAAGAGAGAGAGTGTCTATCTGAGGCG 540
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Db 721 ACCACTGCTAGCTATCTATATGAAGATTAATTAATGGCCAAAGCACTGCTTAA 780
Qy 781 TATGTTGCTGATATGCAATCAAAAAGCAAGATGGCTCACACCACTGTTACTG 840
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Qy 1441 AAAGAGTGGCAAAATATCTCTTGTGAAAAAGCAACCCAGAACAGACTTAAGCTGACA 1500
Db 1441 AAAGAGTGGCAAAATATCTCTTGTGAAAAAGCAACCCAGAACAGACTTAAGCTGACA 1500
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Qy 1801 ATTCTGATGATGAGAAAGCAGATAGAGTGTGTAATAAATGAATTCGAGCTTCT 1860
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Qy 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGCGATGAATAATAGTACGTTGCGGAGAAAT 1920
Db 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGCGATGAATAATAGTACGTTGCGGAGAAAT 1920
Qy 1921 GCCATGCTAAGAGTGAAGTGAAGACATGAAGACATGAGAGCCAGCTAAAAAAGAA 1980
Db 1921 GCCATGCTAAGAGTGAAGTGAAGACATGAAGACATGAGAGCCAGCTAAAAAAGAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 5

US-09-822-827-374
; Sequence 374, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822.827

; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-374

Query Match 100.0%; Score 2000; DB 10; Length 2000;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTGTTGAGTGTGATTCATGCGGCTGCTCTCTCTGTGAAGAAAGCAATTTGCTC 60
Db 1 ATGCTGTTGAGTGTGATTCATGCGGCTGCTCTCTCTGTGAAGAAAGCAATTTGCTC 60

Qy 61 AGAGCAAGATGGGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 61 AGAGCAAGATGGGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

Qy 121 AGCAAGTGGGCACTTGTGGAGACACAGAGACTCTGCTATGAAGACATCAGAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTGTGGAGACACAGAGACTCTGCTATGAAGACATCAGAGAGCAAG 180

Qy 181 ATGGGCAAGTGGTCCGCGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGGTCCGCGCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240

Qy 241 GCGCTTCTGAGACACAGAGACTCTGCTATGAAGACATCAGAGAAAGATGGGCAAG 300
Db 241 GCGCTTCTGAGACACAGAGACTCTGCTATGAAGACATCAGAGAAAGATGGGCAAG 300

Qy 301 TGGTGTGCGCCACTTCCCTGCTGCAAGGGGAGGCGGCAAGAGCAAGTGGGCGTTGG 360
Db 301 TGGTGTGCGCCACTTCCCTGCTGCAAGGGGAGGCGGCAAGAGCAAGTGGGCGTTGG 360

Qy 361 GGAGACTACGATGACAGTGCCTTCATGAGAGCCAGTACCAAGCTCCGTGAGAAAGATCTG 420
Db 361 GGAGACTACGATGACAGTGCCTTCATGAGAGCCAGTACCAAGCTCCGTGAGAAAGATCTG 420

Qy 421 GACAGCTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
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Qy 481 CTCAGGGACACTGACGTGAACAAAGAGCAAGCAAGAAAGAGAGTGTCTACATCTGACC 540
Db 481 CTCAGGGACACTGACGTGAACAAAGAGCAAGCAAGAAAGAGAGTGTCTACATCTGACC 540

Qy 541 TCTGCAATGGGAATTCAGAAATAGTAAACTCTGCTGCAAGAGATGCAACTTAAT 600
Db 541 TCTGCAATGGGAATTCAGAAATAGTAAACTCTGCTGCAAGAGATGCAACTTAAT 600

Qy 601 GTCTTGAACAACAAAGAGAGACAGTCTGATTAAGGCGCTGACAAATGCCAGGAAGATGAA 660
Db 601 GTCTTGAACAACAAAGAGAGACAGTCTGATTAAGGCGCGTACAAATGCCAGGAAGATGAA 660

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Qy	961	GTCAGCCTTACTGTCGCAAAATATGATGTATCTGTCGAAGATCTATCGACAGACG	1020
Dp	961	GTCAGCCTTACTGTCGCAAAATATGATGTATCTTCTCAAGATCTATCGACAGACG	1020
Qy	1021	GCCAGAGATATGCTGTTTCTAGTCATCATATGTAATTTGGCAGTATCTTTCGACTAC	1080
Dp	1021	GCCAGAGATATGCTGTTTCTAGTCATCATATGTAATTTGGCAGTATCTTTCGACTAC	1080
Qy	1081	AAGAAAAACAGATGCTAAAAATCTTCTTGAAAAACGCAATCCGAAACAGACTTAAG	1140
Dp	1081	AAGAAAAACAGATGCTAAAAATCTTCTTGAAAAACGCAATCCGAAACAGACTTAAG	1140
Qy	1141	CTGACATCAGAGGAAGAGTCACAAAGCTTCAAGGACGTAAGAAATAGCACCAGAGAA	1200
Dp	1141	CTGACATCAGAGGAAGAGTCACAAAGCTTCAAGGACGTAAGAAATAGCACCAGAGAA	1200
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Dp	1201	ATGCTCAGAACACAGAAATTAATAGATGGTGATAGAGAGGTTGAAGAAATAGAG	1260
Qy	1261	AAGCATGAAAATATATATGAGGATTAAGTAAAGAAACCTGACTAATAGTGTCACTGTGC	1320
Dp	1261	AAGCATGAAAATATATATGAGGATTAAGTAAAGAAACCTGACTAATAGTGTCACTGTGC	1320
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Dp	1321	AATGCTATATGATTAATCTCTCAAGGAGACGACCAACCTGGAATATCAGCAATTT	1380
Qy	1381	CTTGACAAAGAAAGTAAAGATTCACAGATTTGGCAATTTGTTTCGATACAGAA	1440
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Qy	1441	AAACAGATGCCAAATATCTTCTGAAAAACAGCAACCCAGAACAGACTTAAGCTGCA	1500
Dp	1441	AAACAGATGCCAAATATCTTCTGAAAAACAGCAACCCAGAACAGACTTAAGCTGCA	1500
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Dp	1501	TCGAGAGAAAGTCACAAAGGCTTGAGGGCAGTGAATATGGCCAGCCAGAGCTAGAAAT	1560
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Dp	1561	TTTATGGCTATCGAAGAAATGAAGAAGCAGGAGTACTCATGTGCGATTCCCGAANAAC	1620
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Dp	1621	CTGACTAATGTCGCACTGCTGGCAATGATGATGATTAATTCCTCCAGAGAGAGC	1680
Qy	1681	AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAGATATCACAGTACGAA	1740
Dp	1681	AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAGATATCACAGTACGAA	1740
Qy	1741	CAAAATGATATCTCAGAAAGCAATTTTGTGAAGACAGAACACTGGAATTTACAGATGAG	1800
Dp	1741	CAAAATGATATCTCAGAAAGCAATTTTGTGAAGACAGAACACTGGAATTTACAGATGAG	1800
Qy	1801	ATTCTGATTCATGAGAAAAAGCAGATAGAGTGGTTGAAAAAATGAATTCGAGCTTCT	1860
Dp	1801	ATTCTGATTCATGAGAAAAAGCAGATAGAGTGGTTGAAAAAATGAATTCGAGCTTCT	1860
Qy	1861	CTTATGTTGTAAGAAAGAAAAAGCATCTTGATGAAAAATGATGATCTCGGGAAGAAAT	1920
Dp	1861	CTTATGTTGTAAGAAAGAAAAAGCATCTTGATGAAAAATGATGATCTCGGGAAGAAAT	1920
Qy	1921	GCCATGCTAAGACGCGGAGTCAGACAAATGAAGAAACATCAAGCCACTTAAAAA	1980
Dp	1921	GCCATGCTAAGACGCGGAGTCAGACAAATGAAGAAACATCAAGCCACTTAAAAA	1980
Qy	1981	AAAAAAAAAAAAAAAAAAAA 2000	

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      Db      1981 AAAAAAAAAAAAAAAAAAAAAA 2000
      RESULT 6
      US-09-429-755-302
      ; Sequence 302, Application US/09429755A
      ; Patent No. US2002011467A1
      ; GENERAL INFORMATION:
      ; APPLICANT: Fridakis, Tony N.
      ; APPLICANT: Smith, John M.
      ; APPLICANT: Reed, Steven G.
      ; APPLICANT: Misher, Lynda
      ; APPLICANT: Retter, Marc W.
      ; APPLICANT: Dillon, Davin C.
      ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
      ; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
      ; FILE REFERENCE: 210121.419C6
      ; CURRENT APPLICATION NUMBER: US/09/429,755A
      ; CURRENT FILING DATE: 1999-10-28
      ; NUMBER OF SEQ ID NOS: 315
      ; SOFTWARE: FastSeq for Windows Version 3.0
      ; SEQ ID NO 302
      ; LENGTH: 2000
      ; TYPE: DNA
      ; ORGANISM: Homo sapien
      US-09-429-755-302

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Query Match	100.0%	Score 2000	DB 10	Length 2000
Best Local Similarity	100.0%	Pred. No. 0		
Matches 2000	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY 1	ATGGGAGTTGAGAGTTGATTCCATGGCCGGGTGCGCTCTTGTGTGAAGAGCATTGGTCTC	60		
DB 1	ATGGTGTTGAGAGTTGATTCATGCCCGGCTGCTTTCTGTGAAGAGCATTGGTCTC	60		
QY 61	AGGAGCAGAGTGGGCAAGTGGTGTGCTGCGGTTGCTTCCCTGCTGCAGGAGAGCCGGCAAG	120		
DB 61	AGGAGCAGAGTGGGCAAGTGGTGTGCTGCGGTTGCTTCCCTGCTGCAGGAGAGCCGGCAAG	120		
QY 121	ACCAACGTGGGCACTTCTGGAGAACCAACCAACGACTCTGCTATGAACACCTCAGAGCAAG	180		
DB 121	ACCAACGTGGGCACTTCTGGAGAACCAACGACTCTGCTATGAACACCTCAGAGCAAG	180		
QY 181	ATGGGCAAGTGGTGGCGGCACACTGCTTCCCTCTCTCAGAGGAGATGGCAAGCAAGTG	240		
DB 181	ATGGGCAAGTGGTGGCGGCACACTGCTTCCCTCTCTCAGAGGAGATGGCAAGCAAGTG	240		
QY 241	GGCGCTTCTGGAGACCAGACGACTCTGCTATGAAGACACTGAGAACAACTGGGGCAAG	300		
DB 241	GGCGCTTCTGGAGACCAGACGACTCTGCTATGAAGACACTGAGAACAACTGGGGCAAG	300		
QY 301	TGGTGCTGCACTGCTTCCCTGCTGCAAGGGGGAGACGGCAAGGCAAGGTGGGCGCTTGG	360		
DB 301	TGGTGCTGCACTGCTTCCCTGCTGCTGCAAGGGGGAGACGGCAAGGCAAGGTGGGCGCTTGG	360		
QY 361	GGAGACTACGATGACAGTGGCTTCAATGGAGCCAGGTAACACGCTCCGTGGAGAGATCTG	420		
DB 361	GGAGACTACGATGACAGTGGCTTCAATGGAGCCAGGTAACACGCTCCGTGGAGAGATCTG	420		
QY 421	GACAAAGCTCCAGAGAGCTGGCTGGGGGTAAGTCCCAAGAAAGATCTCATGTGCAATG	480		
DB 421	GACAAAGCTCCAGAGAGCTGGCTGGGGGTAAGTCCCAAGAAAGATCTCATGTGCAATG	480		
QY 481	CTCAGGAGCACTGACGTGTAACAAGAGCAAGCAAAAGAGGACTGCTTACATCTGGCC	540		
DB 481	CTCAGGAGCACTGACGTGTAACAAGAGCAAGCAAAAGAGGACTGCTTACATCTGGCC	540		
QY 541	TCTGCCAATGGGAATTCAGAACTAGTAAACCTCTGCTGGACAGACGATGTCAACTTAAT	600		
DB 541	TCTGCCAATGGGAATTCAGAACTAGTAAACCTCTGCTGGACAGACGATGTCAACTTAAT	600		
QY 601	GTCTCTTGACAAACAAAAGAGGACAGCTCTGATTAAGGCGGTCAATGGCAGGAAGATGAA	660		

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Db 1561 TTTATGGCTATCGAAGAAATGAAGAGCAGGAAATCTATGTCGATTTCCAGAAATC 1620
Qy 1621 CTGACTAATGTCGCACTGCTGGCAATGATGATGATGATGATGATGATGATGATGATGATG 1680
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Qy 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGTGCAATAAATAGTACGTCGGGAGAAAT 1920
Db 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGTGCAATAAATAGTACGTCGGGAGAAAT 1920
Qy 1921 GCCATGCTAAGACTGAGAGCTAGACAAATGAACATCAGACCCAGTAAAAAATTTT 1980
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Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 7
US-09-825-301-7
; Sequence 7, Application US/09825301
; Patent No. US2002009738A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Dillon, David C.
; APPLICANT: Molesh, David A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Zehntner, Barbara
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION
; FILE REFERENCE: 210121.513
; CURRENT APPLICATION NUMBER: US/09/825,301
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-825-301-7

Query Match 97.0%; Score 1940; DB 10; Length 2040;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1995; Conservative 0; Mismatches 0; Indels 45; Gaps 1;

Qy 1 ATGCTGTTGAGTTGATTCATGCGCGGCTGCTCTGTTGAAAGAGCCATTGGTCTC 60
Db 1 ATGCTGTTGAGTTGATTCATGCGCGGCTGCTCTGTTGAAAGAGCCATTGGTCTC 60
Qy 61 AGGAGCAAGATGGGCAAGTGGTGTGCTGCTTCCCTGCTGTCAGAGGAGCGGCAAG 120
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Qy 241 GGGGCTTCTGAGAACACAGAGACTGCTATGAAGACACTCAGAAACAAGATGGGCAAG 300
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Qy 1441 AAACAGATGCCAAAATACTCTTCTGAAAACAGCAACCCAGAACACTTAAAGCTGACA 1500
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Db 1741 CAGCAATTTCTGACACTGAGATGAAGATGATCAGAGTGAAGCAAAATGATACTCAG 1800
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Qy 1816 GAAAGCAGATAGAAAGTGGTTGAAAAATGAATTCGACCTTCTCTAGTTGTAAGAA 1875
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Qy 1876 GAAAAAGACATCTGCTGATGAAAAATAGTACGTGGGAGAAATTCGCTAAGACTG 1935
Db 1921 GAAAAAGACATCTGCTGATGAAAAATAGTACGTGGGAGAAATTCGCTAAGACTG 1980
Qy 1936 GAGCTGACACATGAATGAAATCAGAGCCAGCTGAAAAAAGAAAAAAGAAAAA 1995
Db 1981 GAGCTGACACATGAATGAAATCAGAGCCAGCTGAAAAAAGAAAAAAGAAAAA 2040

RESULT 8
US-09-759-143-375
; Sequence 375, Application US/09759143
; Patent No. US200202248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, JIANGCHUN
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: JIANG, YUQI
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: VEDVICK, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: LI, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yashir A.W.
; APPLICANT: Hepier, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040

TYPE: DNA
ORGANISM: Homo sapien
US-09-759-143-375

Query Match 97.0%: Score 1940; DB 10; Length 2040;
Best Local Similarity 97.8%: Pred. No. 0;
Matches 1995; Conservative 0; Mismatches 0; Indels 45; Gaps 1;

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Db 1 ATGTGGTGTGAGTGTGATTCATCCGCGCTGCTCTTCTGTGAAGAACCATTTGGTCTC 60
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RESULT 9

US-09-780-669-375
Sequence 375, Application us/09780669
Patent No. US20020051977A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitchem, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuxui
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedrick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Ajun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
NUMBER OF SEQ ID NOS: 2001-02-09
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapien
US-09-780-669-375

Query Match 97.0% Score 1940; DB 10; Length 2040;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1995; Conservative 0; Mismatches 0; Indels 45; Gaps 1;

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RESULT 10
US-09-810-936-303
; Sequence 303, Application us/09810936
; Patent No. US20020068285A1
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, AlJun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Day, Craig H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C11
; CURRENT APPLICATION NUMBER: US/09/810.936
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-936-303

Query Match 97.08; Score 1940; DB 10; Length 2040;
Best Local Similarity 97.88; Pred. No. 0;
Matches 1995; Conservative 0; Mismatches 0; Indels 45; Gaps 1;

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RESULT 11
US-09-822-827-375
; Sequence 375, Application US/09822827
; Patent No. US2002081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822.827
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-375

Query Match 97.0%; Score 1940; DB 10; Length 2040;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1995; Conservative 0; Mismatches 0; Indels 45; Gaps 1;

QY 1 ATGCTGTTGAGTTGATTCATGCCGCTGCTCTTCTGTGAAGAAGCAATTTGGTCTC 60
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QY 301 TGGTGTGCACTGCTTCCCTGCTGAGGGGAGGCGGAAAGCAAGGTTGGCGCTTG 360
Db 301 TGGTGTGCACTGCTTCCCTGCTGAGGGGAGGCGGAAAGCAAGGTTGGCGCTTG 360
QY 361 GGAGACTAGATGACAGTCTTCCATGAGCCAGGATACAGTCCCTGGAGAAATCTG 420
Db 361 GGAGACTAGATGACAGTCTTCCATGAGCCAGGATACAGTCCCTGGAGAAATCTG 420
QY 421 GACAACTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421 GACAACTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 CTCAGGAGACTGAGCTGGAAGAAAGAGCAAGCAAGAGAGAGAGAGAGAGAGAG 540
Db 481 CTCAGGAGACTGAGCTGGAAGAAAGAGCAAGCAAGAGAGAGAGAGAGAGAGAG 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGAGAGAGATGCAACTTAAT 600
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAATCTCTGCTGAGAGAGATGCAACTTAAT 600
QY 601 GTCTTGTGACAAAGAAAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 601 GTCTTGTGACAAAGAAAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 661 TGTGCTTAAATGTTGCTGGAACATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 661 TGTGCTTAAATGTTGCTGGAACATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
QY 721 ACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 721 ACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 781 TATGCTGCTGATATGAAATCAAAAAAAGCATGGCTGCTGCTGCTGCTGCTGCTG 840
Db 781 TATGCTGCTGATATGAAATCAAAAAAAGCATGGCTGCTGCTGCTGCTGCTGCTG 840
QY 841 CATGAGCAAAAAAGCAAGTCTGGAATTTTAAATCAAAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAAAGCAAGTCTGGAATTTTAAATCAAAAAAAGCAATTTAAATGCA 900
QY 901 CTGATGATATGAAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 901 CTGATGATATGAAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 GTCAAGCTTCTGCTGAGCAAAAAATTTGATGATCTTCTGCAAGATCTATCTGAGAC 1020
Db 961 GTCAAGCTTCTGCTGAGCAAAAAATTTGATGATCTTCTGCAAGATCTATCTGAGAC 1020

QY	1021	GCACAGATATCTGTTTCTATGTCATCATCTGTAATTTGGCACTTCTTGACATAC	1080
Db	1021	GCACAGAGATATCTGTTTCTATGTCATCATCTGTAATTTGGCACTTCTTGACATAC	1080
QY	1081	AAAGAAAAACAGATGCTAAAAATCTCTTCGTGAAAAACAGCAATCCAGAACAGACTTAAAG	1140
Db	1081	AAAGAAAAACAGATGCTAAAAATCTCTTCGTGAAAAACAGCAATCCAGAACAGACTTAAAG	1140
QY	1141	CTGACATCAGAGAAAGATCACAAAGCTTCAAAAGCAGTGAATAAGCACCAGAGAAA	1200
Db	1141	CTGACATCAGAGAAAGATCACAAAGCTTCAAAAGCAGTGAATAAGCACCAGAGAAA	1200
QY	1201	ATGCTCAAGAACCCAGAAATTAATTAAGATGGGTAGAGAGTTGAAAGAAATGAG	1260
Db	1201	ATGCTCAAGAACCCAGAAATTAATTAAGATGGGTAGAGAGCTTGAAGAAATGAG	1260
QY	1261	AAGCATGAAGTATATATATGTTGGATTAATCTAGAAAAACCTGACTAATGTTGTCACCTG	1320
Db	1261	AAGCATGAAGTATATATATGTTGGATTAATCTAGAAAAACCTGACTAATGTTGTCACCTG	1320
QY	1321	AATGCTATATATGATTAATTCCTCAAGSAGACAGAACCCGGAATAATCAGCAATTT	1380
Db	1321	AATGCTATATATGATTAATTCCTCAAGSAGAGAGAGAACCCGGAATAATCAGCAATTT	1380
QY	1381	CCTGACCAAGAAAGTGAAGATATCACAATAATTTGGATTAATGTTCTGACTACAAAGAA	1440
Db	1381	CCTGACCAAGAAAGTGAAGATATCACAATAATTTGGATTAATGTTCTGACTACAAAGAA	1440
QY	1441	AAACAGATGCCAAATATCTTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA	1500
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QY	1501	TCACAGAAAGATGCACAAAGGCTTGAAGGACAGTGAATAATGGCCAGCC-----	1547
Db	1501	TCAGAGAAAGATGCACAAAGGCTTGAAGGACAGTGAATAATGGCCAGCCAGAGAAAAAGATCT	1560
QY	1548	-----AGAGCTAGAAAAATTTTATGGCTATCGAA	1575
Db	1561	CAAGAACCCAGAAATTAATTAAGATGGTATAGAGACTGAGAAAAATTTTATGGCTATCGAA	1620
QY	1576	GAATGTAAGAACGACGGAATCTCATGTTCGGATTTCCAGAAAACCTGACTATATGTTGCTC	1635
Db	1621	GAATGTAAGAACGACGGAATCTCATGTTCGGATTTCCAGAAAACCTGACTATATGTTGCTC	1680
QY	1636	ACTGCTGGCAATGGTGTATGATGATTAATTTCCGCCAAGSAGACAGACAACCTGAAAGC	1695
Db	1661	ACTGCTGGCAATGGTGTATGATGATTAATTTCCGCCAAGSAGACAGACAACCTGAAAGC	1740
QY	1696	CAGCAATTTCTGCACTGCAATGGAATGGAAGATACACAGTGAAGCAAAATGATACTCAG	1755
Db	1741	CAGCAATTTCTGCACTGCAATGGAATGGAAGATACACAGTGAAGCAAAATGATACTCAG	1800
QY	1756	AAGCAATTTTGTGAAGAACGAAACACTGGAATTTACACAGATGATCTGATTCATGAA	1815
Db	1801	AAGCAATTTTGTGAAGAACGAAACACTGGAATTTACACAGATGATCTGATTCATGAA	1860
QY	1816	GAAGAAGCAGATAGAACGTTTGAAGAAAAATGAATTCGACCTTCTCTTATGTTGAAGAA	1875
Db	1861	GAAGAAGCAGATAGAACGTTTGAAGAAAAATGAATTCGACCTTCTCTTATGTTGAAGAA	1920
QY	1876	GAAAAAAGCATCTTGCATGAAAAATAGTACGTTGCGGGAAGAAATTTGCCATGCTAAGACTG	1935
Db	1921	GAAAAAAGCATCTTGCATGAAAAATAGTACGTTGCGGGAAGAAATTTGCCATGCTAAGACTG	1980
QY	1936	GAGCTAGACACATGAAGAACATCGAGCCAGCTAAAAAATTTTTTTTTTTTTTTTTTTTTT	1995
Db	1961	GAGCTAGACACATGAAGAACATCGAGCCAGCTAAAAAATTTTTTTTTTTTTTTTTTTTTT	2040

```

: GENERAL INFORMATION:
: APPLICANT: Frudakis, Tony N.
: APPLICANT: Smith, John M.
: APPLICANT: Reed, Steven G.
: APPLICANT: Misher, Iynda
: APPLICANT: Reltter, Marc W.
: APPLICANT: Dillon, Davin C.
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
: TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
: FILE REFERENCE: 210121.419C6
: CURRENT APPLICATION NUMBER: US/09/429,755A
: CURRENT FILING DATE: 1999-10-28
: NUMBER OF SEQ ID NOS: 315
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 303
: LENGTH: 2040
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-429-755-303

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RESULT 12
US-09-429-755-303
; Sequence 303, Application US/09429755A
; Patent No. US20020111467A1

	Query Match	Similarity	97.0%	Score	1940:	DB	10:	Length	2040:	
	Best Local	Similarity	97.8%	Pred.	No. 0:					
	Matches	1995:	Conservative	0:	Mismatches	0:	Indels	45:	Gaps	1:
QY	1	ATGGGTGTGAGGTGATGATCCATGCCGGCGTGCCTCTTCTGTGTGAAGAAGCCATTGSGTCTC	60							
Db	1	ATGGGTGTGAGGTGATGATTCATGCCGGCGTGCCTCTTCTGTGTGAAGAAGCATTTGSGTCTC	60							
QY	61	AGGAGCAAGATGGGCAAGTGGTGGCTGGCCGTTGCTTCCCTGCTGCAGAGGAGAGCGGCAAG	120							
Db	61	AGGAGCAAGATGGGCAAGTGGTGGCTGGCCGTTGCTTCCCTGCTGCAGAGGAGAGCGGCAAG	120							
QY	121	AGCAACGTGGGGCAGCTTCTGGAGACACGACGACTCTGCTATGAACAACACTCAGAGACAAG	180							
Db	121	AGCAACGTGGGGCAGCTTCTGGAGACACGACGACTCTGCTATGAACAACACTCAGAGACAAG	180							
QY	181	ATGGGCAAGTGGTGGCGGCACACTGCTTCCCTGCTGCAGGGGGAGTGGCAAGACAAAGCTG	240							
Db	181	ATGGGCAAGTGGTGGCGGCACACTGCTTCCCTGCTGCAGGGGGAGTGGCAAGACAAAGCTG	240							
QY	241	GGCGCTTCTGGAGACACGAGCAGCTCTGTATGAAGACACTAGGAACAAGATGGGGCAAG	300							
Db	241	GGCGCTTCTGGAGACACGAGCAGCTCTGTATGAAGACACTAGGAACAAGATGGGGCAAG	300							
QY	301	TGGTCTGTCGCACTGGCTTCCCTGCTGCAGGGGGAGACGGCAAGGATGGAGGCGCTTGG	360							
Db	301	TGGTCTGTCGCACTGGCTTCCCTGCTGCAGGGGGAGACGGCAAGGATGGAGGCGCTTGG	360							
QY	361	GGAGACTACGATGACGAGTGGCTTCTCATGTGAGACCCAGGATACACGCTCCGTGGAGAGATCTG	420							
Db	361	GGAGACTACGATGACGAGTGGCTTCTCATGTGAGACCCAGGATACACGCTCCGTGGAGAGATCTG	420							
QY	421	GACAAAGCTCCACAGAGCTGCGTGGTGGGTAAAGTCCCAAGAAAGATCTCATCGCAGT	480							
Db	421	GACAAAGCTCCACAGAGCTGCGTGGTGGGTAAAGTCCCAAGAAAGATCTCATCGCAGT	480							
QY	481	CTCAGGGACACTGAGAGTGAACACAGAGGACAAAGAAAAGAGAGACTGCTTACATCTGGCC	540							
Db	481	CTCAGGGACACTGAGAGTGAACACAGAGGACAAAGAAAAGAGAGACTGCTTACATCTGGCC	540							
QY	541	TCTGGCAATGGGAATTCAGAAAGTAAACTCTGCTGTGACAGACAGATGTCAACTTAAT	600							
Db	541	TCTGGCAATGGGAATTCAGAAAGTAAACTCTGCTGTGACAGACAGATGTCAACTTAAT	600							
QY	601	GTCCTTGACACAAAAAAGAGGACACTCTGATTAAGAGCGCTACATGGCCAGGAAGTGA	660							
Db	601	GTCCTTGACACAAAAAAGAGGACACTCTGATTAAGAGCGCTACATGGCCAGGAAGTGA	660							
QY	661	TGTGGCTTAATGTGCTGTGGAACATGGCACTGTATCCAAATATTCCAGATGAGTATGAAAT	720							
Db	661	TGTGGCTTAATGTGCTGTGGAACATGGCACTGTATCCAAATATTCCAGATGAGTATGAAAT	720							
QY	721	ACCACCTGACACTACGCTATCTATTAATGAGATAAATTAAATGGCCAAAGCACTGCTCTTA	780							

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Db 721 ACCACTCTGCTACGCTCTCTATATGAAAGATTAATTAATGCGCAAGACACTGCTTA 780
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Db 781 TATGGCTGATATGATCAAAAAAACAAGCATGGCTTACACCACTGTTACTTGGTGA 840
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Db 841 CATGAGCAAAAAACAGCAATCGTAATTTTAATCAAAAAAAGCAATTTAAATGCA 900
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Db 901 CTGATAGATATGAAAGACTGCTCATATCTGTATGTTGTGATCAGCAAGTATA 960
Qy 961 GTGAGCTTCTACTGAGCAAAATATGATGTAATCTTCAAGATCTATCTGACAGC 1020
Db 961 GTGAGCTTCTACTGAGCAAAATATGATGTAATCTTCAAGATCTATCTGACAGC 1020
Qy 1021 GCGAGAGATATGCTGTTCTAGTCATCATGTAATTTGCGAGTACTTCTGACTAC 1080
Db 1021 GCGAGAGATATGCTGTTCTAGTCATCATGTAATTTGCGAGTACTTCTGACTAC 1080
Qy 1081 AAGAAAAACAGATGCTAAAAATCTCTTCTGAAAACAGCAATCCAGAACAGCTTAAG 1140
Db 1081 AAGAAAAACAGATGCTAAAAATCTCTTCTGAAAACAGCAATCCAGAACAGCTTAAG 1140
Qy 1141 CTGACATCTAGAGAGAGCTCACAAAGGTTCAAGCGATGAAATATGCCAGCAGAAA 1200
Db 1141 CTGACATCTAGAGAGAGCTCACAAAGGTTCAAGCGATGAAATATGCCAGCAGAAA 1200
Qy 1201 ATGTCTCAGAAACAGAAATTAATAGATGGTATGATGAGAGGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAGAAACAGAAATTAATAGATGGTATGATGAGAGGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAAGTAATTAATGTGGATTAATCTAGAAAACCTGACTAATGTGTCACTGGC 1320
Db 1261 AAGCATGAAAGTAATTAATGTGGATTAATCTAGAAAACCTGACTAATGTGTCACTGGC 1320
Qy 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGCAACACCTGAAAAATCGCAATTT 1380
Db 1321 AATGTGATTAATGATTAATCTCTCAAGAGAGAGCAACACCTGAAAAATCGCAATTT 1380
Qy 1381 CCTGACAGAAAGTGAAGATATCAAGATTTGGAATTTGTTCTGCTCAAGAA 1440
Db 1381 CCTGACAGAAAGTGAAGATATCAAGATTTGGAATTTGTTCTGCTCAAGAA 1440
Qy 1441 AAACAGATCCCAAAATACTCTTCTGAAAACAGCAACCCAGAACAGACTTAAGTGACA 1500
Db 1441 AAACAGATCCCAAAATACTCTTCTGAAAACAGCAACCCAGAACAGACTTAAGTGACA 1500
Qy 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGCGAGTGAATAATGCGCAGCC----- 1547
Db 1501 TCAGAGAGAGAGTCAAAAGGCTTGAGGCGAGTGAATAATGCGCAGCC----- 1547
Qy 1548 -----AGAGCTGAAAATTTTATGCTATCGAA 1575
Db 1561 CAAAGAACCAAAATTAATAGATGATAGAGAGCTGAAAAATTTTATGCTATCGAA 1620
Qy 1576 GAAATGAAAGAGACAGAGTACTCATGTGCGATTTCCAGAAAACTGATAATGTTGCC 1635
Db 1621 GAAATGAAAGAGACAGAGTACTCATGTGCGATTTCCAGAAAACTGATAATGTTGCC 1680
Qy 1636 ACTGCTGGCAATGTGATGATTAATTTCTTCCAGAGAGAGAGCAACCTGAAAGC 1695
Db 1681 ACTGCTGGCAATGTGATGATTAATTTCTTCCAGAGAGAGAGCAACCTGAAAGC 1740
Qy 1696 CAGCAATTTCTGACACTGGAATGGAAGTATCAGATGACGAACAAAAATGATCTAG 1755
Db 1741 CAGCAATTTCTGACACTGGAATGGAAGTATCAGATGACGAACAAAAATGATCTAG 1800
Qy 1756 AAGCAATTTTGTGAAGAGAGACACTGGAATTTACAGATGAGATTTCTGATTCGAA 1815
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Db 1801 AAGCAATTTTGTGAAGACAGACACTGGAATATACAGATGAGATTTCTGATTCGAA 1860
Qy 1816 GAAAGACATAGAAATGTTGAAAAAATGAATTCAGACTTCTCTTACTTAAAGAA 1875
Db 1861 GAAAGACATAGAAATGTTGAAAAAATGAATTCAGACTTCTCTTACTTAAAGAA 1920
Qy 1876 GAAAGACATTTGATGAAATATGATGTTCCGGAGAAATTCATGTAAGACTG 1935
Db 1921 GAAAGACATTTGATGAAATATGATGTTCCGGAGAAATTCATGTAAGACTG 1980
Qy 1936 GAGCTAGACAAATGAATCAGACAGCAGCTAAAAAAGAGAGAGAGAGAGAGAGAG 1995
Db 1981 GAGCTAGACAAATGAATCAGACAGCAGCTAAAAAAGAGAGAGAGAGAGAGAGAG 2040

RESULT 13
US-09-759-143-369
; Sequence 369, Application US/09759143
; Patent No. US2002002248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuxui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 369
; LENGTH: 1853
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-369

Query Match 57.4%; Score 1147.6; DB 10; Length 1853;
Best Local Similarity 97.1%; Pred. No. 1,3e-256;
Matches 1163; Conservative 23; Mismatches 7; Indels 5; Gaps 2;
```

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QY 301 TGTGCTGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGTGGCGCTTGG 360
D 523 TGTGCTGCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGCAAGTGGCGCTTGG 582
QY 361 GGAGAGCTACGATGACAGTGCCTTCTATGAGAGCCAGTACACAGTCCGTGGAGAGATG 420
D 583 GGAGAGCTACGATGACAGTGCCTTCTATGAGAGCCAGTACACAGTCCGTGGAGAGATG 642
QY 421 GACAAGCTCCACAGAGTGCCTGCTGAGGAGTAAAGTCCCAAGAGAGATCTATGCTCATG 480
D 643 GACAAGCTCCACAGAGTGCCTGCTGAGGAGTAAAGTCCCAAGAGAGATCTATGCTCATG 702
QY 481 CTCAGAGCACTGACGTGACAGCAAGAGCAAGCAAGAGAGAGTCTCTACATCTGGCC 540
D 703 CTCAGAGCACTGACGTGACAGCAAGAGCAAGCAAGAGAGAGTCTCTACATCTGGCC 762
QY 541 TCTGCAATGGGAATTCAGAGTAGTAAACTCCCTGCTGACAGACAGTCACTTAAT 600
D 763 TCTGCAATGGGAATTCAGAGTAGTAAACTCCCTGCTGACAGACAGTCACTTAAT 822
QY 601 GTCTTGACACAAAAAGAGAGAGTCTGATTAAGGCGGTACATGCGCAGAGAGATGA 660
D 823 GTCTTGACACAAAAAGAGAGAGTCTGATTAAGGCGGTACATGCGCAGAGAGATGA 882
QY 661 TGTGCTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGAGTGAAT 720
D 883 TGTGCTTAATGTTGCTGGAACATGGCACTGATCCAAATATTCAGATGAGTGAAT 942
QY 721 ACCACTGCACTACGCTATCTATATGAGATTAATTAATGCGCAAGCACTGCTTA 780
D 943 ACCACTGCACTACGCTATCTATATGAGATTAATTAATGCGCAAGCACTGCTTA 1002
QY 781 TATGCTGATGATGCAATCAAAAAACAGCATGCGCTCACACCACTGTTACTGGTGA 840
D 1003 TATGCTGATGATGCAATCAAAAAACAGCATGCGCTCACACCACTGTTACTGGTGA 1062
QY 841 CATAGCAAAAAACAGCAAGTGTGAATTTTAATCAAGAAAAAGCAATTT-AAATGC 899
D 1063 CATAGCAAAAAACAGCAAGTGTGAATTTTAATCAAGAAAAAGCAATTT-AAATGC 1122
QY 900 ACTGATGATGATGAGAGAGTGCCTCATCTACTGCTATGTTGGATGAGCAAGAT 959
D 1123 ACTGATGATGATGAGAGAGTGCCTCATCTACTGCTATGTTGGATGAGCAAGAT 1182
QY 960 AGTCAAGCTTACTGAGCAAAATATGATGATCTCTCAAGATCATCTGAGCAAG 1019
D 1183 AGTCAAGCTTACTGAGCAAAATATGATGATCTCTCAAGATCATCTGAGCAAG 1238
QY 1020 GGCCAGAGATGCTGTTTCTAGTCAATCATCATGTAATTTGCCAGTTACTTCTGACTA 1079
D 1239 GGCCAGAGATGCTGTTTCTAGTCAATCATCATGTAATTTGCCAGTTACTTCTGACTA 1298
QY 1080 CAAAGAAAAACAGATGCAAAATCTCTGCAAAAAACAGCAATCCAGAAAGACTTAA 1139
D 1299 CAAAGAAAAACAGATGCAAAATCTCTGCAAAAAACAGCAATCCAGAAAGACTTAA 1358
QY 1140 GCTGACATCAGAGAGAGTCAAGAGTTCAGAAAGAGTGAAGATGAGCCAGAG 1197
D 1359 GCTGACATCAGAGAGAGTCAAGAGTTCAGAAAGAGTGAAGATGAGCCAGAG 1416

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RESULT 14
US-09-780-669-369
; Sequence 369, Application US/09780669
; Patient NO. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.

```

```

; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedivick, Thomas S.
; APPLICANT: Carter, Patrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 369
; LENGTH: 1853
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-780-669-369

Query Match 57.4%; Score 1147.6; DB 10; Length 1853;
Best Local Similarity 97.1%; Pred. No. 1.3e-256;
Matches 1163; Conservative 23; Mismatches 7; Indels 5; Gaps 2;

QY 1 ATGTGTTGAGTGTGATTCATCCAGCCGCTCCTCTCTGTGAAGAACCATTTGCTGC 60
D 223 ATGTGTTGAGTGTGATTCATCCAGCCGCTCCTCTCTGTGAAGAACCATTTGCTGC 282
QY 61 AGAGCAAGATGGCAAGTGTGCTGCCGTTGCTTCCCTGCTCAGAGGAGCGGCAAG 120
D 283 AGAGCAAGATGGCAAGTGTGCTGCCGTTGCTTCCCTGCTCAGAGGAGCGGCAAG 342
QY 121 AGCAAGCGGCGCATCTTGGAGACACAGAGAGTGTGATGAAGACACTGAGAGCAAG 180
D 283 AGCAAGCGGCGCATCTTGGAGACACAGAGAGTGTGATGAAGACACTGAGAGCAAG 342
QY 343 AGCAAGCGGCGCATCTTGGAGACACAGAGAGTGTGATGAAGACACTGAGAGCAAG 402
D 343 AGCAAGCGGCGCATCTTGGAGACACAGAGAGTGTGATGAAGACACTGAGAGCAAG 402
QY 181 ATGGCAAGTGTGCGCCGCACTGCTCCCTGCTGCAAGGGGAGTGGCAAGCAAGTGTG 240
D 403 ATGGCAAGTGTGCGCCGCACTGCTCCCTGCTGCAAGGGGAGTGGCAAGCAAGTGTG 462
QY 241 GGCCCTTGTGAGACACAGAGAGTGTGATGAAGACACTGAGAGCAAGTGTGCAAG 300
D 463 GGCCCTTGTGAGACACAGAGAGTGTGATGAAGACACTGAGAGCAAGTGTGCAAG 522
QY 301 TGTGCTGCGCACTGCTTCCCTGCTGCAAGGGGAGCGCAAGAGAGTGGCGCTTGG 360
D 523 TGTGCTGCGCACTGCTTCCCTGCTGCAAGGGGAGCGCAAGAGAGTGGCGCTTGG 582
QY 523 TGTGCTGCGCACTGCTTCCCTGCTGCAAGGGGAGCGCAAGAGAGTGGCGCTTGG 582
D 523 TGTGCTGCGCACTGCTTCCCTGCTGCAAGGGGAGCGCAAGAGAGTGGCGCTTGG 582
QY 361 GGAGACTACGATGACAGTGCCTTCTATGAGAGCCAGTACACAGTCCGTGGAGAGATG 420
D 583 GGAGACTACGATGACAGTGCCTTCTATGAGAGCCAGTACACAGTCCGTGGAGAGATG 642
QY 421 GACAAGCTCCACAGAGTGCCTGCTGAGGAGTAAAGTCCCAAGAGAGATCTATGCTCATG 480
D 643 GACAAGCTCCACAGAGTGCCTGCTGAGGAGTAAAGTCCCAAGAGAGATCTATGCTCATG 702
QY 481 CTCAGAGCACTGACGTGACAGCAAGAGCAAGCAAGAGAGAGTCTCTACATCTGGCC 540
D 703 CTCAGAGCACTGACGTGACAGCAAGAGCAAGCAAGAGAGAGTCTCTACATCTGGCC 762
QY 541 TCTGCAATGGGAATTCAGAGTAGTAAACTCCCTGCTGACAGACAGTCACTTAAT 600
D 763 TCTGCAATGGGAATTCAGAGTAGTAAACTCCCTGCTGACAGACAGTCACTTAAT 822
QY 601 GTCTTGACACAAAAAGAGAGAGTCTGATTAAGGCGGTACATGCGCAGAGAGATGA 660

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Db 823 GTCTTGACAAACAAAAGAGACACGCTCTGAYAAAGCCGTACAAATGCCAGGAATGAA 882
Qy 661 TGTGGTAAATGTTGCTGACATGACACTGATCCAAATATCCAGATGAGATGAAAT 720
Db 883 TGTGGTAAATGTTGCTGACATGACACTGATCCAAATATCCAGATGAGATGAAAT 942
Qy 721 AACACTGTCAGACTATCTATATAGAGATTAATTAATGAGCAAGCACTGCTCTTA 780
Db 943 AACACTGTCAGACTATCTATATAGAGATTAATTAATGAGCAAGCACTGCTCTTA 1002
Qy 781 TATGTCGTGATATGAAATCAAAAACAGCATGCGCTCACACCACTGTTACTGCTGA 840
Db 1003 TATGTCGTGATATGAAATCAAAAACAGCATGCGCTCACACCACTGTTACTGCTGA 1062
Qy 841 CATGAGCAAAAACAGCATGCTGTAATTTTAAATCAAGAAAACCAATTT-AAATGC 899
Db 1063 CATGAGCAAAAACAGCATGCTGTAATTTTAAATTAAGAAAACCAATTTAAATGC 1122
Qy 900 ACTGATAGATATGAGAGACTGCTCATACTGCTGATGTTGATGATCAGCAAGTAT 959
Db 1123 RCTGGATGATATGAGAGACTGCTCATACTGCTGATGTTGATGATCAGCAAGTAT 1182
Qy 960 AGTACGCTTACTTGTGACAAATATTTGATGATATCTTCTCAAGATCTATCTGACAGAC 1019
Db 1183 AGTACGCTTACTTGTGACAAATATTTGATGATATCTTCTCAAG-ATCTGAGAAAGAC 1238
Qy 1020 GGCCAGAGATATGCTGTTCTAGTCATCATCATGATTAATTTGCCAGTACTTCTGACTA 1079
Db 1239 GGCCAGAGATATGCTGTTCTAGTCATCATCATGATTAATTTGCCAGTACTTCTGACTA 1298
Qy 1080 CAAAGAAAACAGATGCTTAAATCTCTTCTGAAAACAGCAATCCAGAACTATTA 1139
Db 1299 CAAAGAAAACAGATGCTTAAATCTCTTCTGAAAACAGCAATCCAGAACTATTA 1358
Qy 1140 GCTGACATCAAGAGAGAGTCAAAAGCTTCAAGCGAGTGAAATAGCCAGCCAGAG 1197
Db 1359 GCTGACATCAAGAGAGAGTCAAAAGCTTAAAGGAAGTGAAGAAAGCCAGCCAGAG 1416

RESULT 15
US-09-810-936-295
Sequence 295, Application US/09810936
Patent No. US20020068285A1
GENERAL INFORMATION:
APPLICANT: Fridakis, Tony N.
APPLICANT: Reed, Steven G.
APPLICANT: Smith, John M.
APPLICANT: Mishner, Linda E.
APPLICANT: Dillon, Davin C.
APPLICANT: Retter, Marc W.
APPLICANT: Mang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Harlocker, Susan L.
APPLICANT: Day, Craig H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT OF INFLAMMATORY DISEASES
FILE REFERENCE: 210121.419C11
CURRENT APPLICATION NUMBER: US/09/810, 936
CURRENT FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 334
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 295
LENGTH: 1853
TYPE: DNA
ORGANISM: Homo sapien
US-09-810-936-295

Query Match 57.4%; Score 1147.6; DB 10; Length 1853;
Best Local Similarity 97.1%; Pred. No. 1.3e-256;
Matches 1163; Conservative 23; Mismatches 7; Indels 5; Gaps 2;

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Qy 121 AGCAAGTGGGCACTTCTGAGACACAGCAGCAGCTGCTATGAAGACACTGAGAGCAAG 180
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Qy 241 GGCGCTTCTGAGACACAGCAGCAGCTGCTATGAAGACACTGAGAGCAAGTGGGCAAG 300
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Qy 481 CTCAGGACACTGAGCTGTAACAAGAGCACAAGAGAGAGAGAGAGAGAGAGAGAGAG 540
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Db 763 TCTGCCAATGGGAATTCAGAAATAGTAAATCTCTGCTGAGAGAGATGCACTTAAT 822
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Db 823 GTCTTGTGACAAACAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 882
Qy 661 TGTGCTTAAATGTTGCTGGAACATGCACTGATCCAAATATCCAGATGAGTGAAT 720
Db 883 TGTGCTTAAATGTTGCTGGAACATGCACTGATCCAAATATCCAGATGAGTGAAT 942
Qy 721 AACACTGTCAGACTATCTATATAGAGATTAATTAATGAGCAAGCACTGCTCTTA 780
Db 943 AACACTGTCAGACTATCTATATAGAGATTAATTAATGAGCAAGCACTGCTCTTA 1002
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Db 1003 TATGTCGTGATATGAAATCAAAAACAGCATGCGCTCACACCACTGTTACTGCTGA 1062
Qy 841 CATGAGCAAAAACAGCATGCTGTAATTTTAAATCAAGAAAACCAATTT-AAATGC 899
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Db 1183 AGTACGCTTACTTGTGACAAATATTTGATGATATCTTCTCAAG-ATCTGAGAAAGAC 1238
Qy 1020 GGCCAGAGATATGCTGTTCTAGTCATCATCATGATTAATTTGCCAGTACTTCTGACTA 1079
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Qy 1080 CAAAGAAAACAGATGCTTAAATCTCTTCTGAAAACAGCAATCCAGAACTATTA 1139
Db 1299 CAAAGAAAACAGATGCTTAAATCTCTTCTGAAAACAGCAATCCAGAACTATTA 1358

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2002, 02:07:38 ; Search time 3942.08 Seconds
(without alignments)
12755.953 Million cell updates/sec

Title: US-09-924-400-302

Perfect score: 2000

Sequence: 1 atgctgtgtgaggtgattc.....aaaaaaaaaaaaaaaaaaaa 2000

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Pending_Patents_NA_Main:*

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Result				SUMMARIES	
No.	Score	Query Match	Length DB	ID	Description
1	2000	100.0	2000	1	Sequence 302, App
2	2000	100.0	2000	16	Sequence 374, App
3	2000	100.0	2000	16	Sequence 302, App
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5	2000	100.0	2000	18	Sequence 374, App
6	2000	100.0	2000	18	Sequence 374, App
7	2000	100.0	2000	20	Sequence 302, App
8	2000	100.0	2000	20	Sequence 374, App
9	2000	100.0	2000	22	Sequence 374, App
10	2000	100.0	2000	22	Sequence 302, App
11	2000	100.0	2000	22	Sequence 302, App
12	2000	100.0	2000	22	Sequence 374, App
13	2000	100.0	2000	23	Sequence 374, App
14	2000	100.0	2000	24	Sequence 374, App
15	2000	100.0	2000	25	Sequence 374, App
16	2000	100.0	2000	25	Sequence 374, App
17	2000	100.0	2000	26	Sequence 374, App
18	2000	100.0	2000	26	Sequence 374, App
19	2000	100.0	2000	27	Sequence 374, App
20	2000	100.0	2000	27	Sequence 374, App
21	2000	100.0	2000	27	Sequence 302, App

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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23 2000 100.0 2000 29 US-09-759-143-374 Sequence 374, App
24 2000 100.0 2000 30 US-09-780-669-374 Sequence 374, App
25 2000 100.0 2000 31 US-09-810-935-302 Sequence 302, App
26 2000 100.0 2000 31 US-09-822-827-374 Sequence 374, App
27 2000 100.0 2000 31 US-09-825-301-6 Sequence 6, App11
28 2000 100.0 2000 32 US-09-852-911-374 Sequence 374, App
29 2000 100.0 2000 33 US-09-895-793-374 Sequence 374, App
30 2000 100.0 2000 33 US-09-895-814-374 Sequence 374, App
31 2000 100.0 2000 34 US-09-924-400-302 Sequence 302, App
32 2000 100.0 2000 38 US-10-006-920-374 Sequence 374, App
33 2000 100.0 2000 38 US-10-010-940-374 Sequence 374, App
34 2000 100.0 2000 38 US-10-012-895-374 Sequence 374, App
35 2000 100.0 2000 39 US-10-079-137B-302 Sequence 302, App
36 2000 100.0 2000 40 US-10-144-678A-374 Sequence 374, App
37 2000 100.0 2000 42 US-10-212-679-302 Sequence 302, App
38 1940 97.0 2040 1 PCT-US02-24917-303 Sequence 303, App
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40 1940 97.0 2040 16 US-09-289-198-303 Sequence 303, App
41 1940 97.0 2040 18 US-09-429-755-303 Sequence 303, App
42 1940 97.0 2040 18 US-09-443-686-375 Sequence 375, App
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ALIGNMENTS

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RESULT 1
PCT-US02-24917-302
; Sequence 302, Application PC/TUS0224917
; GENERAL INFORMATION:
; APPLICANT: Corixa Corporation
; APPLICANT: Panger, Gary R.
; APPLICANT: Hirstel, Shannon Kathleen
; APPLICANT: Dillon, Davin C.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.41931PC
; CURRENT APPLICATION NUMBER: PCT/US02/24917
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-24917-302
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Query Match 100.0%; Score 2000; DB 1; Length 2000;
Best Local Similarity 100.0%; Pred. No. 2,6e-271;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 ATGCTGTTAGAGTTGATTCATGCGCGGCTCTTCTGTGAAGAACCATTTGGTCTC 60
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DB 61 AGGAGCAAGATGGGCAAGTGGTGTGCTGCTTCCCTGCTGCAAGGAGGAGGCAAG 120
QY 121 AGCAACGTGGGCACTTCTGAGACACAGACACTCTCTATGAAGACACTAGAGCAAG 180
DB 121 AGCAACGTGGGCACTTCTGAGACACAGACACTCTCTATGAAGACACTAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCCGCACTGCTTCCCTGCTGCAAGGAGGAGTGGCAAGCAAGCTG 240
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DB 241 GGGCTTCTGAGACACACAGACACTCTGATGAAGACACTCAGAAACAAGATGGGCAAG 300
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DB 361 GGAGACTACGATGACATGCTGCTTCATGAGCCAGGATACAGCTGCTGGAGAAAGATCTG 420
QY 421 GACAACTCCACAGAGCTGCTGCTGAGGAGTAAAGTCCCGAGAAAGATCTCATGCTCATG 480
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DB 841 CATGAGCAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
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Db	1381	CTTGACAAGCAAAAGTGAAGAGTATCACAATAATTCGGAATTAGTTCAGCTACAAAGAA	1440
QY	1441	AAACAGATGCCAAATATCTCTTCTGAAAACAGCAACCCAGAACAAGACTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAATATCTCTTCTGAAAACAGCAACCCAGAACAAGACTTAAAGCTGACA	1500
QY	1501	TCAGAGAAAGATCACAAAAGCCTTGAGGGCAGTGAATAATGGCCAGCCAGACTAGAAAT	1560
Db	1501	TCAGAGAAAGATCACAAAAGCCTTGAGGGCAGTGAATAATGGCCAGCCAGACTAGAAAT	1560
QY	1561	TTTATGGCTATCGAGAATAATGAAGAAGCAGCAAGTACTCATGTGCGATTCCCAAGAAAC	1620
Db	1561	TTTATGGCTATCGAMAATAATGAAGAAGCAGCAAGTACTCATGTGCGATTCCCAAGAAAC	1620
QY	1621	CTGACATATGTCGCCACTGCTGGCAATGGTGAATGATGATTAATTCCTCAAGGAAGGC	1680
Db	1621	CTGACATATGTCGCCACTGCTGGCAATGGTGAATGATGATGATTAATTCCTCAAGGAAGGC	1680
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Db	1741	CAAAATGATCTCAGAAAGCAATTTTGTGAAGAAGCAACACTGGAATTTACACAGATGAG	1800
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Db	1801	ATTCTGATTCATGAAGAAAAGCAGATAGAGAAGTGTTGAATAATGAATTCTGAGCTTCT	1860
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RESULT 2
; Sequence 374, Application US/09288946
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Milton, Jennifer Lynn
; APPLICANT: Mitcham, David C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C7
; CURRENT APPLICATION NUMBER: US/09/288,946
; CURRENT FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
; S-09-288-946-374

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Query Match	100.0%;	Score 2000;	DB 16;	Length 2000;
Best Local Similarity	100.0%;	Pred. No. 2.6e-271;		
Matches 2000;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Db	181	ATGGGCAAGTGTGTGCGCCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGACCAAGTGTG	240
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QY	361	GGAAGCTACGATGTGACAGTGGCTTCAATGTGAGCCAGGTACCAAGTCCGTGGAGAAAGATCTG	420
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Db	901	CTGAGTATGATATGGAAGAGACTGCTCTCATACTTGTGTAATGTTGTGATCAGCAAGTATA	960
QY	961	GTCAGCCTTCTACTTGAAGCAAAATATTGATGTATCTTCAAGATCTATCTGGACAGAGC	1020
Db	961	GTCAGCCTTCTACTTGAAGCAAAATATTGATGTATCTTCAAGATCTATCTGGACAGAGC	1020
QY	1021	GCCAGAGATGTGCTGTTTCTAGTCATCATATGTAATTTGCCAATTTCTTTCGACATC	1080
Db	1021	GCCAGAGATGTGCTGTTTCTAGTCATCATATGTAATTTGCCAATTTCTTTCGACATC	1080
QY	1081	AAAGAAAAACAGATGCTTAAAAATCTCTTGTGAAAAACAGCAATCCAGAAACAAAGACTTAAAG	1140

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|||||
Db 1081 AAAAGAAAAAGATGCTAAAAATCTCTTCTAAAAACACCAATCCAGAAACAGACTTAAAG 1140
Qy 1141 CTGACATCAGAGAGAACTCACAAGGTTCAAGAGCACTGAAATATGACGACAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAACTCACAAGGTTCAAGAGCACTGAAATATGACGACAGAGAAA 1200
Qy 1201 ATGCTCTAAGAACAGAAATTAATAGAGTGTATAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGCTCTAAGAACAGAAATTAATAGAGTGTATAGAGAGTTGAAGAAATGAAG 1260
Qy 1261 AAGCATGAAATTAATATGTGGATTAATAGAAAACCTGACTAATGTGTCTACTGCTGC 1320
Db 1261 AAGCATGAAATTAATATGTGGATTAATAGAAAACCTGACTAATGTGTCTACTGCTGC 1320
Qy 1321 AATGCTAATTAATGATTAATCTCAAGAGAGACAGAACCCGAAATCAGCAATTT 1380
Db 1321 AATGCTAATTAATGATTAATCTCAAGAGAGACAGAACCCGAAATCAGCAATTT 1380
Qy 1381 CCTGACAAAGAAAGTGAAGAGTATCACAGAAATTTGCGAATTAATTTCTGACTACAAAGAA 1440
Db 1381 CCTGACAAAGAAAGTGAAGAGTATCACAGAAATTTGCGAATTAATTTCTGACTACAAAGAA 1440
Qy 1441 AAACAGATGCCAAATTAATCTTTTGAAGAACGCAACCCAGAACAACTTAAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATTAATCTTTTGAAGAACGCAACCCAGAACAACTTAAAGCTGACA 1500
Qy 1501 TCAGAGAGAAAGTACAAAGAGCTTGAGAGGAGTGAAGTGGCCAGCCAGACTGAGAAAT 1560
Db 1501 TCAGAGAGAAAGTACAAAGAGCTTGAGAGGAGTGAAGTGGCCAGCCAGACTGAGAAAT 1560
Qy 1561 TTTATGCTATCGAAGAAATGAAGAACGACGGAAGTACTCATGTGCGATTTCCACAGAAAC 1620
Db 1561 TTTATGCTATCGAAGAAATGAAGAACGACGGAAGTACTCATGTGCGATTTCCACAGAAAC 1620
Qy 1621 CTGACTAATGTTGCGCAGCTGCGCAATGTGTATGATGATTAATTTCTTCCAGAGAAAGC 1680
Db 1621 CTGACTAATGTTGCGCAGCTGCGCAATGTGTATGATGATTAATTTCTTCCAGAGAAAGC 1680
Qy 1681 AGAACACCTGAAAGCAGACATTTCTGACACTGAGATGAAGATCACAGTGAAGCA 1740
Db 1681 AGAACACCTGAAAGCAGACATTTCTGACACTGAGATGAAGATCACAGTGAAGCA 1740
Qy 1741 CAAATATGATCTCAGAAAGCAATTTTGTGAAGAACGAACTGGAATTTACAGATGAG 1800
Db 1741 CAAATATGATCTCAGAAAGCAATTTTGTGAAGAACGAACTGGAATTTACAGATGAG 1800
Qy 1801 ATTCTGATTTCTGAAGAAACAGATAGAGTGGTTGAAAAATGAATTTCTGAGCTTTCT 1860
Db 1801 ATTCTGATTTCTGAAGAAACAGATAGAGTGGTTGAAAAATGAATTTCTGAGCTTTCT 1860
Qy 1861 CTTAGTTGTAGAAGAAAGAAAGACATCTTTCATGAAATATAGCTTCCGGGAAGAAAT 1920
Db 1861 CTTAGTTGTAGAAGAAAGAAAGACATCTTTCATGAAATATAGCTTCCGGGAAGAAAT 1920
Qy 1921 GCCATGCTAAGAGCTGAGAGCTAGACAAATGAAGCAATCAGAGCCAGCTAAAAA 1980
Db 1921 GCCATGCTAAGAGCTGAGAGCTAGACAAATGAAGCAATCAGAGCCAGCTAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
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RESULT 3

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US-09-289-198-302
; Sequence 302, Application US/09289198
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
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;; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
;; FILE REFERENCE: 210121.419C5
;; CURRENT APPLICATION NUMBER: US/09/289, 198
;; CURRENT FILING DATE: 1999-04-09
;; EARLIER APPLICATION NUMBER: US 09/062,451
;; EARLIER FILING DATE: 1998-04-17
;; EARLIER APPLICATION NUMBER: US 08/991,789
;; EARLIER FILING DATE: 1997-12-11
;; EARLIER APPLICATION NUMBER: US 08/838,762
;; EARLIER FILING DATE: 1997-04-09
;; EARLIER APPLICATION NUMBER: PCT/US97/00485
;; EARLIER FILING DATE: 1997-01-10
;; EARLIER APPLICATION NUMBER: US 08/700,014
;; EARLIER FILING DATE: 1996-08-20
;; EARLIER APPLICATION NUMBER: US 08/585,392
;; EARLIER FILING DATE: 1996-01-01
;; NUMBER OF SEQ ID NOS: 312
;; SOFTWARE: FASTSEQ for Windows Version 3.0
;; SEQ ID NO: 302
;; LENGTH: 2000
;; TYPE: DNA
;; ORGANISM: Homo sapien
US-09-289-198-302

Query Match 100.0%; Score 2000; DB 16; Length 2000;
Best Local Similarity 100.0%; Pred. No. 2,6e-271;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTGCTTGAAGTGGATTCATGCGCGCTGCTTCTTGTGAAACCAATTTGCTCTC 60
Db 1 ATGTGCTTGAAGTGGATTCATGCGCGCTGCTTCTTGTGAAACCAATTTGCTCTC 60
Qy 61 AGAGACAGATGAGGCAATGTGTGCTGCGTTCCTCCCTCTGAGAGAGAGCGCAAG 120
Db 61 AGAGACAGATGAGGCAATGTGTGCTGCGTTCCTCCCTCTGAGAGAGAGCGCGCAAG 120
Qy 121 AGCAAGTGGGCACTTGTGAGACACAGACAGACTCTGTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAAGTGGGCACTTGTGAGACACAGACAGACTCTGTATGAAGACACTCAGAGCAAG 180
Qy 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGACAGGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGGCAAGTGGTGGCGGCACTGCTTCCCTGCTGACAGGGGAGTGGCAAGCAAGCTG 240
Qy 241 GGGCTTCTGAGACACAGAGACACTCTGTATGAAGACACTCAGAGCAAGTGGCGCAAG 300
Db 241 GGGCTTCTGAGACACAGAGACACTCTGTATGAAGACACTCAGAGCAAGTGGCGCAAG 300
Qy 301 TGTGCTGCACTGCTTCCCTGCTGACAGGGGAGCGCAAGAGCAAGTGGCGCTTGG 360
Db 301 TGTGCTGCACTGCTTCCCTGCTGACAGGGGAGCGCAAGAGCAAGTGGCGCTTGG 360
Qy 361 GGAGACTACATGACAGTGCCTTCATAGAGGCCAGGTACCGTCCGGGGAAGATGTG 420
Db 361 GGAGACTACATGACAGTGCCTTCATAGAGGCCAGGTACCGTCCGGGGAAGATGTG 420
Qy 421 GACAAAGCTCCACAGAGCTGCTGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
Db 421 GACAAAGCTCCACAGAGCTGCTGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
Qy 481 CTCAGGACACTGACGTGACAGAGAGAGCAAGCAAAAGAGAGCTCTCATCTGCGC 540
Db 481 CTCAGGACACTGACGTGACAGAGAGAGCAAGCAAAAGAGAGCTCTCATCTGCGC 540
Qy 541 TCTGCAATGGGAATTCAGAGTAGTAATACTCTGCGGAGAGAGCTGCACTTAAT 600
Db 541 TCTGCAATGGGAATTCAGAGTAGTAATACTCTGCGGAGAGAGCTGCACTTAAT 600
Qy 601 GTCCCTTGACAAACAAAAGAGAGAGAGCTGTGATTAAGGCCCTTACATGACAGAGATGAA 660
Db 601 GTCCCTTGACAAACAAAAGAGAGAGAGCTGTGATTAAGGCCCTTACATGAGATGAA 660
Qy 661 TGTGCTTAATGTTGCTGGAACATGGACATGCATCAATATTTCCAGATGAGTGAAT 720
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Db 661 TGTGGTAAATGTTGCTGGACATGGCACTGATCCAAATATTCAGATGATGGAAT 720
Qy 721 ACCACTGCACTAGCTATCTATATGAAGATTAATTAATGAGCCAAACACTGCTTCT 780
Db 721 ACCACTGCTGCACTAGCTATCTATATGAAGATTAATTAATGAGCCAAACACTGCTTCT 780
Qy 781 TATGTTGCTGATATGCAATCAAAAAACAAGCATGGCCCTCACCACTGTTACTGGTGA 840
Db 781 TATGTTGCTGATATGCAATCAAAAAACAAGCATGGCCCTCACCACTGTTACTGGTGA 840
Qy 841 CATGAGCAAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAAAGCGAATTTAAATGCA 900
Db 841 CATGAGCAAAAAACAGCAAGTGTGAAATTTTATCAAGAAAAAAGCGAATTTAAATGCA 900
Qy 901 CTGGATATGATGAAAGAGCTGCTCATCTGCTGATGTTGGTGGATCAGCAAGTATA 960
Db 901 CTGGATATGATGAAAGAGCTGCTCATCTGCTGATGTTGGTGGATCAGCAAGTATA 960
Qy 961 GTCAACCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGGACAGC 1020
Db 961 GTCAACCTTCTACTGAGCAAAATATGATGATCTTCTCAAGATCTATCTGGACAGC 1020
Qy 1021 GCCAAGAGTATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Db 1021 GCCAAGAGTATGCTGTTTCTAGTCATCATGTAATTTGCCAGTTACTTTCTGACTAC 1080
Qy 1081 AAGAAAAACAGATCTAAAAATCTCTCTGAAACAGCAATCCAGAACACTTAAAG 1140
Db 1081 AAGAAAAACAGATCTAAAAATCTCTCTGAAACAGCAATCCAGAACACTTAAAG 1140
Qy 1141 CTGACATCAGAGAGAGTACACAAAGTTCAAGAGCAGTGAATAATAGCCAGCAGAAA 1200
Db 1141 CTGACATCAGAGAGAGTACACAAAGTTCAAGAGCAGTGAATAATAGCCAGCAGAAA 1200
Qy 1201 ATGTTCTAAGAACCAAGAAATTAATAGATGTTGATAGAGAGTTGAAGAAGATGAAG 1260
Db 1201 ATGTTCTAAGAACCAAGAAATTAATAGATGTTGATAGAGAGTTGAAGAAGATGAAG 1260
Qy 1261 AAGCATGAAAGTAAATAGTGGATTAATCTAGAAACCCTGACAAATGCTGCTGCGC 1320
Db 1261 AAGCATGAAAGTAAATAGTGGATTAATCTAGAAACCCTGACAAATGCTGCTGCGC 1320
Qy 1321 AATGTTGATTAATGATTAATCTCTCAAAAGAGAGCAGAAACCTGAAATATAGCAATTT 1380
Db 1321 AATGTTGATTAATGATTAATCTCTCAAAAGAGAGCAGAAACCTGAAATATAGCAATTT 1380
Qy 1381 CCTGACAAAGAAAGTGAAGATATCACAGAAATTTGGAATTAATGTTCTGACTACAAAGAA 1440
Db 1381 CCTGACAAAGAAAGTGAAGATATCACAGAAATTTGGAATTAATGTTCTGACTACAAAGAA 1440
Qy 1441 AAGCATGAAAGTAAATAGTGGATTAATCTAGAAACCCTGACAAATGCTGCTGCGC 1500
Db 1441 AAGCATGAAAGTAAATAGTGGATTAATCTAGAAACCCTGACAAATGCTGCTGCGC 1500
Qy 1501 TCAGAGAGAGTACACAAAGCTTGAAGGAGTGAATAATGAGCAGCAGAGCTAGAAAAAT 1560
Db 1501 TCAGAGAGAGTACACAAAGCTTGAAGGAGTGAATAATGAGCAGCAGAGCTAGAAAAAT 1560
Qy 1561 TTTATGCTATGCAAGAAATGAAGAACGGAAGTACTCATGTCGGATTTCCAGAAAAAC 1620
Db 1561 TTTATGCTATGCAAGAAATGAAGAACGGAAGTACTCATGTCGGATTTCCAGAAAAAC 1620
Qy 1621 CTGACATTAATGTTGCTGCAATGTTGATGATGATTAATTTCTTCAAGAGAAAGAC 1680
Db 1621 CTGACATTAATGTTGCTGCAATGTTGATGATGATTAATTTCTTCAAGAGAAAGAC 1680
Qy 1681 AAGACACCTGAAGAGCAGCAATTTCTGCACTGAGAAATGAAGAGATATCACAGTGAAG 1740
Db 1681 AAGACACCTGAAGAGCAGCAATTTCTGCACTGAGAAATGAAGAGATATCACAGTGAAG 1740
Qy 1741 CAAAATGATATCTCAGAAAGCAATTTTGTGAAGAACAGAACACTGGAATATTACAGATGAG 1800
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Db 1741 CAAAATGATATCTCAGAAAGCAATTTTGTGAAGAACAGAACACTGGAATATTACAGATGAG 1800
Qy 1801 ATTCTGATTCATGAGAAAGAGATAGAGGTTTGAAGAAAAATGAATTCAGAGCTTCT 1860
Db 1801 ATTCTGATTCATGAGAAAGAGATAGAGGTTTGAAGAAAAATGAATTCAGAGCTTCT 1860
Qy 1861 CTTAGTTGTGAAGAAAGAAAGACATCTTGCATGGAATAATGATGTTGGGGAGAAATTT 1920
Db 1861 CTTAGTTGTGAAGAAAGAAAGACATCTTGCATGGAATAATGATGTTGGGGAGAAATTT 1920
Qy 1921 GCCATGCTAAGAGCTGGAGCTAGACACATGAATGAACATCAGAGCAGCTAAAAAAGAAAA 1980
Db 1921 GCCATGCTAAGAGCTGGAGCTAGACACATGAATGAACATCAGAGCAGCTAAAAAAGAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 4
US-09-429-755-302
; Sequence 302, Application US/09429755A
; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, David C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; FILE REFERENCE: 210121.419C6
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-302

Query Match 100.0%; Score 2000; DB 18; Length 2000;
Best Local Similarity 100.0%; Pred. No. 2.6e-271;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 421 GACAGCTCCACAGAGCTGCTGGTAACTCCCCAGAAAAGATCTCATGCTATG 480
 DB 421 GACAGAGCTCCACAGAGCTGCTGGTAACTCCCCAGAAAAGATCTCATGCTATG 480
 QY 481 CTCAGGACATGACGTGACACAAAGAGACAAAGAGAGATGCTCTCATCTGCC 540
 DB 481 CTCAGGACATGACGTGACACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 QY 541 TCTCCATAGGAGATTCAGAGATGATTAATCTGCTGACAGAGATGATCACTTAT 600
 DB 541 TCTCCATAGGAGATTCAGAGATGATTAATCTGCTGACAGAGATGATCACTTAT 600
 QY 601 GTCTTGAACAACAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
 DB 601 GTCTTGAACAACAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
 QY 661 TGTGCGTAAATGTTGCTGAGAACATGCACTATCCAAATATTCAGATGATGAAAT 720
 DB 661 TGTGCGTAAATGTTGCTGAGAACATGCACTATCCAAATATTCAGATGATGAAAT 720
 QY 721 ACCACTGCACTACGCTATCTATATGAAGATTAATGAGCAAGAGAGAGAGAG 780
 DB 721 ACCACTGCACTACGCTATCTATATGAAGATTAATGAGCAAGAGAGAGAGAG 780
 QY 781 TATGCTGATATGATGATCAACAAAAGAGAGAGAGAGAGAGAGAGAGAGAG 840
 DB 781 TATGCTGATATGATGATCAACAAAAGAGAGAGAGAGAGAGAGAGAGAGAG 840
 QY 841 CATAGAGCAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
 DB 841 CATAGAGCAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
 QY 901 CTGATAGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
 DB 901 CTGATAGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
 QY 961 GTGACCTTCTACTGAGCAAAATATGATGATCTCTCAAGATCTATCTGACAG 1020
 DB 961 GTGACCTTCTACTGAGCAAAATATGATGATCTCTCAAGATCTATCTGACAG 1020
 QY 1021 GCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
 DB 1021 GCCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
 QY 1081 AAAG 1140
 DB 1081 AAAG 1140
 QY 1141 CTGACATCAG 1200
 DB 1141 CTGACATCAG 1200
 QY 1201 ATGCTCAAG 1260
 DB 1201 ATGCTCAAG 1260
 QY 1261 AAGCATGAAGATATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
 DB 1261 AAGCATGAAGATATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
 QY 1321 AATGCTGATATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
 DB 1321 AATGCTGATATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
 QY 1381 CTTGACACAG 1440
 DB 1381 CTTGACACAG 1440
 QY 1441 AAACAGATGCAAAATATCTCTTCTGAAAACAGCAACCAAGAGAGAGAGAG 1500
 DB 1441 AAACAGATGCAAAATATCTCTTCTGAAAACAGCAACCAAGAGAGAGAGAG 1500

QY 1501 TCAG 1560
 DB 1501 TCAG 1560
 QY 1561 TTTATGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
 DB 1561 TTTATGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
 QY 1621 CTGACATAGGAG 1680
 DB 1621 CTGACATAGGAG 1680
 QY 1681 AGAACACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
 DB 1681 AGAACACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
 QY 1741 CAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
 DB 1741 CAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1800
 QY 1801 ATTCTGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
 DB 1801 ATTCTGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860
 QY 1861 CTTAGTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
 DB 1861 CTTAGTTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920
 QY 1921 GCCATGCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
 DB 1921 GCCATGCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1980
 QY 1981 AAAAAAAAAAAAAAAAAA 2000
 DB 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 5
 US-09-443-686-374
 : Sequence 374, Application US/09443686
 : GENERAL INFORMATION:
 : APPLICANT: Xu, Jiangchun
 : APPLICANT: Dillon, David C.
 : APPLICANT: Mitcham, Jennifer L.
 : APPLICANT: Harlocker, Susan Louise
 : APPLICANT: Jiang Yuxi
 : APPLICANT: Reed, Steven G.
 : APPLICANT: Kalos, Michael
 : APPLICANT: Fanger, Gary
 : APPLICANT: Retter, Mark
 : APPLICANT: Solk, John
 : APPLICANT: Day, Craly
 : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
 : FILE REFERENCE: 210121.427C9A
 : CURRENT APPLICATION NUMBER: US/09/443,686
 : NUMBER OF SEQ ID NOS: 551
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO 374
 : LENGTH: 2000
 : TYPE: DNA
 : ORGANISM: Homo sapien
 US-09-443-686-374

Query Match 100.0%; Score 2000; DB 18; Length 2000;
 Best Local Similarity 100.0%; Pred. No. 2,6e-271;
 Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGCTGTTAGAGTTGATTCATGCGGCTGCTGAGAGAGAGAGAGAGAGAG 60
 DB 1 ATGCTGTTAGAGTTGATTCATGCGGCTGCTGAGAGAGAGAGAGAGAGAG 60

QY	61	AGAGAGCAAGTGGGCAAGTGGTGGCCCTTACCTTCCCTGGTGGAGGAGCGGGCAAG	120
Db	61	AGAGAGCAAGTGGGCAAGTGGTGGCCCTTACCTTCCCTGGTGGAGGAGCGGGCAAG	120
QY	121	AGCAAGGTGGGCACTTCTGGAGACACGACGACTGCTGATGAAGACACTCAGAGCAAG	180
Db	121	AGCAAGGTGGGCACTTCTGGAGACACGACGACTGCTGATGAAGACACTCAGAGCAAG	180
QY	181	ATGGGCAAGTGGTGGCCCACTGCTTCCCTGCTGACAGGGGAGTGGCAAGACAGTGG	240
Db	181	ATGGGCAAGTGGTGGCCCACTGCTTCCCTGCTGACAGGGGAGTGGCAAGACAGTGG	240
QY	241	GGGGCTTCTGGAGACACGACGACGCTGCTGATGAAGACACTCAGGAACAAGTGGGGCAAG	300
Db	241	GGGGCTTCTGGAGACACGACGACGCTGCTGATGAAGACACTCAGGAACAAGTGGGGCAAG	300
QY	301	TGGTGGTGGCACTGCTTCCCTGCTGTCACAGGGGGAGCGGCAAGCAAGGTGGAGCCTTGG	360
Db	301	TGGTGGTGGCACTGCTTCCCTGCTGTCACAGGGGGAGCGGCAAGCAAGGTGGAGCCTTGG	360
QY	361	GGAGACTACGATACAGTGGCTTTCATGAAGCCAGGTACCAAGTCCGTGGAGAGATGTG	420
Db	361	GGAGACTACGATACAGTGGCTTTCATGAAGCCAGGTACCAAGTCCGTGGAGAGATGTG	420
QY	421	GACAAAGTCCACAGACACTGCTGGTGGGTAAAGTCCACAGAAAGATCTCATGCTCATG	480
Db	421	GACAAAGTCCACAGACACTGCTGGTGGGTAAAGTCCACAGAAAGATCTCATGCTCATG	480
QY	481	CTCAGGACACTACGCTGTAACAGAAAGGACAGCAAAAAGAGATCGCTACATGTGGCC	540
Db	481	CTCAGGACACTACGCTGTAACAGAAAGGACAGCAAAAAGAGATCGCTACATGTGGCC	540
QY	541	TCTGCCANTGGGAATTCAGAAAGTAAACCTCTGCTGGACAGACGATGTCAACTTAAT	600
Db	541	TCTGCCANTGGGAATTCAGAAAGTAAACCTCTGCTGGACAGACGATGTCAACTTAAT	600
QY	601	GTCCTTGACAAACAAAAGAGACGCTGATTAAGGGCCGTACAAATGCCAGGAACAATGA	660
Db	601	GTCCTTGACAAACAAAAGAGACGCTGATTAAGGGCCGTACAAATGCCAGGAACAATGA	660
QY	661	TGTGCGTTAATGTGTGGCAACATGTGCACCTGATCCAAATATTCCAGATGATGGAAT	720
Db	661	TGTGCGTTAATGTGTGGCAACATGTGCACCTGATCCAAATATTCCAGATGATGGAAT	720
QY	721	ACCACTGTGACATACGCTATCTTAATGAAGATTAATTAATGATGATGATGATGATGATGAT	780
Db	721	ACCACTGTGACATACGCTATCTTAATGAAGATTAATTAATGATGATGATGATGATGATGAT	780
QY	781	TATGTCGTCTATATCGAATATCAAAAAACAAGCATGGCTCACACCCTGTACTTGGTGA	840
Db	781	TATGTCGTCTATATCGAATATCAAAAAACAAGCATGGCTCACACCCTGTACTTGGTGA	840
QY	841	CATGAGCAAAAACAGCAAGTCTGTAATTTTAATCAAAAAAGCGAATTTAATCA	900
Db	841	CATGAGCAAAAACAGCAAGTCTGTAATTTTAATCAAAAAAGCGAATTTAATCA	900
QY	901	CTGGATAGATATGGAAGACTGCTCATACTTGTGTATGTTGTGGATCAGCAAGTATA	960
Db	901	CTGGATAGATATGGAAGACTGCTCATACTTGTGTATGTTGTGGATCAGCAAGTATA	960
QY	961	GTCAGCCTTACTTGGAGCAAAATATGATGTATCTTCAAGATCTATCTGGACAGAG	1020
Db	961	GTCAGCCTTACTTGGAGCAAAATATGATGTATCTTCAAGATCTATCTGGACAGAG	1020
QY	1021	GCCAGAGATGCTGTTTCTATCATCATCATCATCATCATCATCATCATCATCATCATCAT	1080
Db	1021	GCCAGAGATGCTGTTTCTATCATCATCATCATCATCATCATCATCATCATCATCATCAT	1080
QY	1081	AAAGAAAAACAGATGCTAAAAATCTTCTGAAACACGAAATCCAGCAACACTTAAG	1140
Db	1081	AAAGAAAAACAGATGCTAAAAATCTTCTGAAACACGAAATCCAGCAACACTTAAG	1140
QY	1141	CTGACATCAGAGAGAGTCCAAAGGTTCCAAAGGCAAGTGAATATGCCAGCCAGAGAA	1200

Db	1141	CTGCAATCAGAGGAAGGCTCCAAAGCTTCAAAAGCAGTGAATAATAGCCAGCAGAGAAA	1200
QY	1201	ATGTCTCAGAACCAGAAATTAAGATGGTGATAGAGAGTTGAAGAAATGAG	1260
Db	1201	ATGTCTCAAGAACCCAGAAATTAAGATGGTGATAGAGAGTTGAAGAAATGAG	1260
QY	1261	AAGCATTAAGTAAATATATGTGGGATATACATGAAGAAACCTGAAATAGTGTACATGCTGGC	1320
Db	1261	AAGCATTAAGTAAATATATGTGGGATATACATGAAGAAACCTGAAATAGTGTACATGCTGGC	1320
QY	1321	AATGCTGATATATGATTAATCTCTCAAGAGAGCAGAAACCTGAAATATCAGCAATTT	1380
Db	1321	AATGCTGATATATGATTAATCTCTCAAGAGAGCAGAAACCTGAAATATCAGCAATTT	1380
QY	1381	CCTGACACAGAAAGTGAAGATATCACAGAAATTTGGCAATTAAGTTCTGACTACAAAGAA	1440
Db	1381	CCTGACACAGAAAGTGAAGATATCACAGAAATTTGGCAATTAAGTTCTGACTACAAAGAA	1440
QY	1441	AAACAGATGCCAAATATCTTTGTGAAAAACGCAACCCGAAACAGACTTAAAGCTGACA	1500
Db	1441	AAACAGATGCCAAATATCTTTGTGAAAAACGCAACCCGAAACAGACTTAAAGCTGACA	1500
QY	1501	TCACAGAGAGAGTCCACAAAGGCTTGAGGGCAGTGAATAATGGCCACCAGACTAGAAAT	1560
Db	1501	TCACAGAGAGAGTCCACAAAGGCTTGAGGGCAGTGAATAATGGCCACCAGACTAGAAAT	1560
QY	1561	TTTATGGCTATCGAAGAAATGAAGAAAGCAACGGAATCTCATGTGCGATTTCCACAGAAAC	1620
Db	1561	TTTATGGCTATCGAAGAAATGAAGAAAGCAACGGAATCTCATGTGCGATTTCCACAGAAAC	1620
QY	1621	CTGCACTAATGGTGGCCACTGCTGGCAATGGTATGATGATTAATTCCTCCAAAGAAAGAC	1680
Db	1621	CTGCACTAATGGTGGCCACTGCTGGCAATGGTATGATGATTAATTCCTCCAAAGAAAGAC	1680
QY	1681	AGAACACCTGAAAGCCGCAATTTCTCGACACTGAGAAATGAAGAGATACACAGTACGAA	1740
Db	1681	AGAACACCTGAAAGCCGCAATTTCTCGACACTGAGAAATGAAGAGATACACAGTACGAA	1740
QY	1741	CAAAATGATACTCAGAAAGCAATTTTGTGAAAGACAGAACACTGGAATATATACACAGATGAG	1800
Db	1741	CAAAATGATACTCAGAAAGCAATTTTGTGAAAGACAGAACACTGGAATATATACACAGATGAG	1800
QY	1801	ATTCTGATTCATGAAGAAAGCCAGATRGAAGTGTGAAAAAATGAATTTCTGAGCTTTCT	1860
Db	1801	ATTCTGATTCATGAAGAAAGCCAGATRGAAGTGTGAAAAAATGAATTTCTGAGCTTTCT	1860
QY	1861	CTTGAGTGTAAAGAAAGAAAGAACATCTTGCAATGAATAATGATACGTGGGGAAGAAATTT	1920
Db	1861	CTTGAGTGTAAAGAAAGAAAGAACATCTTGCAATGAATAATGATACGTGGGGAAGAAATTT	1920
QY	1921	GCCATGCTGAAGACTGAGACTAGACACAAATGAACATCAGAGCCAGCTAAAAAATGAAAAA	1980
Db	1921	GCCATGCTGAAGACTGAGACTAGACACAAATGAACATCAGAGCCAGCTAAAAAATGAAAAA	1980
QY	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
RESULT 6			
US-09-483-672A-374			
Sequence 374, Application US/09483672A			
GENERAL INFORMATION:			
APPLICANT: Xu, Jiangchun			
APPLICANT: Dillon, Davin C.			
APPLICANT: Mitcham, Jennifer L.			
APPLICANT: Harlocker, Susan Louise			
APPLICANT: Jiang Yugu			
APPLICANT: Reed, Steven G.			
APPLICANT: Kalos, Michael D.			
APPLICANT: Fanger, Gary R.			
APPLICANT: Retter, Marc W.			


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: APPLICANT: Solk, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Wang, Aljun
: APPLICANT: Meagher, Madeleine
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.42711C11
: CURRENT APPLICATION NUMBER: US/09/483,672A
: CURRENT FILING DATE: 2000-01-14
: NUMBER OF SEQ ID NOS: 590
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 374
: LENGTH: 2000
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-483-672A-374

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Query Match	100.0%;	Score 2000;	DB 18;	Length 2000;
Best Local Similarity	100.0%;	Pred. No. 2.6e-271;		
Matches 2000; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	ATGGGAGTGTGGGATTGATTCATCCGCGGCGCTTCCTGTGGAAGAACCATTTGGCTC	60
Dp	1	ATGGTGGTGGGATTGATTCATCCGCGGCTTCCTGTGGAAGAACCATTTGGCTC	60
QY	61	AGGAGCAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGCAAGGAGACGGCAAG	120
Dp	61	AGGAGCAAGATGGGCAAGTGTGCTGCGCTTCCCTGCTGCAAGGAGACGGCAAG	120
QY	121	AGCAACGTGGGCACTTCTGGAGACCAGACGACTCTCTATTGAAGACTTCAGAGCAG	180
Dp	121	AGCAACGTGGGCACTTCTGGAGACCAGACGACTCTCTATTGAAGACTTCAGAGCAG	180
QY	181	ATGGGCAAGTGGTCCGCGCACTGCTTCCCGCTGCAAGGGGGATGGCCAGACCACTG	240
Dp	181	ATGGGCAAGTGGTCCGCGCACTGCTTCCCGCTGCAAGGGGGATGGCCAGACCACTG	240
QY	241	GGCGCTTCTGGAGACCAGACGACTCTGCTATGAAGCACTCAGAGCAAGATGGGCAAG	300
Dp	241	GGCGCTTCTGGAGACCAGACGACTCTGCTATGAAGCACTCAGAGCAAGATGGGCAAG	300
QY	301	TGTGTCTGCCACTGCTTCCCTGCTGCCAAGGGGCAAGGCAAGTGGCGCTTGG	360
Dp	301	TGTGTCTGCCACTGCTTCCCTGCTGCCAAGGGGCAAGGCAAGTGGCGCTTGG	360
QY	361	GGAGACTCAGATTGACAGTGCCTTATGGAGCCAGTACACAGCGCTGGAGAAGATCTG	420
Dp	361	GGAGACTCAGATTGACAGTGCCTTATGGAGCCAGTACACAGCTCGTGAGAAGATCTG	420
QY	421	GACAAGCTCCACAGAGCTGCGTGGTGGGGTAAAGTCTCCCAAGAAAGATCTCATCTG	480
Dp	421	GACAAGCTCCACAGAGCTGCGTGGTGGGGTAAAGTCTCCCAAGAAAGATCTCATCTG	480
QY	481	CTCAGGGACACTGACGCTGACACAAAGACAAAGCAAGGAGACTGCTTACATCTGCGC	540
Dp	481	CTCAGGGACACTGACGCTGACACAAAGACAAAGCAAGGAGACTGCTTACATCTGCGC	540
QY	541	TCTGCAATGGGAATTCAGAGTGTGTAAGAACTCCCTGCTGGACAGACATGTCACCTAAT	600
Dp	541	TCTGCAATGGGAATTCAGAGTGTGTAAGAACTCCCTGCTGGACAGACATGTCACCTAAT	600
QY	601	GTCCTTGACAAACAAAAGAGACAGCTCTGTATAAAGCCGTACACATCCACGAGAAGATGA	660
Dp	601	GTCCTTGACAAACAAAAGAGAGACAGCTCTGTATAAAGCCGTACACATCCACGAGAAGATGA	660
QY	661	TGTGCGTTAATGTGTGCTGGAACATGSCACTGATCCAAATATTCCAGATGAGTATGAAAT	720
Dp	661	TGTGCGTTAATGTGTGCTGGAACATGSCACTGATCCAAATATTCCAGATGAGTATGAAAT	720
QY	721	ACCACTCTGCACCTACGCTATCTATAATGAAGATATAATTAATGGCCAAAGCACTGCTTA	780
Dp	721	ACCACTCTGCACCTACGCTATCTATAATGAAGATATAATTAATGGCCAAAGCACTGCTTA	780

QY	781	TATGTCGTGATATCGAATCAAAAAAACAAGCATGGGCTCAGACACCTGTCTTGCGTGA	840
DB	781	TATGTCGTGATATCGAATCAAAAAAACAAGCATGGGCTCAGACACCTGTCTTGCGTGA	840
QY	841	CATGAGCAAAAAACAGCAAGCTGTGAATTTTATATCAAGAAAAAGCAATTTAAATGCA	900
DB	841	CATGAGCAAAAAACAGCAAGCTGTGAATTTTATATCAAGAAAAAGCAATTTAAATGCA	900
QY	901	CTGGATATGATATGGAAGAGACTGCTCTCATCTGCTGATATGTTGGATACAGCAAGTATA	960
DB	901	CTGGATATGATATGGAAGAGACTGCTCTCATCTGCTGATATGTTGGATACAGCAAGTATA	960
QY	961	GTCGACCTTCTACTGTGAGCAAAATATGTGATGTCTCTCAAGATCTATCTGACAGACG	1020
DB	961	GTCGACCTTCTACTGTGAGCAAAATATGTGATGTCTCTCAAGATCTATCTGACAGACG	1020
QY	1021	GCCAGAGATATGCTGTTTCTAGTCATCATATTTTGGCAATCTTTCTGACTAC	1080
DB	1021	GCCAGAGATATGCTGTTTCTAGTCATCATATTTTGGCAATCTTTCTGACTAC	1080
QY	1081	AAAGAAAAACAGATGCTTAAAAATCTCTGTGAAAAACAGCAATCCAGAACAGACTTAAG	1140
DB	1081	AAAGAAAAACAGATGCTTAAAAATCTCTGTGAAAAACAGCAATCCAGAACAGACTTAAG	1140
QY	1141	CTGACATCAGAGAGAGTCACAAAGGTTCAAAAGCATGAAATATGCGACCGACAGAAA	1200
DB	1141	CTGACATCAGAGAGAGTCACAAAGGTTCAAAAGCATGAAATATGCGACCGACAGAAA	1200
QY	1201	ATGTCCTCAAGACACAGAAATTAATTAAGATGGGTAGAGAGCTTGAAAGAAATAGAG	1260
DB	1201	ATGTCCTCAAGACACAGAAATTAATTAAGATGGGTAGAGAGCTTGAAAGAAATAGAG	1260
QY	1261	AAGCATGAAAGTAAATATGTGGGATTTACTAGAAAACCTGACTAATGATGTCACCTGGC	1320
DB	1261	AAGCATGAAAGTAAATATGTGGGATTTACTAGAAAACCTGACTAATGATGTCACCTGGC	1320
QY	1321	AATGCTGATATATGATTTAATTTCTTCAAGAGAGAGAGAGCAACCTGGAAATTCAGCAATTT	1380
DB	1321	AATGCTGATATATGATTTAATTTCTTCAAGAGAGAGAGAGCAACCTGGAAATTCAGCAATTT	1380
QY	1381	CCTGACAACGAAAGTGAAGATATCTACAGAAATTTGCGAATTTAGTTTCTGACTACAAAGAA	1440
DB	1381	CCTGACAACGAAAGTGAAGATATCTACAGAAATTTGCGAATTTAGTTTCTGACTACAAAGAA	1440
QY	1441	AAACAGATGCCAAATATCTTTCTGAAAAACGACACCCAGAACAAAGACTTAAAGCTGACA	1500
DB	1441	AAACAGATGCCAAATATCTTTCTGAAAAACGACACCCAGAACAAAGACTTAAAGCTGACA	1500
QY	1501	TCAGAGGAAGGTACACAAAGGCTTTGAGGGAGTGAATAAGGCCACGACAGACTAGAAAT	1560
DB	1501	TCAGAGGAAGGTACACAAAGGCTTTGAGGGAGTGAATAAGGCCACGACAGACTAGAAAT	1560
QY	1561	TTTATGGCTATCGAAGAAATGAAGAAAGCAGCAAGTACTCATGTGCGATTTCCACAGAAAAAC	1620
DB	1561	TTTATGGCTATCGAAGAAATGAAGAAAGCAGCAAGTACTCATGTGCGATTTCCACAGAAAAAC	1620
QY	1621	CTGACTAATGCTGCCAATCTGTCGCAATGGTGAATGGAATTAATCTCTCAAGAAAGAGGC	1680
DB	1621	CTGACTAATGCTGCCAATCTGTCGCAATGGTGAATGGAATTAATCTCTCAAGAAAGAGGC	1680
QY	1681	AGAACACCTTGAAAGCCAGCAATTTCTGTGACACTGAGAAATGAAGAGACTATCACAGTGACGAA	1740
DB	1681	AGAACACCTTGAAAGCCAGCAATTTCTGTGACACTGAGAAATGAAGAGACTATCACAGTGACGAA	1740
QY	1741	CAAAATGATATCTCGAAGCAATTTTGTGAAAGAACAGAACACTGCGAATTTATCACAGATGAG	1800
DB	1741	CAAAATGATATCTCGAAGCAATTTTGTGAAAGAACAGAACACTGCGAATTTATCACAGATGAG	1800
QY	1801	ATTCGTATTCATGAAGAAAGCAGATAGAAAGGTTGAAAAAATGAATTTGAGAGTTTCT	1860
DB	1801	ATTCGTATTCATGAAGAAAGCAGATAGAAAGGTTGAAAAAATGAATTTGAGAGTTTCT	1860

QY	1861	CTTAGTGGTGAAGAAAGAAAAAGCATTCTTCATGAAATAATGTACTGTTGGGGAGAAATTT	1920
Db	1861	CTTAGTGGTGAAGAAAGAAAAAGCATTCTTCATGAAATAATGTACTGTTGGGGAGAAATTT	1920
QY	1921	GCCATGCTGAAGACTGGAGCTAGACACATCAATGAACATCAGAGCCAGCTATAAAAAAAAAAAAA	1980
Db	1921	GCCATGCTGAAGACTGGAGCTAGACACATCAATGAACATCAGAGCCAGCTATAAAAAAAAAAAAA	1980
QY	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAAA 2000	

RESULT 7
US-09-534-825A-302

; Sequence 302, Application US/09534825A

APPLICANT: Frudakis, Tony N.

APPLICANT: SMITH, JOHN M.
APPLICANT: Reed, Steven G

APPLICANT: Misher, Lynda

APPLICANT: Dillon, Davin C

TREATMENT AND DIAGNOSIS OF BREAST COMPOSITIONS AND METHODS FOR THE

FILE REFERENCE: 210121.419C/
CURRENT APPLICATION NUMBER: IIS/009/534 825A

; CURRENT FILING DATE: 2000-03-23
 ; REVISED OR CTD TO: 0000-00-00

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; SOFTWARE: FastSEQ for windows Version 3.0

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; LENGTH: 2

TYPE: DNA
ORGANISM: Homo sapien

US-09-534-825A-302

Query Match	100.0%	Score 2000;	DB 2000;	Length 2000;
Best Local Similarity	100.0%	Pred. No. 2.6e-271;		
Matches 2000; Conservative	0;	Mismatches	0;	Gaps 0;

QY	1	ATATGGTTAGAGTTGATTTCACATCCGCGGCTGCCTCTTCTGTGAAGAAGCATTTGGTCTC	60
Db	1	ATGGTGGTTAGAGTTGATTTCACATCCGCGGCTGCCTCTTCTGTGAAGAAGCATTTGGTCTC	60
QY	61	AGGAGCAAGATGGGCAAGTGGTGGCTCCCGTGGTTCCCTCGTGCAGGAGAGCGGCAAG	120
Db	61	AGGAGCAAGATGGGCAAGTGGTGGCTCCCGTGGTTCCCTCGTGCAGGAGAGCGGCAAG	120
QY	121	AGCAACTGGGGCACTTCTGGAGACACACGACGACTCTGCTATATGAAGCACTCAGGAGCAAG	180
Db	121	AGCAACTGGGGCACTTCTGGAGACACACGACGACTCTGCTATATGAAGCACTCAGGAGCAAG	180
QY	181	ATGGGGCAAGTGTGTGCGCGCACTGCTTCCCTCGTGCAGGAGGAGTGTGCNAAGCAACGTG	240
Db	181	ATGGGGCAAGTGTGTGCGCGCACTGCTTCCCTCGTGCAGGAGGAGTGTGCNAAGCAACGTG	240
QY	241	GCGCGCTTCTGGAGACACACGACGACTCTGCTATATGAAGCACTCAGGAGCAAGTGGGCAAG	300
Db	241	GCGCGCTTCTGGAGACACACGACGACTCTGCTATATGAAGCACTCAGGAGCAAGTGGGCAAG	300
QY	301	TGGTGTGTGACACTGCTTCCCTGCTGCAGGAGGAGCGGCAAGAGCAAGTGGGCGCTTGG	360
Db	301	TGGTGTGTGACACTGCTTCCCTGCTGCAGGAGGAGCGGCAAGAGCAAGTGGGCGCTTGG	360
QY	361	GGAACATACGATGACATGCTGCCCTTCATGGAAGCCAGGTATCCACAGTCCGTTGGAGAGATGTG	420
Db	361	GGAACATACGATGACATGCTGCCCTTCATGGAAGCCAGGTATCCACAGTCCGTTGGAGAGATGTG	420
QY	421	GACAAAGTCCACAGAGCTGCTGGTGGGGAAGATCCCGAAGAAAGATTCATCTGCATG	480
Db	421	GACAAAGTCCACAGAGCTGCTGGTGGGGAAGATTCAGTGGGGAAGATTCATCTGCATG	480
QY	481	CTCAGGACACTGACGTGAACAGAAAGACAGACAAAGAGAGACTGCTCTACATCTGCC	540

Db	481	CTCAGGGCACTGACGTGAACCAAGAGAGCAACCAAAAGAGACGTGCTTACATCTGGCC	540
QY	541	TCTGCAATGGGAATTCAGAAGTAGTAAAACCTCGTCTGGACAGACATGTCACCTTAT	600
Db	541	TCTGCCAATGGGAATTCAGAAGTAGTAAAACCTCGTCTGGACAGACATGTCACCTTAT	600
QY	601	GTCCTTGACAACAAAAGAGAGACGCTGTGATAAAGGGCGTACATGCCCAGGAAGATGA	660
Db	601	GTCCTTGACAACAAAAGAGAGACGCTGTGATAAAGGGCGTACATGCCCAGGAAGATGA	660
QY	661	TGTGCTTAATGTTGCTGGAAACATGGCAGCTATCCAAATATTCCAGATGAGATGGAAT	720
Db	661	TGTGCTTAATGTTGCTGGAAACATGGCAGCTATCCAAATATTCCAGATGAGATGGAAT	720
QY	721	ACCACTGCACTACGGCTATCTTAATGAAGATTAATTAATGGCCAAAGCACTGCTCTTA	780
Db	721	ACCACTGCACTACGGCTATCTTAATGAAGATTAATTAATGGCCAAAGCACTGCTCTTA	780
QY	781	TATGCTGTGATATCGAATCAAAAACAAAGCATGGCCTCACACCACTGTTACTTGCTGA	840
Db	781	TATGCTGTGATATCGAATCAAAAACAAAGCATGGCCTCACACCACTGTTACTTGCTGA	840
QY	841	CATGAGCAAAAACGCAAGTCGTGAATTTTATATACAAAAAGCGAATTTAAATGCA	900
Db	841	CATGAGCAAAAACGCAAGTCGTGAATTTTATATACAAAAAGCGAATTTAAATGCA	900
QY	901	CTGGATACATATGGAAGAGACTGGCTCATCTGCTGATGTTGGATCAGCAGATGA	960
Db	901	CTGGATACATATGGAAGAGACTGGCTCATCTGCTGATGTTGGATCAGCAGATGA	960
QY	961	GTCACCTTCTACTTTGAGCAAAATATTGATGATCTTCTCAAGATCTATCTGGACAGC	1020
Db	961	GTCACCTTCTACTTTGAGCAAAATATTGATGATCTTCTCAAGATCTATCTGGACAGC	1020
QY	1021	GCCAGAGATATGCTGTTTCTAGTCATCATATCTAATTTGCCAGTTACTTTCTGACTAC	1080
Db	1021	GCCAGAGATATGCTGTTTCTAGTCATCATATCTAATTTGCCAGTTACTTTCTGACTAC	1080
QY	1081	AAAGAAAAACGATGCTAAAAATCTCTTGAAAACAGCAATCCAGAAACACACTTAAG	1140
Db	1081	AAAGAAAAACGATGCTAAAAATCTCTTGAAAACAGCAATCCAGAAACACACTTAAG	1140
QY	1141	CTGACATCAGAGGAAGATCAAAAAGGTTCAAAAGGCAGTGAATAATAGCCAGCCAGAAA	1200
Db	1141	CTGACATCAGAGGAAGATCAAAAAGGTTCAAAAGGCAGTGAATAATAGCCAGCCAGAAA	1200
QY	1201	ATGTCACAAGACCAGAATTAATTAAGATGCTGATAGAGAGTTGAGAGAAATGAAG	1260
Db	1201	ATGTCACAAGACCAGAATTAATTAAGATGCTGATAGAGAGTTGAGAGAAATGAAG	1260
QY	1261	AAGCATGAAGATTAATTAATGCGGTTTCTTGAAAACCTGCACTAATAGGTGTCACCTGGC	1320
Db	1261	AAGCATGAAGATTAATTAATGCGGTTTCTTGAAAACCTGCACTAATAGGTGTCACCTGGC	1320
QY	1321	AATGCTGATTAATGATTAATTTCTTCAAAAGGAGAGCAGAACCTGAAAAATCAGCAATTT	1380
Db	1321	AATGCTGATTAATGATTAATTTCTTCAAAAGGAGAGCAGAACCTGAAAAATCAGCAATTT	1380
QY	1381	CCTGACAACGAAGTGAAGAGTATCACGAAATTTGGCAATTAAGTTTCTGACTACAAAGA	1440
Db	1381	CCTGACAACGAAGTGAAGAGTATCACGAAATTTGGCAATTAAGTTTCTGACTACAAAGA	1440
QY	1441	AAACGATGCCAAAATCTCTTGAAAACAGCAACCCAGAACAAAGACTTAAGCTGACA	1500
Db	1441	AAACGATGCCAAAATCTCTTGAAAACAGCAACCCAGAACAAAGACTTAAGCTGACA	1500
QY	1501	TCAGAGGAAGATCAACAAGGCTTGAGAGGCAATGGAATAATGGCCAGCAGAGCTAGAAT	1560
Db	1501	TCAGAGGAAGATCAACAAGGCTTGAGAGGCAATGGAATAATGGCCAGCAGAGCTAGAAT	1560
QY	1561	TTTATGGCTATCGAAGAAATGAGAGACACGGAAGTACTCATGTGGGATTTCCACAAAC	1620
Db	1561	TTTATGGCTATCGAAGAAATGAGAGACACGGAAGTACTCATGTGGGATTTCCACAAAC	1620

Db 1561 TTATGGCTATCGAAGAAATGAAGACAGGAAAGTACTCATGTGCGATTCCAGAAAC 1620
QY 1521 CTGACTAATGGTGGCTGCTGGCAATGGTATGATGGATTAAATCTCCAGAGAAAGC 1680
Db 1621 CTGACTAATGGTGGCTGCTGGCAATGGTATGATGGATTAAATCTCCAGAGAAAGC 1680
QY 1681 AGAACCCTGAAACCGACCAATTTCTGACACTGAGAAATGAAGATACACAGTACGAA 1740
Db 1681 AGAACCCTGAAACCGACCAATTTCTGACACTGAGAAATGAAGATACACAGTACGAA 1740
QY 1741 CAAATATATCTCGAAGCAATTTTGTGAAGACAGAACTGGAAATTTACAGATAG 1800
Db 1741 CAAATATATCTCGAAGCAATTTTGTGAAGACAGAACTGGAAATTTACAGATAG 1800
QY 1801 ATTCTGATTCATGAAGAAAGCAGATAGAACTGTTGAAAAATGAATTCAGACTTCT 1860
Db 1801 ATTCTGATTCATGAAGAAAGCAGATAGAACTGTTGAAAAATGAATTCAGACTTCT 1860
QY 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGATGAAATAGTACGTTGGGAAAGAAAT 1920
Db 1861 CTTAGTGTGAAGAAAGAAAGACATCTTGATGAAATAGTACGTTGGGAAAGAAAT 1920
QY 1921 GCCATGCTAAGACTGAGCTAGACACATGACATGACAGCCAGCTAAAAAAGAAAA 1980
Db 1921 GCCATGCTAAGACTGAGCTAGACACATGACATGACAGCCAGCTAAAAAAGAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 8
US-09-536-857-374
Sequence 3/4, Application US/09536857
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuyui
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Scolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42712C12
CURRENT APPLICATION NUMBER: US/09/536.857
NUMBER OF SEQ ID NOS: 592
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 374
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-536-857-374

Query Match 100.0% Score 2000: DB 20: Length 2000:
Best Local Similarity 100.0% Pred. No. 2,6e-271:
Matches 2000: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 ATGGTGGTGAAGTTGATTCATGCCGCTGCTCTTCTGTGAAGAACCATTTGTCTC 60
Db 1 ATGGTGGTGAAGTTGATTCATGCCGCTGCTCTTCTGTGAAGAACCATTTGTCTC 60
QY 61 AGAGCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGACGAGGAGCGGCAAG 120
Db 61 AGAGCAAGATGGGCAAGTGTGCTGCTTCCCTGCTGACGAGGAGCGGCAAG 120
QY 121 AGCAAGTGGCACTTCTGAGACCCAGAGACTCTCTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAAGTGGCACTTCTGAGACCCAGAGACTCTCTATGAAGACACTCAGAGCAAG 180

Db 121 AGCAAGTGGCACTTCTGAGACCCAGAGACTCTCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGCAAGTGGTCCGCGCACTGCTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
Db 181 ATGGCAAGTGGTCCGCGCACTGCTCCCTGCTGCAAGGGGAGTGGCAAGCAAGCTG 240
QY 241 GGGCTTCTGAGAACACGACGACTCTGCTATGAAGACCTTCAGAACAGATGGCAAG 300
Db 241 GGGCTTCTGAGAACACGACGACTCTGCTATGAAGACCTTCAGAACAGATGGCAAG 300
QY 301 TGGTGGTCCGCACTGCTCCCTGCTGCAAGGGGAGGCGGCAAGCAAGTGGGCTTGG 360
Db 301 TGGTGGTCCGCACTGCTCCCTGCTGCAAGGGGAGGCGGCAAGCAAGTGGGCTTGG 360
QY 361 GGAGACTACGATGACAGTGCCTTCATGAGGCCAGGTACACGTCCTGGAGAAAGATCTG 420
Db 361 GGAGACTACGATGACAGTGCCTTCATGAGGCCAGGTACACGTCCTGGAGAAAGATCTG 420
QY 421 GACAAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
Db 421 GACAAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATGTCATG 480
QY 481 CTCAGGGGACATGACGTGAACAAGAGACAAAGAAAGAGAGACTGCTCATCTGGCC 540
Db 481 CTCAGGGGACATGACGTGAACAAGAGACAAAGAAAGAGAGACTGCTCATCTGGCC 540
QY 541 TCTGCAATGGGAATTCAGAAAGTGAATAAACTCTGCTGACAGACGATGCAACTTAAT 600
Db 541 TCTGCAATGGGAATTCAGAAAGTGAATAAACTCTGCTGACAGACGATGCAACTTAAT 600
QY 601 GTCTTGAACAACAAAGAGAGACGCTGTATTAAGCCGCTACAAATGCGAGGAAGTGA 660
Db 601 GTCTTGAACAACAAAGAGAGACGCTGTATTAAGCCGCTACAAATGCGAGGAAGTGA 660
QY 661 TGTGCGTTAATGTTGCTGGAACATGGCAGCTGATTAAGGCGCTACAAATGCGAGGAAGTGA 720
Db 661 TGTGCGTTAATGTTGCTGGAACATGGCAGCTGATTAAGGCGCTACAAATGCGAGGAAGTGA 720
QY 721 ACCACTGCACTACGCTATCTATTAATGAAGATTAATGAGCAAGCAAGCTGCTTA 780
Db 721 ACCACTGCACTACGCTATCTATTAATGAAGATTAATGAGCAAGCAAGCTGCTTA 780
QY 781 TATGCTGCTGATATGCAATCAAAAAACAGCATGCGCTCACACCAGTCTACTGGTGA 840
Db 781 TATGCTGCTGATATGCAATCAAAAAACAGCATGCGCTCACACCAGTCTACTGGTGA 840
QY 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGGAATTTAAATGA 900
Db 841 CATGAGCAAAAAACAGCAAGTGTGAATTTTATCAAGAAAAAGGAATTTAAATGA 900
QY 901 CTGATGATATGGAAGAGACTGCTCTCATACTTCTGATGTTGGATCGACAAATATA 960
Db 901 CTGATGATATGGAAGAGACTGCTCTCATACTTCTGATGTTGGATCGACAAATATA 960
QY 961 GTACGCTTCTACTTGAACAAATATTGATGATCTTCTCAAGATCTATCTGACAGAG 1020
Db 961 GTACGCTTCTACTTGAACAAATATTGATGATCTTCTCAAGATCTATCTGACAGAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGATTAATTTGCCATTTCTGACATAC 1080
Db 1021 GCCAGAGATATGCTGTTTCTAGTCATCATCATGATTAATTTGCCATTTCTGACATAC 1080
QY 1081 AAAGAAAAACAGATGCTAAATCTCTTCTGAAAAACGACATCCAGAACAGACTTAAG 1140
Db 1081 AAAGAAAAACAGATGCTAAATCTCTTCTGAAAAACGACATCCAGAACAGACTTAAG 1140
QY 1141 CTGACATCAAGAGAAAGTCAAAAGGTTCAAAAGCAAGTGAATTAAGCCAGAGAA 1200
Db 1141 CTGACATCAAGAGAAAGTCAAAAGGTTCAAAAGCAAGTGAATTAAGCCAGAGAA 1200
QY 1201 ATGCTCAAGAACCCAGAAATTAATTAAGATGCTATGACAGGTGAAGAAATGAAG 1260
Db 1201 ATGCTCAAGAACCCAGAAATTAATTAAGATGCTATGACAGGTGAAGAAATGAAG 1260

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OY 1261 AAGCATGAAGTAATATGTGGATTACTAGAAAACCTGACATAAGTGTGCTGCGC 1320
      |||||||
Db 1261 AAGCATGAAGTAATATGTGGATTACTAGAAAACCTGACATAAGTGTGCTGCGC 1320
OY 1321 AATGTGATTAATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
      |||||||
Db 1321 AATGTGATTAATGATTAATTCCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
OY 1381 CCTGACACGAAAGTGAAGATATCAGAGATTTGCGAATTAAGTTCTGACTACAAAGAA 1440
      |||||||
Db 1381 CCTGACACGAAAGTGAAGATATCAGAGATTTGCGAATTAAGTTCTGACTACAAAGAA 1440
OY 1441 AAACAGATGCCAAATATCTTCTGAAAACAGAACCCAGAACAAACTTAAGCTGACAA 1500
      |||||||
Db 1441 AAACAGATGCCAAATATCTTCTGAAAACAGAACCCAGAACAAACTTAAGCTGACAA 1500
OY 1501 TCAGAGAGAGAGTCAACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCAGAGCTAGAAAAT 1560
      |||||||
Db 1501 TCAGAGAGAGAGTCAACAAAGGCTTGAGGGCAGTGAATAATGGCCAGCAGAGCTAGAAAAT 1560
OY 1561 TTTATGTGCTATCGAAGAAATGAAGAACGACGAGATCTCATGTGCGAATTCGCAAGAAAC 1620
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Db 1561 TTTATGTGCTATCGAAGAAATGAAGAACGACGAGATCTCATGTGCGAATTCGCAAGAAAC 1620
OY 1621 CTGACTAATGTGCTGCTGCTGCAATGGATGATGATGATTAATTCCTCCAGAGAGAGC 1680
      |||||||
Db 1621 CTGACTAATGTGCTGCTGCTGCAATGGATGATGATGATTAATTCCTCCAGAGAGAGC 1680
OY 1681 AGAAGACCTGAAGAGCCAGCAATTTCTGACACTGAGATGAAGAGATATCAGATGACGAA 1740
      |||||||
Db 1681 AGAAGACCTGAAGAGCCAGCAATTTCTGACACTGAGATGAAGAGATATCAGATGACGAA 1740
OY 1741 CAAATATGATCTCAGAGCAATTTTGTGAAGAACAGAACACTGGAATTTACACGATGAG 1800
      |||||||
Db 1741 CAAATATGATCTCAGAGCAATTTTGTGAAGAACAGAACACTGGAATTTACACGATGAG 1800
OY 1801 ATTCTGATTCATGAAGAAAGCAGATAGAAGTGTGAAAATAATGAATTCGTGCTTCT 1860
      |||||||
Db 1801 ATTCTGATTCATGAAGAAAGCAGATAGAAGTGTGAAAATAATGAATTCGTGCTTCT 1860
OY 1861 CTTAGTTGTGAAGAAAGAAAGACATCTTGCAATGAATAATGATGCTTGGGGAGAAAT 1920
      |||||||
Db 1861 CTTAGTTGTGAAGAAAGAAAGACATCTTGCAATGAATAATGATGCTTGGGGAGAAAT 1920
OY 1921 GCCATGCTTAAGACTGAGCTAGACCAATGAAGCAATCAGAGCCAGCTTAAGAAAAA 1980
      |||||||
Db 1921 GCCATGCTTAAGACTGAGCTAGACCAATGAAGCAATCAGAGCCAGCTTAAGAAAAA 1980
OY 1981 AAAAAAAAAAAAAAAAAA 2000
      |||||||
Db 1981 AAAAAAAAAAAAAAAAAA 2000

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RESULT 9
US-09-568-100A-374
; Sequence 374, Application US/09568100A
; GENERAL INFORMATION:

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; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedryck, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun

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; APPLICANT: Skelky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; TITLE REFERENCE: 210121.42713C13
; CURRENT APPLICATION NUMBER: US/09/568,100A
; NUMBER OF SEQ ID NOS: 701
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-568-100A-374

Query Match      100.0%; Score 2000; DB 22; Length 2000;
Best Local Similarity 100.0%; Pred. No. 2.6e-271;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AATGTGTTGAGGTGATTCATGCGGCGTCCCTTCTGTGAAGAGCCATTGGCTC 60
      |||||||
Db 1 AATGTGTTGAGGTGATTCATGCGGCGTCCCTTCTGTGAAGAGCCATTGGCTC 60
OY 61 AGGAGCAAGATGGGCAAGTGTGCTGCGTCCCTGCTGCAAGGAGAGCGCAAG 120
      |||||||
Db 61 AGGAGCAAGATGGGCAAGTGTGCTGCGTCCCTGCTGCAAGGAGAGCGCAAG 120
OY 121 AGCAAGCTGGGCACTTCTGAGACACAGACGATCTGCTATGAAGACCTCAGAGCAAG 180
      |||||||
Db 121 AGCAAGCTGGGCACTTCTGAGACACAGACGATCTGCTATGAAGACCTCAGAGCAAG 180
OY 181 ATGGGCAAGTGTGCGGCGCACTGCTCCCTGCTGAGAGGGGAGTGGCAAGCTG 240
      |||||||
Db 181 ATGGGCAAGTGTGCGGCGCACTGCTCCCTGCTGAGAGGGGAGTGGCAAGCTG 240
OY 241 GGGGCTTGTGAGACACGACGACTGCTATGAAGACACTCAGAAACAAGATGGCAAG 300
      |||||||
Db 241 GGGGCTTGTGAGACACGACGACTGCTATGAAGACACTCAGAAACAAGATGGCAAG 300
OY 301 TGGTGTGCTGCTGCTTCCCTGCTGAGGGGAGGGGCAAGAGTGGGCGCTTGG 360
      |||||||
Db 301 TGGTGTGCTGCTGCTTCCCTGCTGAGGGGAGGGGCAAGAGTGGGCGCTTGG 360
OY 361 GGAGACTAGATGACAGTGTGCTGATGAGACCCAGGTACCACTGCTGAGAAATCTG 420
      |||||||
Db 361 GGAGACTAGATGACAGTGTGCTGATGAGACCCAGGTACCACTGCTGAGAAATCTG 420
OY 421 GACAACTCCACAGAGCTGCTGCTGAGGAGTAAAGTCCCGAGAAAGATCTCATG 480
      |||||||
Db 421 GACAACTCCACAGAGCTGCTGCTGAGGAGTAAAGTCCCGAGAAAGATCTCATG 480
OY 481 CTCAGGAGACACTAGCTGAACAAAGAGACAAAGAGAGAGAGAGAGAGAGAGAG 540
      |||||||
Db 481 CTCAGGAGACACTAGCTGAACAAAGAGAGACAAAGAGAGAGAGAGAGAGAGAG 540
OY 541 TCTGCCAATGGGAATTCAGAAAGTAAAGTCTGCTGAGAGAGAGATCAACTTAAT 600
      |||||||
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAAGTCTGCTGAGAGAGAGATCAACTTAAT 600
OY 601 GTCCCTTGACAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
      |||||||
Db 601 GTCCCTTGACAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
OY 661 TGTGCGTTAATGTGCTGGAACATGGCAGTCACTCAAAATTAATCAATGATGTGAAT 720
      |||||||
Db 661 TGTGCGTTAATGTGCTGGAACATGGCAGTCACTCAAAATTAATCAATGATGTGAAT 720
OY 721 ACCACTCTGACATACCTATCTAATGAAGATTAATTAATGAGCAAGAGAGAGAG 780
      |||||||
Db 721 ACCACTCTGACATACCTATCTAATGAAGATTAATTAATGAGCAAGAGAGAGAG 780
OY 781 TATGAGTGTGATATGCAATCAAAAGCAAGCAATGGCTCAGACCACTGTTACTTGTG 840
      |||||||
Db 781 TATGAGTGTGATATGCAATCAAAAGCAAGCAATGGCTCAGACCACTGTTACTTGTG 840

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QY 841 CATGAGCAAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTTAAATCA 900
DB 841 CATGAGCAAAAAACAGCAAGTGTGAAATTTTAAATCAAGAAAAAGCAATTTTAAATCA 900
QY 901 CTGATAGATATGGAAGAGCTGCTCTCATCTTGTGTATGTGTGGATCAAGAGTATA 960
DB 901 CTGATAGATATGGAAGAGCTGCTCTCATCTTGTGTATGTGTGGATCAAGAGTATA 960
QY 961 GTCAGCCCTTCTACTTGAGCAAAATATTGATGTATCTTCAAGATCTATGAGCAGAG 1020
DB 961 GTCAGCCCTTCTACTTGAGCAAAATATTGATGTATCTTCAAGATCTATGAGCAGAG 1020
QY 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTATTTGCCATTTCTTCTGACATAC 1080
DB 1021 GCCAGAGATATGCTGTTTCTAGTCATCATGTATTTGCCATTTCTTCTGACATAC 1080
QY 1081 AAAAGAAAAAGATGCTTAAAAATCTCTTCTGAAAAACAGCAATCCAGAAACAGCTTAAAG 1140
DB 1081 AAAAGAAAAAGATGCTTAAAAATCTCTTCTGAAAAACAGCAATCCAGAAACAGCTTAAAG 1140
QY 1141 CTGACATCAGAGAGAGTCAAAAGTTTCAAAAGGCTGAAAAATAGCCAGCAGAGAAA 1200
DB 1141 CTGACATCAGAGAGAGTCAAAAGTTTCAAAAGGCTGAAAAATAGCCAGCAGAGAAA 1200
QY 1201 ATGTCCTAAGAACAGAAATTAATTAAGGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
DB 1201 ATGTCCTAAGAACAGAAATTAATTAAGGATGCTGATAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAATTAATTAATGTTGGATTAATAGAAAACTGACTAATGCTGCTGCTG 1320
DB 1261 AAGCATGAAATTAATTAATGTTGGATTAATAGAAAACTGACTAATGCTGCTGCTG 1320
QY 1321 AATGCTGATTAATGATTAATCTCTCAAAAGAGAGCAGAACCTGAAATCAGCAATTT 1380
DB 1321 AATGCTGATTAATGATTAATCTCTCAAAAGAGAGCAGAACCTGAAATCAGCAATTT 1380
QY 1381 CCTGACAAAGAAAGTGAAGAGTATCACAGAAATTTGCCAATTAATGTTCTGACTACAAAGAA 1440
DB 1381 CCTGACAAAGAAAGTGAAGAGTATCACAGAAATTTGCCAATTAATGTTCTGACTACAAAGAA 1440
QY 1441 AAAAGATGCCAAATTAATCTTCTGAAAAACAGCAACCCAGAAACAGCTTAAAGTCA 1500
DB 1441 AAAAGATGCCAAATTAATCTTCTGAAAAACAGCAACCCAGAAACAGCTTAAAGTCA 1500
QY 1501 TCAGAGAGAGAGTCAAAAGGCTGAGGAGCTGAAAAATGGCCAGCCAGCTGAAAT 1560
DB 1501 TCAGAGAGAGAGTCAAAAGGCTGAGGAGCTGAAAAATGGCCAGCCAGCTGAAAT 1560
QY 1561 TTTATGCTATCGAAGAAATGAAGAGCAGAAAGTACTCATGTCGATTTCCAGAAAAAC 1620
DB 1561 TTTATGCTATCGAAGAAATGAAGAGCAGAAAGTACTCATGTCGATTTCCAGAAAAAC 1620
QY 1621 CTGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
DB 1621 CTGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
QY 1681 AGAAGACCTGAAAGCCAGCAATTTCTGAGACCTGAGATGAAGATCAAGAGAGAA 1740
DB 1681 AGAAGACCTGAAAGCCAGCAATTTCTGAGACCTGAGATGAAGATCAAGAGAGAA 1740
QY 1741 CAAAATGATCTCAGAAAGCAATTTTGTGAAGACAGAACTGGAATTAACAGATAG 1800
DB 1741 CAAAATGATCTCAGAAAGCAATTTTGTGAAGACAGAACTGGAATTAACAGATAG 1800
QY 1801 ATTCTGATCTCAGAAAGCAATTAAGAGTGTGTAAGAAATTAATTTCTGAGCTTTCT 1860
DB 1801 ATTCTGATCTCAGAAAGCAATTAAGAGTGTGTAAGAAATTAATTTCTGAGCTTTCT 1860
QY 1861 CTTAGTGTGAAGAAAGAAAGACATCTGATGAAAAATAGTACGTTGGGGAAGAAAT 1920
DB 1861 CTTAGTGTGAAGAAAGAAAGACATCTGATGAAAAATAGTACGTTGGGGAAGAAAT 1920

QY 1921 GCCATGCTAAGACCTGGAGCTAGACAAATGAATACTAGAGCCAGCTTAAAAA 1980
DB 1921 GCCATGCTAAGACCTGGAGCTAGACAAATGAATACTAGAGCCAGCTTAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAA 2000
DB 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 10
US-09-577-505B-302
Sequence 302, Application US/09577505B
GENERAL INFORMATION:
APPLICANT: Fridakis, Tony N.
APPLICANT: Reed, Steven G.
APPLICANT: Smith, John M.
APPLICANT: Misher, Linda E.
APPLICANT: Dillon, Davin C.
APPLICANT: Retter, Marc W.
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITILE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.419C8
CURRENT APPLICATION NUMBER: US/09/577.505B
CURRENT FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 324
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 302
LENGTH: 2000
TYPE: DNA
ORGANISM: Homo sapien
US-09-577-505B-302

Query Match 100.0%; Score 2000; DB 22; Length 2000;
Best Local Similarity 100.0%; Pred. No. 2,6e-271;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGTGTTGAGTGTGATTCCATGCGCGCTGCTCTCTGTAAGAAACCATTTGGTCTC 60
DB 1 ATGGGTGTTGAGTGTGATTCCATGCGCGCTGCTCTCTGTAAGAAACCATTTGGTCTC 60
QY 61 AGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTTCCCTCTGCAAGGAGAGCGGCAAG 120
DB 61 AGAGCAAGATGGGCAAGTGTGCTGCCGTTGCTTCCCTCTGCAAGGAGAGCGGCAAG 120
QY 121 AGCAAGCTGGGCACTTCTGAGAGCAGACGACACTCTGTATGAAGACACTGAGAGCAAG 180
DB 121 AGCAAGCTGGGCACTTCTGAGAGCAGACGACACTCTGTATGAAGACACTGAGAGCAAG 180
QY 181 ATGGGCAAGTGGTGGCGGCACTGCTCCCTGCTGTCAGAGGGGAGTGGCAAGACGCTG 240
DB 181 ATGGGCAAGTGGTGGCGGCACTGCTCCCTGCTGTCAGAGGGGAGTGGCAAGACGCTG 240
QY 241 GGGCTTCTGAGAGACACAGAGACTTGTCTATGAAGACACTGAGAACATGGGCAAG 300
DB 241 GGGCTTCTGAGAGACACAGAGACTTGTCTATGAAGACACTGAGAACATGGGCAAG 300
QY 301 TGTGTCTGCCACTGCTTCCCTGCTGTCAGAGGGGAGGCAAGACCAAGTGGGCTTGG 360
DB 301 TGTGTCTGCCACTGCTTCCCTGCTGTCAGAGGGGAGGCAAGACCAAGTGGGCTTGG 360
QY 361 GGAAGCTAGATGACAGAGTGGCTTTCATGAGAGCCAGAGTCCAGTCCGCGGAGAGATCTG 420
DB 361 GGAAGCTAGATGACAGAGTGGCTTTCATGAGAGCCAGAGTCCAGTCCGCGGAGAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGTTGAGTAAAGTCCCAAGAAAGATCTCATCTCATG 480
DB 421 GACAAGCTCCACAGAGCTGCTGTTGAGTAAAGTCCCAAGAAAGATCTCATCTCATG 480
QY 481 CTCAGGGACACTGACGTGAACAAAGAGCAAGCAAGAAAGAGACTGCTCTCATCTGCCC 540
DB 481 CTCAGGGACACTGACGTGAACAAAGAGCAAGCAAGAAAGAGACTGCTCTCATCTGCCC 540

Qy	541	TCGCCAATGGGAATTCAGAAAGTAAAGAAAACCTCGCTGGACAGACAGATGTCAACTTAAT	600
Db	541	TTCTCCCATGTGGAAATTCAGAAAGTAAAGTAAACCTCGCTGGACAGACAGATGTCAACTTAAT	600
Qy	601	GTCCTTGACAACAAAAGAGAGACGCTCTGATAAAGGCCGTGTCAATGGCAGAGAAGATGA	660
Db	601	GTCCTTGACAACAAAAGAGAGACGCTCTGATAAAGGCCGTGTCAATGGCAGAGAAGATGA	660
Qy	661	TGTCCGTTAATGTTTGGTGGAAACATGGCACTGATCCAAATATTCCAGATGAGTATGGAAT	720
Db	661	TGTCCGTTAATGTTTGGTGGAAACATGGCACTGATCCAAATATTCCAGATGAGTATGGAAT	720
Qy	721	ACCACTGTGCACACGCTATCTATATGGAAGATTAATTTATGGCCAAAGCACTGCTCTTA	780
Db	721	ACCACTGTGCACACGCTATCTATATGGAAGATTAATTTATGGCCAAAGCACTGCTCTTA	780
Qy	781	TATGGTGTCTATATTCGATATCAAAAAACAAGCATGGCCTCACACCACTGTACTTGGTGTA	840
Db	781	TATGGTGTCTATATTCGATATCAAAAAACAAGCATGGCCTCACACCACTGTACTTGGTGTA	840
Qy	841	CATGAGCAAAAACAGCAAGCTGTGAATTTTAATTCAGAAAAAGCCAAATTTAAATGCA	900
Db	841	CATGAGCAAAAACAGCAAGCTGTGAATTTTAATTCAGAAAAAGCCAAATTTAAATGCA	900
Qy	901	CTGGATATGATGGAAGAGACGTGCTCATCATCTTGTGTATGTTGTGATCAGCAAGTATA	960
Db	901	CTGGATATGATGGAAGAGACGTGCTCATCATCTTGTGTATGTTGTGATCAGCAAGTATA	960
Qy	961	GTCAGCCTTACTACTTGAGCAAAATATTGATGTATCTTCAAGATCTATCTGGACAGCG	1020
Db	961	GTCAGCCTTACTACTTGAGCAAAATATTGATGTATCTTCAAGATCTATCTGGACAGCG	1020
Qy	1021	GCCAGAGATATGCTGTTTCTAGTCTCATCATCATATGTATGGCAGTATCTTCTGCAGATC	1080
Db	1021	GCCAGAGATATGCTGTTTCTAGTCTCATCATCATATGTATGGCAGTATCTTCTGCAGATC	1080
Qy	1081	AAAGAAAACAGATGCTAAAAATCTCTTGTAACACGCAATCCAGAACAGACTTAAAG	1140
Db	1081	AAAGAAAACAGATGCTAAAAATCTCTTGTAACACGCAATCCAGAACAGACTTAAAG	1140
Qy	1141	CTGACATCAGAGAAAGGTACACAAGGTTCAAGGACAGTGAANAATAGCAGCAGAGAAA	1200
Db	1141	CTGACATCAGAGAAAGGTACACAAGGTTCAAGGACAGTGAANAATAGCAGCAGAGAAA	1200
Qy	1201	ATGTCTCAAGAACCGAATTAATAAAGATGGTATAGAGAGTTGAAGAAAGAAATGAG	1260
Db	1201	ATGTCTCAAGAACCGAATTAATAAAGATGGTATAGAGAGTTGAAGAAAGAAATGAG	1260
Qy	1261	AAAGATGAAGTAAATATATGTGGATTAATAGAAAACCTGACTAATGGTGTCACTGTGCGC	1320
Db	1261	AAAGATGAAGTAAATATATGTGGATTAATAGAAAACCTGACTAATGGTGTCACTGTGCGC	1320
Qy	1321	AATGGTATATGATTAATTTCTCTCAAGAGAGACAGAAACCTGGAANAATCAGCAATTT	1380
Db	1321	AATGGTATATGATTAATTTCTCTCAAGAGAGACAGAAACCTGGAANAATCAGCAATTT	1380
Qy	1381	CCTGACACAGAAAGTGAAGGTATCCACAGATTTGCGAATTAGTTTGTGACTACAAAGAA	1440
Db	1381	CCTGACACAGAAAGTGAAGGTATCCACAGATTTGCGAATTAGTTTGTGACTACAAAGAA	1440
Qy	1441	AAAGAGATGCCAAAATCTCTTCTGAAAAACAGAACCCGGAACAAGACTTAAAGCTGCA	1500
Db	1441	AAAGAGATGCCAAAATCTCTTCTGAAAAACAGAACCCGGAACAAGACTTAAAGCTGCA	1500
Qy	1501	TCAGAGAAAGTTCACAAAAGCTTTGAGGGCAGTGAANAATGGCCAGCCAGAGCTGANAAT	1560
Db	1501	TCAGAGAAAGTTCACAAAAGCTTTGAGGGCAGTGAANAATGGCCAGCCAGAGCTGANAAT	1560
Qy	1561	TTTATGGCTATCGAAGAAATGAAGAAGCAACGGAAGTACTCATGTGGGATTCGCCAGAAAC	1620
Db	1561	TTTATGGCTATCGAAGAAATGAAGAAGCAACGGAAGTACTCATGTGGGATTCGCCAGAAAC	1620

Oy	1621	CTACTATATGGGCGACACGTCGGCGCAATGTGTATGTATGATTAATTCCTCCGAAGAAAGGC	1680
Db	1621	CTGACTAATATGGGCGACACGTCGGCGCAATGTGTATGTATTAATTCCTCCGAAGAAAGGC	1680
Oy	1681	AGAACACCTGAAAGCGACACAATTTCTCTACACTGTGAATGGAAGAGTATCACAGTACCAA	1740
Db	1681	AGAACACCTGAAAGCGACACAATTTCTCTACACTGTGAATGGAAGAGTATCACAGTACCAA	1740
Oy	1741	CAAAATGATPACTCAGAACCAATTTTGTGAAGAACAGAACTCTGAAATATTCACAGATGAG	1800
Db	1741	CAAAATGATPACTCAGAACCAATTTTGTGAAGAACAGAACTCTGAAATATTCACAGATGAG	1800
Oy	1801	ATTCGATTCATGAAAGAAAGCAGATPAGAAGGCTTGAAAAATGAATTCGAGCTTCT	1860
Db	1801	ATTCGATTCATGAAAGAAAGCAGATPAGAAGGCTTGAAAAATGAATTCGAGCTTCT	1860
Oy	1861	CTTAGTTGTAGAAAGAAAGACATCTTGCGATGAAATAGTACGCTTCGGGAACAAATT	1920
Db	1861	CTTAGTTGTAGAAAGAAAGACATCTTGCGATGAAATAGTACGCTTCGGGAACAAATT	1920
Oy	1921	GCCATGCTPAGACTGGAGCTAGACACAATGAACAATCAGAGCCAGCTTAAAAAAAAAAAAA	1980
Db	1921	GCCATGCTPAGACTGGAGCTAGACACAATGAACAATCAGAGCCAGCTTAAAAAAAAAAAAA	1980
Oy	1981	AAAAAAAAAAAAAAAAAAAAA 2000	
Db	1981	AAAAAAAAAAAAAAAAAAAAA 2000	

RESULT 11
US-09-590-583-302
; Sequence 302, Application US/09590583

```

1 GENERAL INFORMATION:
2 APPLICANT: Fridakis, Tony N.
3 APPLICANT: Reed, Steven G.
4 APPLICANT: Smith, John M.
5 APPLICANT: Misher, Linda E.
6 APPLICANT: Dillon, David C.
7 APPLICANT: Reltter, Marc W.
8 APPLICANT: Wang, Aljun
9 APPLICANT: Skelky, Yasir A.W.
10 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
11 FILE REFERENCE: 210121.419C9
12 CURRENT APPLICATION NUMBER: US/09/590.583
13 CURRENT FILING DATE: 2000-06-08
14 NUMBER OF SEQ ID NOS: 324
15 SOFTWARE: FastSeq for Windows Version 3.0
16 SEQ ID NO 302
17 LENGTH: 2000
18 TYPE: DNA
19 ORGANISM: Homo sapien
20 US-09-590-583-302

```

Query Match	100.0%;	Score 2000;	DB 22;	Length 2000;
Best Local Similarity	100.0%;	Pred. No. 2.6e-271;		
Matches 2000; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	ATTGTGTTAAGGTTAATTCACAGCCGGTGCCTCTCTGTGAAACAACCACTTTGGTCTC	60
Db	1	ATGTGTGTTAAGGTGTGATTCACATGCCGGTGCCTCTCTGTGTAAACAACCACTTTGGTCTC <th>60</th>	60
QY	61	AGAGACAAGATGGGCAAGTGGTGCCTGCCTTCCCTGCTGCAGGAGAACGGCAAG <th>120</th>	120
Db	61	AGGAGCAAGATGGGCAAGTGGTGCCTGCCTTCCCTGCTGCAGGAGAACGGCGCAAG <th>120</th>	120
QY	121	AGCAACGTGGGCACTTCTGTGAGACCAACGACACTGTGATGAAACACTCAGGAGCAAG <th>180</th>	180
Db	121	AGCAACGTGGGCACTTCTGTGAGACCAACGACACTGTGATGAAACACTCAGGAGCAAG <th>180</th>	180
QY	181	ATGGGCAAGTGTGTCCGCCCACTGCTTCCCTGCTGCAGGGGAGTGTGCAAGACAAGCTG <th>240</th>	240
Db	181	ATGGGCAAGTGTGTCCGCCCACTGCTTCCCTGCTGCAGGGGAGTGTGCAAGACAAGCTG <th>240</th>	240

QY 241 GGCCTTCTGGAGACACGAGACTCTGCTATGAAAGACACTCAGGAACAGATGGCAG 300
| | | | |
Db 241 GGCCTTCTGGAGACACGAGACTCTGCTATGAAAGACACTCAGGAACAGATGGCAG 300
QY 301 TGGTGTGCCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGAGTGGCGCTTGG 360
| | | | |
Db 301 TGGTGTGCCACTGCTTCCCTGCTGCAAGGGGAGCGGCAAGAGAGTGGCGCTTGG 360
QY 361 GGAGACTACGATGACAGTGGCTTATGAGAGCCAGGTACCAAGTCCGATGGAGAGATCTG 420
| | | | |
Db 361 GGAGACTACGATGACAGTGGCTTATGAGAGCCAGGTACCAAGTCCGATGGAGAGATCTG 420
QY 421 GACAAGCTCCACAGAGTGGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATGCTATG 480
| | | | |
Db 421 GACAAGCTCCACAGAGTGGCTGGTGGGTAAAGTCCCAAGAAAGATCTCATGCTATG 480
QY 481 CTCAGGACACTGACGTGAACAGAGACAGCAAGAGAGACTGCTTACATCTGGCC 540
| | | | |
Db 481 CTCAGGACACTGACGTGAACAGAGACAGCAAGAGAGACTGCTTACATCTGGCC 540
QY 541 TCTGCCAATGGAAATGAGAAGTAAAGTCTGCTGGGACAGAGATGCACTTAAT 600
| | | | |
Db 541 TCTGCCAATGGAAATGAGAAGTAAAGTCTGCTGGGACAGAGATGCACTTAAT 600
QY 601 GTCTTGACAAACAAAAGAGAGACAGCTCTGATAAAGCCGTAACATGCGAGAGATGAA 660
| | | | |
Db 601 GTCTTGACAAACAAAAGAGAGACAGCTCTGATAAAGCCGTAACATGCGAGAGATGAA 660
QY 661 TGTGCGCTTAATGTGTGCTGGAACATGCGCATGATCCAAATATTCAGATGATGGAAT 720
| | | | |
Db 661 TGTGCGCTTAATGTGTGCTGGAACATGCGCATGATCCAAATATTCAGATGATGGAAT 720
QY 721 ACCACTGTGACACTGCTATCTATATGAAGATAAATTAATGGCAAGACCTGCTTA 780
| | | | |
Db 721 ACCACTGTGACACTGCTATCTATATGAAGATAAATTAATGGCAAGACCTGCTTA 780
QY 781 TATGCTGCTGATATGCAATCAAAAACAGCATGGCTCACACACAGTTCCTGGTGA 840
| | | | |
Db 781 TATGCTGCTGATATGCAATCAAAAACAGCATGGCTCACACACAGTTCCTGGTGA 840
QY 841 CATGAGCAAAAACAGCAAGTCTGTAATTTTATCAAGAAAAAGCAATTTTAAATGCA 900
| | | | |
Db 841 CATGAGCAAAAACAGCAAGTCTGTAATTTTATCAAGAAAAAGCAATTTTAAATGCA 900
QY 901 CTGATATGATATGGAAGAGACTGCTCTCATCTTCTGATGTTGGATGCAAGTATA 960
| | | | |
Db 901 CTGATATGATATGGAAGAGACTGCTCTCATCTTCTGATGTTGGATGCAAGTATA 960
QY 961 GTGAGCCTTCTACTTGAAGCAAAATATTTGATGATCTTCTCAAGATCTATCTGACAGC 1020
| | | | |
Db 961 GTGAGCCTTCTACTTGAAGCAAAATATTTGATGATCTTCTCAAGATCTATCTGACAGC 1020
QY 1021 GCCAGAGAGTATGCTGTTTCTAGTCATCATCTATTTTCCAGTACTTCTGACTAC 1080
| | | | |
Db 1021 GCCAGAGAGTATGCTGTTTCTAGTCATCATCTATTTTCCAGTACTTCTGACTAC 1080
QY 1081 AAAGAAAAAGAGATGCTAAATAATCTTCTGAAAACAGCAATCCAGAACAAAGATTAAAG 1140
| | | | |
Db 1081 AAAGAAAAAGAGATGCTAAATAATCTTCTGAAAACAGCAATCCAGAACAAAGATTAAAG 1140
QY 1141 CTGACATCAGAGAGAGAGTACAAAAGGTTCAAGGAGTGAATAATAGCCAGAGAAA 1200
| | | | |
Db 1141 CTGACATCAGAGAGAGAGTACAAAAGGTTCAAGGAGTGAATAATAGCCAGAGAAA 1200
QY 1201 ATGTCTTAAGAACAGAAATTAATAGAGTGTGATAGAGAGTTGAAGAAATGAAG 1260
| | | | |
Db 1201 ATGTCTTAAGAACAGAAATTAATAGAGTGTGATAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGCATGAAGTAAATATGTGGGATTAAGTAAAGCTGACTATAGTGTGACAGTGGC 1320
| | | | |
Db 1261 AAGCATGAAGTAAATATGTGGGATTAAGTAAAGCTGACTATAGTGTGACAGTGGC 1320

QY 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGACAGACACTGAATAATCAGCAATTT 1380
| | | | |
Db 1321 AATGTGATTAATGATTAATTTCTCAAGAGAGAGACAGACACTGAATAATCAGCAATTT 1380
QY 1381 CCTGACACAGAAATGAAAGATATCAGAGATTTTCCGAATTAATTTTCTGATACAAAGAA 1440
| | | | |
Db 1381 CCTGACACAGAAATGAAAGATATCAGAGATTTTCCGAATTAATTTTCTGATACAAAGAA 1440
QY 1441 AAACAGATGCCAAATATCTCTTGAATAACAGCAACCCAGAACAAAGATTAAAGCTGACA 1500
| | | | |
Db 1441 AAACAGATGCCAAATATCTCTTGAATAACAGCAACCCAGAACAAAGATTAAAGCTGACA 1500
QY 1501 TCAGAGAGAGAGTACAAAAGGCTTGAGGCGAGTGAATAATGGCCAGCAGAGCTGAAAAT 1560
| | | | |
Db 1501 TCAGAGAGAGAGTACAAAAGGCTTGAGGCGAGTGAATAATGGCCAGCAGAGCTGAAAAT 1560
QY 1561 TTTATGGCTATCGAAGAAATGAAGACAGCAGGAAAGTACTCATGTGCGATTTCCAGAAAAC 1620
| | | | |
Db 1561 TTTATGGCTATCGAAGAAATGAAGACAGCAGGAAAGTACTCATGTGCGAATTTCCAGAAAAC 1620
QY 1621 CTGACTAATGCTGGCCTGCTGCGCAATGATGATGATGATTAATTTCTCCAAAGAGAGC 1680
| | | | |
Db 1621 CTGACTAATGCTGGCCTGCTGCGCAATGATGATGATGATTAATTTCTCCAAAGAGAGC 1680
QY 1681 AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAGATACACAGTGACGAA 1740
| | | | |
Db 1681 AGAACACCTGAAAGCCAGCAATTTCTGACACTGAGATGAAGATACACAGTGACGAA 1740
QY 1741 CAAATGATATCTCGAAGCAATTTTGTGAAGAAACAGAACTGGAAATTTACAGATGAG 1800
| | | | |
Db 1741 CAAATGATATCTCGAAGCAATTTTGTGAAGAAACAGAACTGGAAATTTACAGATGAG 1800
QY 1801 ATTCTGATTCATGAAGAAACAGATAGAAAGTGTGAAAAATGAATTTCTGACCTTCT 1860
| | | | |
Db 1801 ATTCTGATTCATGAAGAAACAGATAGAAAGTGTGAAAAATGAATTTCTGACCTTCT 1860
QY 1861 CTTAGTTGTAAAGAAAGAAAGACATCTTGATGAAATTAATGATGAGGGAAGAAAT 1920
| | | | |
Db 1861 CTTAGTTGTAAAGAAAGAAAGACATCTTGATGAAATTAATGATGAGGGAAGAAAT 1920
QY 1921 GCCATGCTAAGACGTGAGCTGAGACAAATGAACATCAGAGCCAGTAAAAAGAAAA 1980
| | | | |
Db 1921 GCCATGCTAAGACGTGAGCTGAGACAAATGAACATCAGAGCCAGTAAAAAGAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
| | | | |
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

RESULT 12
US-09-593-793A-374
; Sequence 374, Application US/09593793A
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Helper, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.42715C15


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QY 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 13
US-09-605-783A-374
; Sequence 374, Application US/09605783A
; GENERAL INFORMATION:
; APPLICANT: Xu, Jlangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,783A
; NUMBER OF FILING DATE: 2000-06-27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-605-783A-374

Query Match 100.0%; Score 2000; DB 23; Length 2000;
Best Local Similarity 100.0%; Pred. No. 2,6e-271;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGTGTTAGGTTGATTCATGCGCGCTGCTCTTCTGTGAAGAACCATTTGCTC 60
Db 1 ATGGGTGTTAGGTTGATTCATGCGCGCTGCTCTTCTGTGAAGAACCATTTGCTC 60

QY 61 AGGAGCAAGATGGGCAAGTGTGTGCTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAGT 120
Db 61 AGGAGCAAGATGGGCAAGTGTGTGCTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAGT 120

QY 121 AGCAACTGGGCACTTGTGAGACACAGACGACTCTGTATGAAGACACTCAGAGCAAG 180
Db 121 AGCAACTGGGCACTTGTGAGACACAGACGACTCTGTATGAAGACACTCAGAGCAAG 180

QY 181 ATGGGCAAGTGTGTGCGCCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAGT 240
Db 181 ATGGGCAAGTGTGTGCGCCCACTGCTTCCCTGCTGCAAGGGGAGTGGCAAGCAGT 240

QY 241 GGGCTTCTGAGAGCCAGACGACTGTGTATGAAGACACTCAGAGCAAGATGGGCAAG 300
Db 241 GGGCTTCTGAGAGCCAGACGACTGTGTATGAAGACACTCAGAGCAAGATGGGCAAG 300

QY 301 TGGTGTGCGCACTGCTTCCCTGCTGCAAGGGGAGCGCAAGAGCAAGTGGGCGCTTG 360
Db 301 TGGTGTGCGCACTGCTTCCCTGCTGCAAGGGGAGCGCAAGAGCAAGTGGGCGCTTG 360

QY 361 GGAAGTACAGATGACAGTGTCTTATGAGAGCCAGATACAGTCCGTGGAGAGATCTG 420
Db 361 GGAAGTACAGATGACAGTGTCTTATGAGAGCCAGATACAGTCCGTGGAGAGATCTG 420

QY 421 GACAAGCTCCACAGAGCTGCTGTGGGTAAAGTCCCAAGAAAGATCTCATGTGTCATG 480
Db 421 GACAAGCTCCACAGAGCTGCTGTGGGTAAAGTCCCAAGAAAGATCTCATGTGTCATG 480
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Db 421 GACAAGCTCCACAGAGCTGCTGTGGGTAAAGTCCCAAGAAAGATCTCATGTGTCATG 480
QY 481 CTCAGGACACTGACGTGAACAAGAGACAGCAAGAGAGAGACTGCTTACATCTGCGC 540
Db 481 CTCAGGACACTGACGTGAACAAGAGAGACAGCAAGAGAGAGACTGCTTACATCTGCGC 540

QY 541 TCTGCCAATGGGAATTGAGAAGTAGTAAACCTCCTGCTGAGACAGACATGCTCAAT 600
Db 541 TCTGCCAATGGGAATTGAGAAGTAGTAAACCTCCTGCTGAGACAGACATGCTCAAT 600

QY 601 GTCTTACACAACAAAAGAGACAGCTGTGATAAAGCCCTACAAATCCACGGAAGTAA 660
Db 601 GTCTTACACAACAAAAGAGACAGCTGTGATAAAGCCCTACAAATCCACGGAAGTAA 660

QY 661 TGTGCGTTAATGTTGTCGAACATGGCAGCATGATCCAAATATTCAGATGATGGAAT 720
Db 661 TGTGCGTTAATGTTGTCGAACATGGCAGCATGATCCAAATATTCAGATGATGGAAT 720

QY 721 ACCACTGCACTAGCTAGCTATCTATATGAAGATTAATTAATGAGCAAGCACTGCTTA 780
Db 721 ACCACTGCACTAGCTAGCTATCTATATGAAGATTAATTAATGAGCAAGCACTGCTTA 780

QY 781 TATGTGCTGATATCCGAATCAAAAAACAGCATGCGCTCACACACTGTACTGTGCTA 840
Db 781 TATGTGCTGATATCCGAATCAAAAAACAGCATGCGCTCACACACTGTACTGTGCTA 840

QY 841 CATGAGCAAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900
Db 841 CATGAGCAAAAACAGCAAGTCGTGAATTTTATCAAGAAAAAGCAATTTAAATGCA 900

QY 901 CTGGATGATATGGAAGAGAGTCTCTCATCTTGTGATGTTGTGATCAGCAAGTATA 960
Db 901 CTGGATGATATGGAAGAGAGTCTCTCATCTTGTGATGTTGTGATCAGCAAGTATA 960

QY 961 GTGAGCTTCTACTGAGCAAAATATGATGTATCTTCAAGATCTATGTCAGACAGAG 1020
Db 961 GTGAGCTTCTACTGAGCAAAATATGATGTATCTTCAAGATCTATGTCAGACAGAG 1020

QY 1021 GCCAGAGATATGCTGTTTGTAGTATCATCATGATTAATTTGCCAGTACTTTCGATAC 1080
Db 1021 GCCAGAGATATGCTGTTTGTAGTATCATCATGATTAATTTGCCAGTACTTTCGATAC 1080

QY 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGTGAANAACAGCAATCCAGAACACTTAAG 1140
Db 1081 AAAGAAAAACAGATGCTAAAAATCTCTTGTGAANAACAGCAATCCAGAACACTTAAG 1140

QY 1141 CTGACATCAGAGAGAGTCAAAAAGGTTCAAGGGCAGTAAATAGCCAGCAAGAAA 1200
Db 1141 CTGACATCAGAGAGAGTCAAAAAGGTTCAAGGGCAGTAAATAGCCAGCAAGAAA 1200

QY 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGTGATAGAGGTTGAAGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGTGATAGAGGTTGAAGAAGAAATGAAG 1260

QY 1261 AAGCATGAAGATTAATTAATGCGGATTAAGTAAAGCTGTGATGCTGCTGCGC 1320
Db 1261 AAGCATGAAGATTAATTAATGCGGATTAAGTAAAGCTGTGATGCTGCTGCGC 1320

QY 1321 AATGTGATTAATGATTAATTCCTCAAGAGAGAGCAAGACACTGAAATTCAGCAATTT 1380
Db 1321 AATGTGATTAATGATTAATTCCTCAAGAGAGAGCAAGACACTGAAATTCAGCAATTT 1380

QY 1381 CTTGACAAAGAAAGTAAAGTATACAGAGATTTGCAATTTAGTTTCTGACTCAAGAA 1440
Db 1381 CTTGACAAAGAAAGTAAAGTATACAGAGATTTGCAATTTAGTTTCTGACTCAAGAA 1440

QY 1441 AAACAGATGCCAAATATCTTCTGAAAACAGCAACCCAGAACAGACTTTAAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATATCTTCTGAAAACAGCAACCCAGAACAGACTTTAAAGCTGACA 1500

QY 1501 TCAGAGGAAGAATCACAAAGCTTTGAGGCGATGTAAGTATGCGCAGCAGAGCTAGAAAT 1560
Db 1501 TCAGAGGAAGAATCACAAAGCTTTGAGGCGATGTAAGTATGCGCAGCAGAGCTAGAAAT 1560
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QY 1561 TTTATGCTATCGAAGAAATGAAGACAGAGAGTACTCATGTGCGATTCCAGAAAAC 1620
| | | | |
Db 1561 TTTATGCTATCGAAGAAATGAAGACAGAGAGTACTCATGTGCGATTCCAGAAAAC 1620
QY 1621 CTGACTAATGTCGCCACTCTGTGCAATGGTGATGATGATTAATTCCTCCAGAGAAAGC 1680
| | | | |
Db 1621 CTGACTAATGTCGCCACTCTGTGCAATGGTGATGATGATTAATTCCTCCAGAGAAAGC 1680
QY 1681 AGAACCCGTAAGCCAGCAATTCCTGACACGAGAAATGAAGATATCAAGTACAGAA 1740
| | | | |
Db 1681 AGAACCCGTAAGCCAGCAATTCCTGACACGAGAAATGAAGATATCAAGTACAGAA 1740
QY 1741 CAAATGATACCTAGAACAAATTTGTGAAGAACAGACACTGGATTTACACGATGAG 1800
| | | | |
Db 1741 CAAATGATACCTAGAACAAATTTGTGAAGAACAGACACTGGATTTACACGATGAG 1800
QY 1801 ATTCTGATTCATGAGAAAAGCAGATAGAAAGTGTGAAAATAATGTAATTCGAGCTTTGT 1860
| | | | |
Db 1801 ATTCTGATTCATGAGAAAAGCAGATAGAAAGTGTGAAAATAATGTAATTCGAGCTTTGT 1860
QY 1861 CTTAGTGTGAAGAAAGCAATCTTCATGAAATATGATCGTTGGGGGAGAAAT 1920
| | | | |
Db 1861 CTTAGTGTGAAGAAAGCAATCTTCATGAAATATGATCGTTGGGGGAGAAAT 1920
QY 1921 GCCATGCTAAGACTGAGCTAGACACATGAAACATCAGAGCCGTTAAAAA 1980
| | | | |
Db 1921 GCCATGCTAAGACTGAGCTAGACACATGAAACATCAGAGCCGTTAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAA 2000
| | | | |
Db 1981 AAAAAAAAAAAAAAAAAA 2000

RESULT 14
US-09-636-215-374
; Sequence 374, Application US/09636215
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolck, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darlick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-636-215-374

Query Match 100.0%; Score 2000; DB 24; Length 2000;
Best Local Similarity 100.0%; Pred. No. 2.6e-271;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTGTTGAGGTGATTCCATGCCGCTCTTCTGTGTAAGAACCAATTTGGTCTC 60

Db 1 ATGGTGTTGAGGTGATTCCATGCCGCTCTTCTGTGTAAGAACCAATTTGGTCTC 60
61 AGAGACAAGATGGGCAAGTGTGCTCCGTGTTCCCTGCTGCGAGGGAGAGCGGCAAG 120
61 AGAGACAAGATGGGCAAGTGTGCTCCGTGTTCCCTGCTGCGAGGGAGAGCGGCAAG 120
QY 121 AGCAAGTGGGCACTTCTGAGACACGAGACGACTGCTATGAAGACACTCAGAGCAAG 180
| | | | |
Db 121 AGCAAGTGGGCACTTCTGAGACACGAGACGACTGCTATGAAGACACTCAGAGCAAG 180
QY 181 ATGGGCAAGTGTGCGCCCACTGCTTCCCTGCTGAGGGGAGGAGGCAAGCAACGTCG 240
| | | | |
Db 181 ATGGGCAAGTGTGCGCCCACTGCTTCCCTGCTGAGGGGAGGAGGCAAGCAACGTCG 240
QY 241 GGGGCTTCTGAGACACGAGACGACTGCTATGAAGACACTCAGGAACAAGATGGCAAG 300
| | | | |
Db 241 GGGGCTTCTGAGACACGAGACGACTGCTATGAAGACACTCAGGAACAAGATGGCAAG 300
QY 301 TGGTGTGCACTGCTTCCCTGCTGAGGGGAGGCAAGCAAGGAGGCGCTTGG 360
| | | | |
Db 301 TGGTGTGCACTGCTTCCCTGCTGAGGGGAGGCAAGCAAGGAGGCGCTTGG 360
QY 361 GGAGACTAGATGACAGTGTGCTTCAATGAGCCAGGTACAGCTCCGAGAGATCTG 420
| | | | |
Db 361 GGAGACTAGATGACAGTGTGCTTCAATGAGCCAGGTACAGCTCCGAGAGATCTG 420
QY 421 GACAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCAAGAAAGATCTCATGCTATG 480
| | | | |
Db 421 GACAGCTCCACAGAGCTGCTGTGGGGTAAAGTCCCAAGAAAGATCTCATGCTATG 480
QY 481 CTCAGGACACAGCTGAGCAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
| | | | |
Db 481 CTCAGGACACAGCTGAGCAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
QY 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGAGAGAGATGCAACTTAAT 600
| | | | |
Db 541 TCTGCCAATGGGAATTCAGAAAGTAAACTCTGCTGAGAGAGATGCAACTTAAT 600
QY 601 GTCTTGTGACAAACAAAAGAGAGAGAGCTGTGATTAAGCCGCTACATCCAGGAATGAA 660
| | | | |
Db 601 GTCTTGTGACAAACAAAAGAGAGAGAGCTGTGATTAAGCCGCTACATCCAGGAATGAA 660
QY 661 TGTGGCTTAATGTTGTGGAACATGACAGTCCAAATATTCACATGATGTAAT 720
| | | | |
Db 661 TGTGGCTTAATGTTGTGGAACATGACAGTCCAAATATTCACATGATGTAAT 720
QY 721 ACCACTCTGACAGCTATCTATTAATGAAGATTAATTAATGAGCCAAACACTGCTTA 780
| | | | |
Db 721 ACCACTCTGACAGCTATCTATTAATGAAGATTAATTAATGAGCCAAACACTGCTTA 780
QY 781 TATGTTGCTGATATGCAATCAAAAAAAGCATGAGCTTCAACACACTGTTACTGGTGA 840
| | | | |
Db 781 TATGTTGCTGATATGCAATCAAAAAAAGCATGAGCTTCAACACACTGTTACTGGTGA 840
QY 841 CATGACCAAAAAAGCAAGCTGGAATTTTAATCAAAAAAGCAATTAATTAATGA 900
| | | | |
Db 841 CATGACCAAAAAAGCAAGCTGGAATTTTAATCAAAAAAGCAATTAATTAATGA 900
QY 901 CTGATATGATTAAGAGAGAGCTGCTCATACTGCTATGTTGTTGATCAGCAATATA 960
| | | | |
Db 901 CTGATATGATTAAGAGAGAGCTGCTCATACTGCTATGTTGTTGATCAGCAATATA 960
QY 961 GTGAGCTTCTACTGAGCAAAATATGATGATGATGATGATGATGATGATGATGATGAT 1020
| | | | |
Db 961 GTGAGCTTCTACTGAGCAAAATATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1021 GCCAGAGTATGCTGTTCTGCTCATCATCATCATCATCATCATCATCATCATCATCAT 1080
| | | | |
Db 1021 GCCAGAGTATGCTGTTCTGCTCATCATCATCATCATCATCATCATCATCATCATCAT 1080
QY 1081 AAGAGAAACAGATGCTAAATCTCTTCTGAAGACCAATCCAAAGCAAGCAAGCAAG 1140
| | | | |

```

Db 1081 AAGAGAAAAAGATGCTAAAAATCTTTGAAAAACGCAATTCAGAACAGACTTAAG 1140
QY 1141 CTGACATCAGAGAGAGATCACAAGAGTTCAAGAGCAGTGAATAATAGCCAGAGAAA 1200
Db 1141 CTGACATCAGAGAGAGAGTCCAAAGGTTCAAAGCAGTGAATAATAGCCAGAGAAA 1200
QY 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGGTATAGAGAGTTGAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAACAGAAATTAATTAAGATGGTATAGAGAGTTGAAGAAATGAAG 1260
QY 1261 AAGATATAAGTATATATGCGGATTAAGAAACCTGACTATATGCTGACAGTGGC 1320
Db 1261 AAGATATAAGTATATATGCGGATTAAGAAACCTGACTATATGCTGACAGTGGC 1320
QY 1321 AATGTGATATATGATTAATTCCTCAAGAGAGAGAGACCTGAAATACAGCAATTT 1380
Db 1321 AATGTGATATATGATTAATTCCTCAAGAGAGAGAGACCTGAAATACAGCAATTT 1380
QY 1381 CTGACACAAGAGAGAGATATCAGAGAAATTTGCGAATTAATTTCTGACTACAGAA 1440
Db 1381 CTGACACAAGAGAGATATCAGAGAAATTTGCGAATTAATTTCTGACTACAGAA 1440
QY 1441 AAGAGATGCGCAAAATCTCTTGAAGAACAGCAACCCAGAGCAAGCTTAAGCTGCA 1500
Db 1441 AAGAGATGCGCAAAATCTCTTGAAGAACAGCAACCCAGAGCAAGCTTAAGCTGCA 1500
QY 1501 TCAGAGAGAGAGATCACAAGAGCTTGAGGAGAGTGAATAATGCGCAGAGAGCTGA 1560
Db 1501 TCAGAGAGAGAGATCACAAGAGCTTGAGGAGAGTGAATAATGCGCAGAGAGCTGA 1560
QY 1561 TTTTGTGCTATCGAAGAAATGAGAGACGAGAGTACTATGTCGATTCGCCAGAAAC 1620
Db 1561 TTTTGTGCTATCGAAGAAATGAGAGACGAGAGTACTATGTCGATTCGCCAGAAAC 1620
QY 1621 CTGACTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
Db 1621 CTGACTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
QY 1681 AGAAGACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
Db 1681 AGAAGACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
QY 1741 CAAATATGATCTCAGAAAGCAATTTTGTGAAGAACAGAACTGGAATATTTACAGATGAG 1800
Db 1741 CAAATATGATCTCAGAAAGCAATTTTGTGAAGAACAGAACTGGAATATTTACAGATGAG 1800
QY 1801 ATTTGATTTCTGAAGAAAGAGATGAAAGTGGTTGAAATAATTTCTGAGCTTTCT 1860
Db 1801 ATTTGATTTCTGAAGAAAGAGATGAAAGTGGTTGAAATAATTTCTGAGCTTTCT 1860
QY 1861 CTGAGTTGTAAGAAAGAGAGATCTTGCATGAAATATAGCTTGCAGGAGAGAAAT 1920
Db 1861 CTGAGTTGTAAGAAAGAGAGATCTTGCATGAAATATAGCTTGCAGGAGAGAAAT 1920
QY 1921 GCCATGCTAAGAGCTGAGAGCTAGACAAATGAACATCAGAGCCAGCTAAAAA 1980
Db 1921 GCCATGCTAAGAGCTGAGAGCTAGACAAATGAACATCAGAGCCAGCTAAAAA 1980
QY 1981 AAAAAAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAAAAAA 2000

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RESULT 15

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US-09-651-236-374
; Sequence 374, Application US/09651236
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.

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```

; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42718C18
; CURRENT APPLICATION NUMBER: US/09/651,236
; NUMBER OF SEQ. ID NOS: 865
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 374
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-651-236-374

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Query Match 100.0%; Score 2000; DB 25; Length 2000;
Best Local Similarity 100.0%; Pred. No. 2,6e-271;
Matches 2000; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGTGTTAGTGTGTTGATTCATGCGGCTGCTCTCTGTAAGAGCAATTTGGTCTC 60
Db 1 ATGTGTGTTAGTGTGTTGATTCATGCGGCTGCTCTCTCTGTAAGAGCAATTTGGTCTC 60
QY 61 AGGAGCAAGATGAGGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 61 AGGAGCAAGATGAGGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
QY 121 AGCAAGTGGGCACTTGTGAGACACAGACAGACTGCTGTATGAAGACACTGAGACAG 180
Db 121 AGCAAGTGGGCACTTGTGAGACACAGACAGACTGCTGTATGAAGACACTGAGACAG 180
QY 181 ATGGGCAAGTGTGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 181 ATGGGCAAGTGTGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 241 GGCCCTTCTGAGAGCCAGAGACTGCTGTAAGAACTCAGAGAACAGATGGGCAAG 300
Db 241 GGCCCTTCTGAGAGCCAGAGACTGCTGTAAGAACTCAGAGAACAGATGGGCAAG 300
QY 301 TGTGTGCTGCACTGCTTCCCTGCTGCAAGGGGAGCGCAAGAGTGGCGCTTGG 360
Db 301 TGTGTGCTGCACTGCTTCCCTGCTGCAAGGGGAGCGCAAGAGTGGCGCTTGG 360
QY 361 GGAGACTAGATGACAGTCTTATGATGAGGCCAGGTACCAAGTGGGAGAGATCTG 420
Db 361 GGAGACTAGATGACAGTCTTATGATGAGGCCAGGTACCAAGTGGGAGAGATCTG 420
QY 421 GACAAGCTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 421 GACAAGCTCCACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
QY 481 CTCAGGAGACTGACGTGAACAGAGAGCAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 481 CTCAGGAGACTGACGTGAACAGAGAGCAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 TCTGCAATGGGAATTCAGAAATAGTAAATCTCTGCTGCAACAGATGCAACTTAAT 600
Db 541 TCTGCAATGGGAATTCAGAAATAGTAAATCTCTGCTGCAACAGATGCAACTTAAT 600
QY 601 GTCTTTCAGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 601 GTCTTTCAGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 TGTGCTTAATGTTGTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 720

```

Db 661 TGGGCTTAATGTGCTGGAACATGGCAGCTGATCCAAATATTCACAGATGATGAAAT 720
Qy 721 ACCACCTCTCAGCTAGCTATCTATATGAAGATAATTAATGGCCAAAGCAGCTCTTA 780
Db 721 ACCACCTCTCAGCTAGCTATCTATATGAAGATAATTAATGGCCAAAGCAGCTCTTA 780
Qy 781 TATGGCTGATATGAAATCAAAAAACAAGCAGCTGACACCACTGTTACTGGTGA 840
Db 781 TATGGCTGATATGAAATCAAAAAACAAGCAGCTGACACCACTGTTACTGGTGA 840
Qy 841 CATGAGCAAAAAACAGCACTGTAATTTTATCAAAAAAAGCGAATTTAAATGA 900
Db 841 CATGAGCAAAAAACAGCACTGTAATTTTATCAAAAAAAGCGAATTTAAATGA 900
Qy 901 CTGAGTATGATGGAAGCACTGCTCATCTGATCTGATGTTGGTGAACAGCTATA 960
Db 901 CTGAGTATGATGGAAGCACTGCTCATCTGATCTGATGTTGGTGAACAGCTATA 960
Qy 961 GTGAGCCTCTAAGCAAAATATGATGATCTTCACAGATCTATCTGGACAGAG 1020
Db 961 GTGAGCCTCTAAGCAAAATATGATGATCTTCACAGATCTATCTGGACAGAG 1020
Qy 1021 GCCAGAGATATCTGTTCTAGTCATCATCTGATTTGGCAGTTACTTTCTGACTAC 1080
Db 1021 GCCAGAGATATCTGTTCTAGTCATCATCTGATTTGGCAGTTACTTTCTGACTAC 1080
Qy 1081 AAGAAAAACAGATGCTAAAAATCTCTTGAAACAGCAATCCAGACAGACTTAAAG 1140
Db 1081 AAGAAAAACAGATGCTAAAAATCTCTTGAAACAGCAATCCAGACAGACTTAAAG 1140
Qy 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAGGCGATGAATAGCCAGCAGAGAA 1200
Db 1141 CTGACATCAGAGAGAGTCAAAAGGTTCAAGGCGATGAATAGCCAGCAGAGAA 1200
Qy 1201 ATGTCTCAAGAAACAGAAATTAATAGATGGTATGATAGAGAGTTGAAAGAAATGAAG 1260
Db 1201 ATGTCTCAAGAAACAGAAATTAATAGATGGTATGATAGAGAGTTGAAAGAAATGAAG 1260
Qy 1261 AAGCATGAAAGTATATGATGGGATTAAGAAACCTGACTAATGTTGCTGCTGCGC 1320
Db 1261 AAGCATGAAAGTATATGATGGGATTAAGAAACCTGACTAATGTTGCTGCTGCGC 1320
Qy 1321 AATGGTAAATGATTAATTCCTCAAGAGAGCAGAAACCTGAAATACGCAATTT 1380
Db 1321 AATGGTAAATGATTAATTCCTCAAGAGAGCAGAAACCTGAAATACGCAATTT 1380
Qy 1381 CCTGACAAAGAAAGTAAAGATATCAGAAATTTGCAATTTAGTTCTGACTCAAGAA 1440
Db 1381 CCTGACAAAGAAAGTAAAGATATCAGAAATTTGCAATTTAGTTCTGACTCAAGAA 1440
Qy 1441 AAACAGATGCCAAATACTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Db 1441 AAACAGATGCCAAATACTCTTCTGAAAAACAGCAACCCAGAACAGACTTAAAGCTGACA 1500
Qy 1501 TCAGAGGAAGATCAAAAGGCTTGAGGCGAGTGAATGGCCAGCCAGAGCTAGAAAT 1560
Db 1501 TCAGAGGAAGATCAAAAGGCTTGAGGCGAGTGAATGGCCAGCCAGAGCTAGAAAT 1560
Qy 1561 TTTATGGCTATGAGAAATGAAGAAAGCAGCAAGTACTCATGTCGATTTCCAGAAAAAC 1620
Db 1561 TTTATGGCTATGAGAAATGAAGAAAGCAGCAAGTACTCATGTCGATTTCCAGAAAAAC 1620
Qy 1621 CTGACTAATGTCGCACTGCTGCAATGGTATGATGATTAATTCCTCAAGGAAGAGC 1680
Db 1621 CTGACTAATGTCGCACTGCTGCAATGGTATGATGATTAATTCCTCAAGGAAGAGC 1680
Qy 1681 AGAACAACCTGAAGAGCAATTTCTGACACTGAGAAATGAAGAGTATCACAGTGACGAA 1740
Db 1681 AGAACAACCTGAAGAGCAATTTCTGACACTGAGAAATGAAGAGTATCACAGTGACGAA 1740
Qy 1741 CAAAATGATACTCAGAAAGCAATTTTGTGAAGAACAGAACCTGGAATATTACAGATGAG 1800
Db 1741 CAAAATGATACTCAGAAAGCAATTTTGTGAAGAACAGAACCTGGAATATTACAGATGAG 1800

Db 1741 CAAAATGATACTCAGAAAGCAATTTTGTGAAGAACAGAACCTGGAATATTACAGATGAG 1800
Qy 1801 ATTCTGATTCATGAAGAAAAAGCAGATAGAAGTGGTTGAAAAAATGAATTTCTGAGCTTTCT 1860
Db 1801 ATTCTGATTCATGAAGAAAAAGCAGATAGAAGTGGTTGAAAAAATGAATTTCTGAGCTTTCT 1860
Qy 1861 CTTAGTTGTGAAGAAAGAAAGACATCTTGATGAATATGATGTTGGGGGAAGAAAT 1920
Db 1861 CTTAGTTGTGAAGAAAGAAAGACATCTTGATGAATATGATGTTGGGGGAAGAAAT 1920
Qy 1921 GCCATGCTAAGACTGAGCTAGACACAAATGAACATCAGAGCCAGCTAAAAAAGAAAAA 1980
Db 1921 GCCATGCTAAGACTGAGCTAGACACAAATGAACATCAGAGCCAGCTAAAAAAGAAAAA 1980
Qy 1981 AAAAAAAAAAAAAAAAAA 2000
Db 1981 AAAAAAAAAAAAAAAAAA 2000

Search completed: November 8, 2002, 08:45:42
Job time : 3948.08 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 8, 2002, 02:17:58 : Search time 209.406 Seconds
(without alignments) 1500.171 Million cell updates/sec

Title: US-09-924-400-302

Perfect score: 2000

Sequence: 1 atggtgtgtgtgtgtgtgtc.....aaaaaaaaaaaaaaaaaaaa 2000

Scoring table:

Gapop 10.0 , Gapext 1.0

Searched: 205966 seqs, 78536166 residues

Total number of hits satisfying chosen parameters: 411932

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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7: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	205.4	10.3	298	US-09-513-999C-3605	Sequence 3605, Ap
2	170.6	8.5	1041	US-10-131-813A-21	Sequence 21, Appl
3	170.6	8.5	1041	US-10-131-819A-21	Sequence 21, Appl
4	170.6	8.5	1041	US-10-131-823A-21	Sequence 21, Appl
5	170.6	8.5	1041	US-10-131-824A-21	Sequence 21, Appl
6	170.6	8.5	1041	US-10-131-826A-21	Sequence 21, Appl
7	170.6	8.5	1041	US-10-131-829A-21	Sequence 21, Appl
8	170.6	8.5	1041	US-10-125-926A-21	Sequence 21, Appl
9	170.6	8.5	1041	US-10-127-829A-21	Sequence 21, Appl
10	170.6	8.5	1041	US-10-127-831A-21	Sequence 21, Appl
11	170.6	8.5	1041	US-10-127-835A-21	Sequence 21, Appl
12	170.6	8.5	1041	US-10-127-837A-21	Sequence 21, Appl
13	170.6	8.5	1041	US-10-127-842A-21	Sequence 21, Appl
14	170.6	8.5	1041	US-10-127-850A-21	Sequence 21, Appl
15	170.6	8.5	1041	US-10-127-901A-21	Sequence 21, Appl
16	170.6	8.5	1041	US-10-128-689A-21	Sequence 21, Appl
17	170.6	8.5	1041	US-10-131-830A-21	Sequence 21, Appl
18	170.6	8.5	1041	US-10-131-833A-21	Sequence 21, Appl
19	170.6	8.5	1041	US-10-131-837A-21	Sequence 21, Appl
20	170.6	8.5	1041	US-10-125-930A-21	Sequence 21, Appl
21	170.6	8.5	1041	US-10-127-825A-21	Sequence 21, Appl
22	170.6	8.5	1041	US-10-127-838A-21	Sequence 21, Appl
23	170.6	8.5	1041	US-10-127-843A-21	Sequence 21, Appl
24	170.6	8.5	1041	US-10-127-849A-21	Sequence 21, Appl
25	170.6	8.5	1041	US-10-128-684A-21	Sequence 21, Appl
26	170.6	8.5	1041	US-10-128-685A-21	Sequence 21, Appl

27	170.6	8.5	1041	US-10-128-686A-21	Sequence 21, Appl
28	170.6	8.5	1041	US-10-128-690A-21	Sequence 21, Appl
29	170.6	8.5	1041	US-10-128-693A-21	Sequence 21, Appl
30	170.6	8.5	1041	US-10-131-821A-21	Sequence 21, Appl
31	170.6	8.5	1041	US-10-131-826A-21	Sequence 21, Appl
32	170.6	8.5	1041	US-10-137-872A-21	Sequence 21, Appl
33	170.6	8.5	1041	US-10-137-873A-21	Sequence 21, Appl
34	170.6	8.5	1041	US-10-125-921A-21	Sequence 21, Appl
35	170.6	8.5	1041	US-10-125-928A-21	Sequence 21, Appl
36	170.6	8.5	1041	US-10-127-821A-21	Sequence 21, Appl
37	170.6	8.5	1041	US-10-127-822A-21	Sequence 21, Appl
38	170.6	8.5	1041	US-10-127-824A-21	Sequence 21, Appl
39	170.6	8.5	1041	US-10-127-827A-21	Sequence 21, Appl
40	170.6	8.5	1041	US-10-127-830A-21	Sequence 21, Appl
41	170.6	8.5	1041	US-10-127-832A-21	Sequence 21, Appl
42	170.6	8.5	1041	US-10-127-834A-21	Sequence 21, Appl
43	170.6	8.5	1041	US-10-127-836A-21	Sequence 21, Appl
44	170.6	8.5	1041	US-10-127-839A-21	Sequence 21, Appl
45	170.6	8.5	1041	US-10-127-840A-21	Sequence 21, Appl

ALIGNMENTS

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RESULT 1
US-09-513-999C-3605
; Sequence 3605, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Mline Edwards, J.B.
; APPLICANT: Duclet, A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59, US2, REG.
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 3605
; LENGTH: 298
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 77..298
US-09-513-999C-3605

Query Match          10.3% Score 205.4; DB 5; Length 298;
Best local similarity 97.2%; Pred. No. 2,9e+40;
Matches 209; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 809 AGCATGCGCTCACACACACTGTACTGTGTACATGACCAAAACAGCAAGTCGTGAAT 868
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 81 ATCATGCGCTCACACACACTGTACTGTGTACATGACCAAAACAGCAAGTCGTGAAT 140

QY 869 TTTTAAACAGAAAAGCAATTTAAATGACATGATATATGAAAGCATGCTCTCA 928
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 141 TTTTAAACAGAAAAGCAATTTAAATGACATGATATATGAAAGCATGCTCTCA 200

QY 929 TACTTCCTGATGTGTGTGATGACAGATATATGACCCCTTCTACTTGACCAAAATATG 988
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 201 TACTTCCTGATGTGTGTGATGACAGATATATGACCCCTTCTACTTGACCAAAATATG 260

QY 989 ATGTATCTTCAAGATCTATCTGACAGAGCGCC 1023
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 261 ATGTATCTTCAAGATCTATCTGACAGAGCGCC 295

RESULT 2
US-10-131-813A-21
; Sequence 21, Application US/10131813A
; GENERAL INFORMATION:
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? APPLICANT: Baker, Kevin P.
? APPLICANT: Beresini, Laureen
? APPLICANT: DeForge, Laura
? APPLICANT: Desnoyers, Luc
? APPLICANT: Filvaroff, Ellen
? APPLICANT: Gao, Wei-Qiang
? APPLICANT: Geriltsen, Mary E.
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Gurney, Austin L.
? APPLICANT: Sherwood, Steven
? APPLICANT: Smith, Victoria
? APPLICANT: Stewart, Timothy A.
? APPLICANT: Tumas, Daniel
? APPLICANT: Watanabe, Colin K
? APPLICANT: Wood, William
? APPLICANT: Zhang, Zemin
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
? FILE REFERENCE: P3330R1C139
? CURRENT APPLICATION NUMBER: US/10/131,813A
? PRIOR FILING DATE: 2002-04-24
? PRIOR APPLICATION NUMBER: 60/049911
? PRIOR FILING DATE: 1997-06-18
? PRIOR APPLICATION NUMBER: 60/056974
? PRIOR FILING DATE: 1997-08-26
? PRIOR APPLICATION NUMBER: 60/059113
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059115
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059117
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059122
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059184
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059263
? PRIOR FILING DATE: 1997-09-18
? PRIOR APPLICATION NUMBER: 60/059352
? PRIOR FILING DATE: 1997-09-19
? PRIOR APPLICATION NUMBER: 60/059588
? PRIOR FILING DATE: 1997-09-19
? Remaining Prior Application data removed - See File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 550
? SEQ ID NO 21
? LENGTH: 1041
? TYPE: DNA
? ORGANISM: Homo Sapien
? US-10-131-813A-21

Query Match      8.5%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 9e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

? 378 TGCCTTCATGAGCCCGACGATCCGTCGAGAGAAATCTGGACAAAGCTCCACAGAGC 437
? 300 TGGCTTCGCAATTTCCCAATACCCCAATTAACCGTATCATCTGAAGAGATCCACAGAGC 359
? 438 TGCCTGGTGGGTAAAGTCCCGACAGAAAGTATCATGCTCATGCTCAAGGACACTGACGT 497
? 360 TGTCTTACATGTAATCTAGAGAAAGTAA--GTACCTTCTGCTCACGTAATATGACGC 416
? 498 GAACAAGAGAGACAGAAAGAGAGACTGCTGTACATCTGCGCTTGCATGGAATTC 557
? 417 CATAAGAGAGACAGAGAAAGAGACCGCCCTACATTTGGCTGCTGCACCTGGCCAC 476
? 558 AGAAGTAGTAAACTCCTGCTGACAGAGATGTCACATTAAATGCTCTGACAAACAAA 617
? 477 GGAAGATGTACATCTCTGCTGTCCAGAAAGATGTGAGCTTAACCTGCGACCGTGA 536
? 618 GAGAGAGCTGTGATAAGCGCTACATGCCAGGAAGATGTGCGTATGTGCT 677
? 537 CAGGACACCTGTGATCAAGCGTGTACAACTGAGGACGAGGCTTGTCACCTCTGCT 596
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? 678 GGAACATGGCAGTATCCAAATATTCAGATGAGTAAGAAATACCACTGTGACACTAGC 737
? 597 GCAAAATGGCCCCAATCCAAATATATAGGATTTCTTTGGAAGAGACTGCTGCACTAGC 656
? 738 TATCTATATGAGATAAATTAATGAGCAAGCACTGCTTATATATGCTGATATGCA 797
? 657 TGTATATATGAGATATCATCATGATAGAAAACTTCTTACATGATGTAACAAATATGTA 716
? 798 ATCAAAAACAG 810
? 717 AGAATGCGACAG 729

RESULT 3
US-10-131-819A-21
? Sequence 21, Application US/10131819A
? GENERAL INFORMATION:
? APPLICANT: Baker, Kevin P.
? APPLICANT: Beresini, Laureen
? APPLICANT: DeForge, Laura
? APPLICANT: Desnoyers, Luc
? APPLICANT: Filvaroff, Ellen
? APPLICANT: Gao, Wei-Qiang
? APPLICANT: Geriltsen, Mary E.
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Gurney, Austin L.
? APPLICANT: Sherwood, Steven
? APPLICANT: Smith, Victoria
? APPLICANT: Stewart, Timothy A.
? APPLICANT: Tumas, Daniel
? APPLICANT: Watanabe, Colin K
? APPLICANT: Wood, William
? APPLICANT: Zhang, Zemin
? TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
? FILE REFERENCE: P3330R1C134
? CURRENT APPLICATION NUMBER: US/10/131,819A
? PRIOR FILING DATE: 2002-04-24
? PRIOR APPLICATION NUMBER: 60/049911
? PRIOR FILING DATE: 1997-06-18
? PRIOR APPLICATION NUMBER: 60/056974
? PRIOR FILING DATE: 1997-08-26
? PRIOR APPLICATION NUMBER: 60/059113
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059115
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059117
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059122
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059184
? PRIOR FILING DATE: 1997-09-17
? PRIOR APPLICATION NUMBER: 60/059263
? PRIOR FILING DATE: 1997-09-18
? PRIOR APPLICATION NUMBER: 60/059352
? PRIOR FILING DATE: 1997-09-19
? PRIOR APPLICATION NUMBER: 60/059588
? PRIOR FILING DATE: 1997-09-19
? Remaining Prior Application data removed - See File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 550
? SEQ ID NO 21
? LENGTH: 1041
? TYPE: DNA
? ORGANISM: Homo Sapien
? US-10-131-819A-21

Query Match      8.5%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 9e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

? 378 TGCCTTCATGAGCCCGACGATCCGTCGAGAGAAATCTGGACAAAGCTCCACAGAGC 437
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Db 300 TGGCTTCGCAATTTCCCAATACCCCAATTAACCGTATCATCTGAGAGAGATCCACAGAGC 359
Qy 438 TGCCCTGGGGGTAAAGTCCCAAGAGATCTCATGCTCATGCTCAGGAGACAGTACGT 497
Db 360 TGTCTTACATGGTAAATCTAGAGAAACTGAA--GTACCTTCTGCTCAGCTATATTAGAGCG 416
Qy 498 GAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 557
Db 417 CAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 476
Qy 558 AGAGTAGTAAACTCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 617
Db 477 GGAATAGTACATCTCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 536
Qy 618 GAGGACACCTCTGATTAAGGCGCTGATGCTGATGCTGATGCTGATGCTGATGCTGCT 677
Db 537 CAGGACACCTCTGATTAAGGCGCTGATGCTGATGCTGATGCTGATGCTGATGCTGCT 596
Qy 678 GGAACATGCGACACTGATCCAAATATTCAGATGATGAGAAATACCACTGCTGCTACAGC 737
Db 597 GCAAAATGGCGCCCAATCCAAATATTTACGATTTCTTTGAGAGAGAGCTGCTGCTACAGC 656
Qy 738 TATCTATATGAAGATTAATTAATGCGCAAGACACTGCTTATATGCTGATGATGCA 797
Db 657 TGTGTATATGAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 716
Qy 798 ATCAAAAAACAG 810
Db 717 AGAATGACAGCAG 729
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RESULT 4

US-10-131-823A-21

Sequence 21, Application US/10131823A

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3330R1C143

CURRENT APPLICATION NUMBER: US/10/131, 823A

PRIOR FILING DATE: 2002-04-24

PRIOR APPLICATION NUMBER: 60/049911

PRIOR FILING DATE: 1997-06-18

PRIOR APPLICATION NUMBER: 60/056974

PRIOR FILING DATE: 1997-08-26

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059115

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059117

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059122

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059184

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059263

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; PRIOR FILING DATE: 1997-09-18
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; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 21
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-823A-21
Query Match      8.5%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 9e-37;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;
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Qy 378 TGCCCTTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 437
Db 300 TGGCTTCGCAATTTCCCAATACCCCAATTAACCGTATCATCTGAGAGAGATCCACAGAGC 359
Qy 438 TGCCCTGGGGGTAAAGTCCCAAGAGATCTCATGCTCATGCTCAGGAGACAGTACGT 497
Db 360 TGTCTTACATGGTAAATCTAGAGAAACTGAA--GTACCTTCTGCTCAGCTATATTAGAGCG 416
Qy 498 GAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 557
Db 417 CAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 476
Qy 558 AGAGTAGTAAACTCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 617
Db 477 GGAATAGTACATCTCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 536
Qy 618 GAGGACACCTCTGATTAAGGCGCTGATGCTGATGCTGATGCTGATGCTGATGCTGCT 677
Db 537 CAGGACACCTCTGATTAAGGCGCTGATGCTGATGCTGATGCTGATGCTGATGCTGCT 596
Qy 678 GGAACATGCGACACTGATCCAAATATTCAGATGATGAGAAATACCACTGCTGCTACAGC 737
Db 597 GCAAAATGGCGCCCAATCCAAATATTTACGATTTCTTTGAGAGAGAGCTGCTGCTACAGC 656
Qy 738 TATCTATATGAAGATTAATTAATGCGCAAGACACTGCTTATATGCTGATGATGCA 797
Db 657 TGTGTATATGAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 716
Qy 798 ATCAAAAAACAG 810
Db 717 AGAATGACAGCAG 729
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RESULT 5

US-10-131-824A-21

Sequence 21, Application US/10131824A

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3330R1C143

CURRENT APPLICATION NUMBER: US/10/131, 824A

PRIOR FILING DATE: 2002-04-24

PRIOR APPLICATION NUMBER: 60/049911

PRIOR FILING DATE: 1997-06-18

PRIOR APPLICATION NUMBER: 60/056974

PRIOR FILING DATE: 1997-08-26

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059115

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059117

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059122

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059184

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059263

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; FILE REFERENCE: P3330R1C126
; CURRENT APPLICATION NUMBER: US/10/131, 826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 350
; SEQ ID NO 21
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-826A-21

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Query Match      8.5%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 9e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

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QY 378 TGCCTTATGAGCCCGACGATCCGCTCGTGAGAAATCTGGACAAGCTCCACAGAGC 437
DB 300 TGGCTTCGATTTCCCAATACCCCATTAACCGTATCATCTGAAGAGATCCACAGAGC 359
QY 438 TGCCTGTGGGGTAAATGCCCAAGAAAGATTCATGTCATGCTGAGGACACTGAGT 497
DB 360 TGTCTTACATGATATAGAGAAACTGAA---GTACCTTCTGCTCAGTATTTATGACGC 416
QY 498 GAACAGAGAGACAGCAAGCAAAAGAGACTGCTTACATCTGACCTTCCCAATGGGAATTC 557
DB 417 CAATTAAGAGAGAGAGAAAGAGACCGCCCTCATTTGCGCTGCGACCTGGCAACC 476
QY 558 AGAAGTAGTAAACTCTGCTGGACAGACATGTCACACTTAATGTCCTTGACAACAAAAA 617
DB 477 GGAATGTGTACATCTCTGCTGTCTCCAGAAAGATGTGAGCTTAACCTTGCACCGTGAAG 536
QY 618 GAGGACAGCTCTGATTAAGCCCGTACCAATGCGAGAGATGAATGTGCGTTAATGTTGCT 677
DB 537 CAGGACACCTCTGATCAAGGCTGTACACTGAGGACGAGAGCTTGTCAACTCTTCTGCT 596
QY 678 GGAACATGAGCATGATCAATATTCAGATGATGAAATPACCACTGTGCACTACGC 737
DB 597 GCAAAATGGCGCAATCAATATTTACGATTTCTTTGGAAGAGCTGCTGTGCACTACGC 656
QY 738 TATCTATAATGAAGATAATTAATGGCAAGACACTGCTTATATGCTGTGATATGCA 797
DB 657 TGTGTATAATGAAGATATCATCATGATATGAAAAAATTCTTTCACATGTGTAATATTTGA 716
QY 798 ATCAAAAAACAAG 810
DB 717 AGAATGCAAGCAAG 729

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RESULT 6
US-10-131-826A-21
; Sequence 21, Application US/10131826A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.

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; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Oiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131, 826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 350
; SEQ ID NO 21
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-826A-21

```

```

Query Match      8.5%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 9e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

```

```

QY 378 TGCCTTATGAGCCCGACGATCCGCTCGTGAGAAATCTGGACAAGCTCCACAGAGC 437
DB 300 TGGCTTCGATTTCCCAATACCCCATTAACCGTATCATCTGAAGAGATCCACAGAGC 359
QY 438 TGCCTGTGGGGTAAATGCCCAAGAAAGATTCATGTCATGCTGAGGACACTGAGT 497
DB 360 TGTCTTACATGATATAGAGAAACTGAA---GTACCTTCTGCTCAGTATTTATGACGC 416
QY 498 GAACAGAGAGACAGCAAGCAAAAGAGACTGCTTACATCTGACCTTCCCAATGGGAATTC 557
DB 417 CAATTAAGAGAGAGAGAAAGAGACCGCCCTATCATTTGCGCTGTGCACTGGCCAGC 476
QY 558 AGAAGTAGTAAACTCTGCTGTGACAGACATGTCACACTTAATGTCCTTGACAACAAAAA 617
DB 477 GGAATGTGTACATCTCTGCTGTCTCCAGAAAGATGTGAGCTTAACCTTGCACCGTGAAG 536
QY 618 GAGGACAGCTCTGATTAAGCCCGTACCAATGCGAGAGATGAATGTGCGTTAATGTTGCT 677
DB 537 CAGGACACCTCTGATCAAGGCTGTACAAAGAGGACGAGAGCTTGTGCAACTCTTCTGCT 596

```


Qy	678	GAAGACGGGACATGCATCAATATATCCAGATGATGAAATACCACTGTGACATACG	727
Db	597	GCAAAATGGGCGCATTCCAATATATACGAGATTTCTTTTGGAAAGGACCTGTGACATACG	656
Qy	738	TATCTATATGAAGATTAATTAATGGCCAAAGCAGCTCTTTATATGGTGTGATATGA	797
Db	657	TGTGTATATGAAGATTCATTCATGATGAAAACTCTTTCACATGGTACAAATATTTGA	716
Qy	798	ATCAAAAACCAAG	810
Db	717	AGATGACGACAG	729

RESULT 7
US-10-131-829A-21
; Sequence 21, Application US/10131829A
; GENERAL INFORMATION.

```

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Mei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C138
CURRENT APPLICATION NUMBER: US/10/131,829A
CURRENT FILING DATE: 2002-04-27
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059352
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
Remainder of SEQ ID Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 21
LENGTH: 1041
TYPE: DNA
ORGANISM: Homo Sapien
OS-10-131-829A-21

```

	Query Match	8.5%	Score 170.6;	DB 6;	Length 1041;	
	Best Local Similarity	63.7%;	Pred. No. 9e-32;			
	Matches 276; Conservative	0;	Mismatches 154;	Indels 3;	Gaps 1.	
OY	378 TGCCTTATGAGACCCACGTACACGTCCTCGTGGAAGAATGTCGGACAAGCCTCACAGACC	437				

Db	300	TGCGTTGCAATTTCCCAATTAACCCCAATTAACGGTATCATCTGAAGAGATCCACAGAG	359
QY	438	TGCGTTGGGGTAAGTGTCCCGAAGAAAGATCTCATGTCATGCTCAGGAGACGTGACGT	497
Db	360	TGCTTACATAGGTATATCTAGAGAACTGAA--GTACCTTCCTGCTCAGTATATTAGCGC	416
QY	498	GAACACAGAAGACACAGCAAAAGAGAGACTGCTTTCATCTTGCCCTCTGCCAATGGAAATTC	557
Db	417	CAATTAAGAGAGACAGGAAGAAAGAGACCGCCCTACATTTTGGCTGTGGCCACTGGCCAAAC	476
QY	558	AGAACTGTATAAAGTCTGCTGGACAGACATGTCAACTTAATGTCTTACACAACAAAA	617
Db	477	GGAATGTGTACATCTCCTGGTGTCCAAAGAAATGTGAGACTTAACCTCGCCACGGTAGA	536
QY	618	GAGACAGCTCTGATTAAGGCCGCTACACATGCCAGGAATGCAATGTGCGTTAATGTTGCT	677
Db	537	CAGGACACCTCTGATTCAGAGCTGTACAACTGAGGACAGAGAGCTGTGGCAACTTGTGCT	596
QY	678	GGAACATAGCAGCTGATCCAAATATTCAGAGTAGTAGTAAAGAAATACCACTTGGACATACG	737
Db	597	GCAAAATGGGCGCAATCAATATATTAGGATTTCTTTGGAAGAGACTGCTGTGCATACGC	656
QY	738	TATCTATATGAAGATTAATTAATAGGCCCAAGCAGCTCTTATATGGTGTCTATATCGA	797
Db	657	TGTGTATATGAAGATACATTCATGATAGAAAAACTTCTTTCACATGTGTACAAATATTGA	716
QY	798	ATCAAAAACAAAG	810
Db	717	AGAAATGCAAGAG	729

RESULT 8
US-10-125-926A-21
; Sequence 21, Application US/10125926A

```

GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerilsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Guney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OR INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P93330R1C80
CURRENT APPLICATION NUMBER: US/10/125, 926A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059122
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18

```

```
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 350
; SEQ ID NO 21
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-125-926a-21

Query Match      8.5%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 9e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 378 TGCCTTATGAGCCCGGACGTCCTGGAGAAATCTGGACAAAGCTCCACAGC 437
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 300 TGGCTTGCATTTCCCAATACCCCATTAACCGTATCATCTGAAGAGATCCAGAGC 359
QY 438 TGCCTGGGGTAAAGTCCCAAGAAAGATCTCATGCTCAGGACACTGACGT 497
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 360 TGTCTTACATGTAATCTAGAAACTGAA--GTACTTCTGCTCAGTAATTATGAGC 416
QY 498 GAACAGAGGACAAAGAAAGAGACTGCTTACATCTGGCTTCCCAATGGAAATTC 557
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 417 CAATTAAGAGAGACGAAAGAAAGACCGCCCTACATTTGGCTGTGCCACTGGCCAAC 476
QY 558 AGAAGTAAACTCTGCTGGACACATGTCACACTTAATCTCTTGACAAACAAA 617
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 477 GGAATGTATCATCTCTGGTGTCCAGAAAGATGAGACTTAACCTTACCGCTGAGA 536
QY 618 GAGGACAGCTCTGTAATAAGCCGTCACATGCAAGAGATGATGCTGTTAATGTTGCT 677
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 537 CAGGACACCTCTGTATCAAGGCTGTACAACTGAGGACAGAGGCTTGTCACTCTTCTGCT 596
QY 678 GGAACATGCACTGATCCAAATATTTCCAGATGATGAAATACCACTGTGACACTGAC 737
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 597 GCAAAATGGCGCCCAATCAATATTTACGATTTCTTGAAGAGACTGCTGTGCACTACGC 656
QY 738 TATCTATAATGAAGATTAATTAATGAGCCAAAGCACTGCTTATATGTGCTGATATGCA 797
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 657 TGTGTATAATGAAGATCATCATCATGATAGAAAACCTTCTTACATGTGTAATATTTGA 716
QY 798 ATCAAAAACAAAG 810
    ||||| |||||
Db 717 AGAATGCAGCAAG 729

RESULT 9
US-10-127-829a-21
; Sequence 21, Application US/10127829a
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Laureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Geo, Mei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C85
```

```
; CURRENT APPLICATION NUMBER: US/10/127,829a
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 350
; SEQ ID NO 21
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-829a-21

Query Match      8.5%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 9e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 378 TGCCTTATGAGCCCGGACGTCCTGGAGAAATCTGGACAAAGCTCCACAGC 437
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 300 TGGCTTGCATTTCCCAATACCCCATTAACCGTATCATCTGAAGAGATCCAGAGC 359
QY 438 TGCCTGGGGTAAAGTCCCAAGAAAGATCTCATGCTCAGGACACTGACGT 497
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 360 TGTCTTACATGTAATCTAGAAACTGAA--GTACTTCTGCTCAGTAATTATGAGC 416
QY 498 GAACAGAGGACAAAGAAAGAGACTGCTTACATCTGGCTTCCCAATGGAAATTC 557
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 417 CAATTAAGAGAGACGAAAGAAAGACCGCCCTACATTTGGCTGTGCCACTGGCCAAC 476
QY 558 AGAAGTAAACTCTGCTGGACACATGTCACACTTAATCTCTTGACAAACAAA 617
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 477 GGAATGTATCATCTCTGGTGTCCAGAAAGATGAGACTTAACCTTACCGCTGAGA 536
QY 618 GAGGACAGCTCTGTAATAAGCCGTCACATGCAAGAGATGATGCTGTTAATGTTGCT 677
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 537 CAGGACACCTCTGTATCAAGGCTGTACAACTGAGGACAGAGGCTTGTCACTCTTCTGCT 596
QY 678 GGAACATGCACTGATCCAAATATTTCCAGATGATGAAATACCACTGTGACACTGAC 737
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 597 GCAAAATGGCGCCCAATCAATATTTACGATTTCTTGAAGAGACTGCTGTGCACTACGC 656
QY 738 TATCTATAATGAAGATTAATTAATGAGCCAAAGCACTGCTTATATGTGCTGATATGCA 797
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 657 TGTGTATAATGAAGATCATCATCATGATAGAAAACCTTCTTACATGTGTAATATTTGA 716
QY 798 ATCAAAAACAAAG 810
    ||||| |||||
Db 717 AGAATGCAGCAAG 729

RESULT 10
US-10-127-831a-21
; Sequence 21, Application US/10127831a
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Laureen
```

```

; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C107
; CURRENT APPLICATION NUMBER: US/10/127,831A
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 21
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-127-831A-21

Query Match      8.5%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 9e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 378 TGCCTTCATGAGCCAGGAGTCCGCTGAGAGATCTGGACAAGCTCCAGAGC 437
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 300 TGGCTTCGATTTCCCAATACCCATTAACCGTATCATGTAAGAGATCCAGAGC 359
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 438 TGGCTTCGAGTAAAGTCCCGAGAAAGATCTCATGCTGCTAGGAGACCTACGT 497
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 360 TGTCTTACATGGTAATCTAGAGAACTGAA--GTACCTTGTCTACGTATTATGACG 416
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 498 GACACAGAGAGCAAGCAAAAGAGAGCTGCTACATCTGGCCTCGCAATGGAAATTC 557
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 417 CAATAGAGAGAGAGAGAAAGAGAGCCGCCCTACATTTGGCCTGCGCAGCCGCAAGC 476
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 558 AGAAGTAGTAACCTCTCTCTGAGACAGACGATCTCACTTATGCTCTTGACAACAAA 617
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 477 GGAATAGTACATCTCTGCTGTCAGAAAGATGTGAGCTTAACCTCTGCGACCGTGAAG 536
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 618 GAGGACAGCTGTATAAGGCGGTACAAATGCCAGAAATGATGTGCGTTATGTGCT 677
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 537 CAGGACACCTCTGTAAAGGCTGTACACTGAGGCGAGGCGTTGGCAATCTTCTGCT 596
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 678 GGAACATGGCACTGATCAAAATATTCCAGATGATGAAATATACCACTCTGCACTACGC 737
```

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DB 597 GCAAAATGGCGCCAAATCAAAATATTTACGATTTCTTTGGAAGAGACTGCTGCACTACGC 656
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 738 TATCTATATGAAGATAAATTAATGCGCAAGACACTGCTTATATGTCGATATCA 797
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 657 TGTGTATTAATGAAGATACATGATAGAAAACCTTCTTCACTGATGCAAAATATTGA 716
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 798 ATCAAAAACAG 810
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 717 AGAATGACAGCAAG 729
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
US-10-127-835A-21
; Sequence 21, Application US/10127835A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C102
; CURRENT APPLICATION NUMBER: US/10/127,835A
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 21
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-127-835A-21

Query Match      8.5%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 9e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 378 TGCCTTCATGAGCCAGGAGTCCGCTGAGAGATCTGGACAAGCTCCAGAGC 437
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 300 TGGCTTCGATTTCCCAATACCCATTAACCGTATCATGTAAGAGATCCAGAGC 359
```

```
QY 438 TGCCTGGTGGGTAAGTCCCGAGAAAGATCTCANTGCTCATGCTCAGGGACACTGACGT 497
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 360 TGTCTTACATGTGTAATCTAGAGAAACTGAA---GTACCTTCTGCTCAGATATATGACGC 416
QY 498 GAACAAGAAGACAGCAAAAAGAGACTGCTCTACATCTGGCCCTTCCCATGGGAATTC 557
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 417 CAATTAAGAGACAGAGAAAGAGACCGCCATGATTTGGCCCTGCTGACCTGGCCAAAC 476
QY 558 AGAAGTGTAAACTCTGCTGGACAGACATGTCAACTTAATGTGCTTGACACAACAAAA 617
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 477 GGAATATGTATCATCTCTGCTGCTCAGAAAGATGTGACCTTACCTTGGCAGCCTGAA 536
QY 618 GAGCAGCTCTGTATTAAGCCCGTACATGCCAGGAAGATGATGCTGATATGTTGCT 677
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 537 CAGGACACCTCTGTATCAAGGCTGTACAACTGAGGACGAGGCTGTGCAACTCTTCTGCT 596
QY 678 GGAACATGGACATGTCACCAATATTCAGATGAGTATGGAATATCCACTGTGCACTACGC 737
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 597 GCAAAATGGCGCCCAATCAATATATACGATTTCTTTGGAAGACCTCTGCACTACGC 656
QY 738 TATCTATATGAAGATTAATTAATGCGCAAGACACTGCTCTTATATGTGCTGATATCGA 797
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 657 TGTCTATATGAAGATATCATCATCATGATAGAAAACTTCTTTCACATGTGACAAATATTTGA 716
QY 798 ATCAAAAAACAG 810
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 717 AGAATGCAGCAAG 729
```

```
RESULT 12
US-10-127-837A-21
; Sequence 21, Application US/10127837A
; GENERAL INFORMATION:
```

```
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C96
; CURRENT APPLICATION NUMBER: US/10/127, 837A
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
```

```
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 21
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-127-837A-21
```

```
Query Match 8.5%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 9e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;
```

```
QY 378 TGCCTTATGAGAGCCAGTACACGCTCCGTCGAGATCTGCAAGCAAGCTCCACAGAGC 437
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 300 TGGCTTGACATTTCCCAATRACCCATTAAACGCTATCATCTGAAAGAGATCCACAGAGC 359
QY 438 TGCCTGGTGGGTAAGTCCCGAGAAAGATCTCATGCTCATGCTCAGGGACACTGACGT 497
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 360 TGTCTTACATGTGTAATCTAGAGAAACTGAA---GTACCTTCTGCTCAGATATATGACGC 416
QY 498 GAACAAGAAGACAGCAAAAAGAGACTGCTCTACATCTGGCCCTTCCCATGGGAATTC 557
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 417 CAATTAAGAGACAGAGAAAGAGACCGCCATGATTTGGCCCTGCTGACCTGGCCAAAC 476
QY 558 AGAAGTGTAAACTCTGCTGGACAGACATGTCAACTTAATGTGCTTGACACAACAAAA 617
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 477 GGAATATGTATCATCTCTGCTGCTCAGAAAGATGTGACCTTACCTTGGCAGCCTGAA 536
QY 618 GAGCAGCTCTGTATTAAGCCCGTACATGCCAGGAAGATGATGCTGATATGTTGCT 677
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 537 CAGGACACCTCTGTATCAAGGCTGTACAACTGAGGACGAGGCTGTGCAACTCTTCTGCT 596
QY 678 GGAACATGGACATGTCACCAATATTCAGATGAGTATGGAATATCCACTGTGCACTACGC 737
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 597 GCAAAATGGCGCCCAATCAATATATACGATTTCTTTGGAAGACCTCTGCACTACGC 656
QY 738 TATCTATATGAAGATTAATTAATGCGCAAGACACTGCTCTTATATGTGCTGATATCGA 797
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 657 TGTCTATATGAAGATATCATCATCATGATAGAAAACTTCTTTCACATGTGACAAATATTTGA 716
QY 798 ATCAAAAAACAG 810
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 717 AGAATGCAGCAAG 729
```

```
RESULT 13
US-10-127-842A-21
; Sequence 21, Application US/10127842A
; GENERAL INFORMATION:
```

```
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C100
; CURRENT APPLICATION NUMBER: US/10/127, 842A
```

```

: CURRENT FILING DATE: 2002-10-15
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059184
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059352
: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/059588
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 21
: LENGTH: 1041
: TYPE: DNA
: ORGANISM: Homo Sapien
US-10-127-842A-21

```

```

Query Match      8.5%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 9e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

```

```

QY 378 TCCCTTCATGAGGCCAGGTACCGTCCGTGAGAGATCTCGAGACACTCCACAGAGC 437
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 300 TGGCTTCGCATTTCCTCCCAATACCCATTAAACCGTATCTGAAGAGATCCACAGAGC 359
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 438 TGCCTGGTGGTAAAGTCCCAAGAGATCTCATCGTCATGCTCAGGAGACATGAGCT 497
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 360 TGTCTTACATGCTATCTAGAGAACTGAA---GTACCTTCTGCTCAGCTATATATGACGC 416
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 498 GAACAAGAGAGCAAGCAAAAGAGAGACTGCTCTACATCTGGCCCTGCCAATGGAAATTC 557
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
-DB 417 CAATAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 476
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 558 AGAAGTAGTAAATCTCTGCTGAGACAGATGTCACTTAATGTCCTTGACACAAAAA 617
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 477 GGAATGTGACATCTCTGCTGTCGTCAGAGATGTGAGCTTAACCTCTGCGACCGTGAAGA 536
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 618 GAGGACAGCTGTGATTAAGGCGGTACCAATGCGCAGAGATGTAATGCGTTATGTTGCT 677
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 537 CAGGACAGCTCTGTATCAAGGCTGTACACTGAGGAGGCGTTGTGCAACTCTTCTGCT 596
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 678 GGAACATGGCACTGTATCCAAATATTCAGATAGTATGGAATATACCACTCTGCACACGC 737
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 597 GCAAAATGGCGCAATCCAAATATTTAGCGATTCTTTGGAAGAGACGCTCTGCACACGAGC 656
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 738 TATCTATATGAAGATTAATTAATGCGCAAGACACTGCTTATATATGCTGTGATATGCA 797
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 657 TGTGATATATGAAGATACATCATGATAGAAAAAATCTTCTTCAACATGATGAATATTTGA 716
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 798 ATCAAAAAACAAG 810
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 717 AGAATGACGACAAG 729
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

RESULT 14
US-10-127-850A-21
: Sequence 21, Application US/10127850A
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: Deforge, Laura

```

```

: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C110
: CURRENT FILING DATE: 2002-10-15
: PRIOR APPLICATION NUMBER: 60/049911
: PRIOR FILING DATE: 1997-06-18
: PRIOR APPLICATION NUMBER: 60/056974
: PRIOR FILING DATE: 1997-08-26
: PRIOR APPLICATION NUMBER: 60/059113
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059115
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059117
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059122
: PRIOR FILING DATE: 1997-09-17
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059352
: PRIOR FILING DATE: 1997-09-19
: PRIOR APPLICATION NUMBER: 60/059588
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 21
: LENGTH: 1041
: TYPE: DNA
: ORGANISM: Homo Sapien
US-10-127-850A-21

```

```

Query Match      8.5%; Score 170.6; DB 6; Length 1041;
Best Local Similarity 63.7%; Pred. No. 9e-32;
Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

```

```

QY 378 TCCCTTCATGAGGCCAGGTACCGTCCGTGAGAGATCTCGAGACACTCCACAGAGC 437
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 300 TGGCTTCGCATTTCCTCCCAATACCCATTAAACCGTATCTGAAGAGATCCACAGAGC 359
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 438 TGCCTGGTGGTAAAGTCCCAAGAGATCTCATCGTCATGCTCAGGAGACATGAGCT 497
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 360 TGTCTTACATGCTATCTAGAGAACTGAA---GTACCTTCTGCTCAGCTATATATGACGC 416
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 498 GAACAAGAGAGCAAGCAAAAGAGAGACTGCTCTACATCTGGCCCTGCCAATGGAAATTC 557
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 417 CAATAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 476
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 558 AGAAGTAGTAAATCTCTGCTGAGACAGATGTCACTTAATGTCCTTGACACAAAAA 617
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 477 GGAATGTGACATCTCTGCTGTCGTCAGAGATGTGAGCTTAACCTCTGCGACCGTGAAGA 536
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 618 GAGGACAGCTGTGATTAAGGCGGTACCAATGCGCAGAGATGTAATGCGTTATGTTGCT 677
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 537 CAGGACAGCTCTGTATCAAGGCTGTACACTGAGGAGGCGTTGTGCAACTCTTCTGCT 596
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 678 GGAACATGGCACTGTATCCAAATATTCAGATAGTATGGAATATACCACTCTGCACACGC 737
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

Db 597 GCAAAATGGCCCAATCCAAATATTACGATTTCTTGGAGGACAGCTGCTGCACTACGC 656
 QY 738 TATCTATATGAGATTAATTAATGCGCAAGACAGCTGCTTTATATGCTGATATGCA 797
 Db 657 TGTATATATGAGATTAATTAATGCGCAAGACAGCTGCTTTATATGCTGATATGCA 716
 QY 798 ATCAAAAAACAG 810
 Db 717 AGAATGCAGCAG 729

RESULT 15
 US-10-127-901A-21
 ; Sequence 21, Application US/10127901A
 ; GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
 APPLICANT: Beresini, Maureen
 APPLICANT: Deforge, Laura
 APPLICANT: Desnoyers, Luc
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerlitsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Sherwood, Steven
 APPLICANT: Smith, Victoria
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P330R1C86
 CURRENT APPLICATION NUMBER: US/10/127, 901A
 CURRENT FILING DATE: 2002-10-15
 PRIOR APPLICATION NUMBER: 60/049911
 PRIOR FILING DATE: 1997-06-18
 PRIOR APPLICATION NUMBER: 60/056974
 PRIOR FILING DATE: 1997-08-26
 PRIOR APPLICATION NUMBER: 60/059113
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059115
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059117
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059122
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059184
 PRIOR FILING DATE: 1997-09-17
 PRIOR APPLICATION NUMBER: 60/059263
 PRIOR FILING DATE: 1997-09-18
 PRIOR APPLICATION NUMBER: 60/059352
 PRIOR FILING DATE: 1997-09-19
 PRIOR APPLICATION NUMBER: 60/059588
 PRIOR FILING DATE: 1997-09-19
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 550
 SEQ ID NO 21
 LENGTH: 1041
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-10-127-901A-21

Query Match 8.58; Score 170.6; DB 6; Length 1041;
 Best Local Similarity 63.7%; Pred. No. 9e-32;
 Matches 276; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 378 TGCCTTATGAGCCGATGACGATGCGTGGAGAGATGAGCAAGCTCCACAGAGC 437
 Db 300 TGGCTTGCATTTCCCAATACCCCAATTAACGATATCATCTGAAGAGATCCACAGAGC 359

QY 438 TGCCTGTTGGGTAAGATCCCAAGAGATCTCATGCTCATGCTCAGGACACTGACGT 497
 Db 360 TGTCTTACATGTAATCTAGAGAACTGAA---GTACTCTCTGCTCAGATATATGACGC 416
 QY 498 GAGCAGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 557
 Db 417 CAAATAGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 476
 QY 558 AGAAGTAGTAAGAACTCCTGCTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 617
 Db 477 GGAATATGATATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 536
 QY 618 GAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 677
 Db 537 CAGGACACCTCTGATCAAGGCTGTACAACTGAGCAGAGAGGCTGTGCAACTCTTCTGCT 596
 QY 678 GGAACATGCGCACTATCCCAATATTCCAGATGATATGAAATACCACTGCGCTACGC 737
 Db 597 GCAAAATGGCCCAATCCAAATATTACGATTTCTTGGAGGACCTGCTGCACTACGC 656
 QY 738 TATCTATATGAGATTAATTAATGCGCAAGACAGCAGCTGCTTTATATGCTGATATGCA 797
 Db 657 TGTATATATGAGATTAATTAATGCGCAAGACAGCTGCTTTATATGCTGATATGCA 716
 QY 798 ATCAAAAAACAG 810
 Db 717 AGAATGCAGCAG 729

Search completed: November 8, 2002, 08:52:58
 Job time : 214.406 secs